CHAPTER I

INTRODUCTION

The total load of human misery and suffering from communicable disease in the world today is incalculable and presents a formidable challenge to public health authorities, epidemiologists, parapsychologists, entomologists, bio mathematicians and any other experts whose skills may have some bearing on the problems involved.

Modern medicine can have now do much to alleviate or cure many infectious diseases once they have been contracted. The elimination of poverty and hunger and the provision of adequate social and public health measures such as quarantine, isolation of infections cases, provision of clean water supplied, proper disposal of sewage, vaccination and inoculation etc have provided the main contributions to the fight against disease.

Let us use some models to study the large – scale population phenomena of immediate relevance to any social and public health measures that might be advocated or undertaken. In particular, let us know more about the transmission and spread of infectious disease, about trying to predict the course of an epidemic, and about the recognition of threshold densities of population which must be surpassed before a flare-up is likely.

In the context of epidemic disease, let us require to know more about how the endemic level is related factors, which can be controlled by public health intervention. Let us need to develop models that will assist the decision – making process by helping to evaluate the consequences of choosing one of the alternative strategies available . Therefore mathematical models of the dynamics of a communicable disease can have a direct bearing on the choice of an immunization of control or eradication techniques.

Suppose let us consider an individual who has been exposed to interface (i.e) who has received infectious material by some means such as direct physical contact with an infectious person, breathing in infectious organisms or eating contaminated food, An actively infectious individual and the appearance of symptoms is normally called the incubation period and the period from the observation of symptoms is one case to the observation of symptoms in a second case directly infected from the first is the second interval. When symptoms in occur either during or immediately after the end of the infectious period the incubation period is exactly equal to the sum of the latent period and the part of the infectious period during which the patient is still a danger to other.

It is supposed for the group of individuals at any instant there is a certain chance of contact between any two individuals sufficient for the transmission of disease of one is an infective and one a susceptible. When there are several

infectious in a group, a given susceptible will remain true of disease only if happens to escape adequate contact with any of them with continuous infection models a suitable analogous assumption is that the chance of one new case in a very short interval of time is jointly proportional to the length of the interval, the number of susceptibles and the number of infectives. Such ideas regarding lead to mathematical equations describing the whole process.

Carriers are the individuals who although apparently healthy themselves, harbour infections which can be transmitted to others.

Methodological Aspects

Let us consider briefly a number of methodological aspects concentrating more on the general philosophical Implications.

Let us first look at the simplest type of epidemic model in which infection spreads by contact between the members of a community but in which there is no removal from circulation by death, recovery or isolation. Ultimately all susceptibles therefore become infected. When dealing with large number of both susceptibles and infectives, let as should expect the effect of statistical fluctuations on large – scale phenomena to be much reduced. In such circumstances if not unreasonable to use a first approximation a deterministic model in which, let us assume that for given number of susceptibles and infectives and for a given attack rate, certain definite numbers of new infectives

will occur in any specified time. In stochastic models probability distribution of the numbers of susceptibles or infectives occurring at any instant replace the point values of deterministic treatments. In general, the form of behavious predicted by a stochastic model is likely to be very similar by the corresponding deterministic version when the number of susceptibles or infectives are both sufficiently large but in other situations there may be important differences.

Moreover, there is a good reason to suppose that the assumptions of homogeneous mixing is approximately valid for epidemic in only comparatively small as individual household where statistical fluctuations may be large.

A major part of the work on stochastic epidemic models has been on the general stochastic epidemic a name given by Bailey we give a simpler proof for the threshold theorem due to Williams and whittle using Rajarshi technique.

A major complication of many diseases is the existence of so-called carriers (i.e) individuals who although apparently healthy themselves are already infected and are capable of transmitting the infection to others. Philippe Picard gives some applications of martingale to epidemics. All the results are in connection with stopping times T and include the expression of the joint generating function Laplace transform of X_T, $\int x_u\ y_u\, du$ and $\int y_u\, du$ and relation between moments of these three variables. The relation between Downston's model and the general epidemic is discussed and finally a generalization of one of Daniel's classical results is given.

In a real epidemic the increase of the number of infectives usually generates sanitary measures in order to isolate infectives and prevent contacts with susceptibles. Therefore Picard [32] in the general epidemic model considered the parameters are as functions of infectives which gives a better approximation. In these cases the martingale approach proves very valuable and gives explicit results quite easily.

The considerable literature now existing on stochastic models is mainly concerned with closed population epidemics, such as the general stochastic epidemic and thus is of limited direct use in modeling most AIDS epidemics where immigrations into and deaths from the class of susceptibles can be an important feature.

AIDS needs no introductions. AIDS (Acquired Immune Deficiency Syndrome) which breaks down the body's natural immune system is transmitted primarily by sexual contact or by bodily fluids exchanged between drug addicts, who share needles. AIDS epidemic an explosive spread of disease was first diagonised almost 12 years ago. To understand AIDS one must know a little about the functioning of the human body and its resistance power, or capacity of the body or immune system.

The AIDS is caused be a germ HIV which enters the body's while blood cells and makes it impossible for the body to defined itself against illness. The HIV doesn't kill the people directly. But it weakens the body's resistance power

and finally destroys the body's immune system. The major signs of AIDS are loss of more than 10% of normal body weight and servere diarrhea for more than a month and continuous fever for more that one month. However standard stochastic epidemic theory is often still not applicable because the infection process is modeled slightly differently. The usual xy term (where x and y are the number of susceptibles and infectives respectively) for the rate of new infections is replaced by $\beta xy/x + y$. The justification for the new term is that AIDS spread by individuals changing sexual partners. So if we removed individuals are no longer available as sexual partners, then the probability that a new partner of a given susceptibles infected is $y/x + y$.

John A. Jacquez Philiponeille compare the threshold results for the deterministic and stochastic versions of the homogeneous SI model with recruitment death due to the disease a background death rate and transmission rate. A fundamental concept that has come out the deterministic mathematical theory of epidemics is that of the basic reproduction number.

Let us examine the deterministic and stochastic formulation for the SI, SIS, SIR and SIRS models for homogeneous populations. Finally Frankball Philpo'neill consider a model for the spread of an epidemic in a closed, homogeneously mixing population in which new infection occur at rate $\beta xy/x + y$ where x and y are the number of susceptibles and infectious individuals respectively and β is the infection rate. This differs with the

standards general epidemic in which new infectious occur at rate βxy. Both the deterministic and stochastic versions of the modified epidemic are analysed.

Simple and General Epidemics

Let us first look at the simplest type of epidemic model in which infection spreads by contact between the members of a community but in which there is no removal from circulation by death, recovery or isolation. When dealing with large number of both susceptibles and infectives, let us expect the effect of statistical fluctuations on large scale to be reduced.

In general the form of behaviour predicted by a stochastic model is likely to be very similar to that entailed by the corresponding deterministic version when the number of susceptibles and infectives are both sufficiently large but in other situations there may be important differences. Let us use the concept of the epidemic curve defined by the rate at which new cases are recognized.

Deterministic model

In the simplest deterministic formulation, let us suppose that let us have homogeneously mixing group of individuals of total size n + 1 and that the epidemic is started off at time t = 0 by just one individual becoming infections, the remaining n individuals all being susceptible, but as yet un infected.

In general at time t, let us write x and y are continuous for the numbers of susceptibles and infectives so that $x + y = n + 1$. The actual numbers of new infections in the time interval Δt is $\beta xy\Delta t$, where β is the infection rate.

$$\Delta t = -\beta xy\Delta t$$

$$dx / dt = -\beta xy = \beta x (n - x + 1)$$

If $\tau = \beta t$, then

$$dx / d\tau = - x (n - x + 1)$$

With $x = n$, $\tau = 0$

$$x = n (n + 1) / n + e^{(n+1)\tau}$$

the number of infective at time τ is

$$y = n - x + 1 = (n + 1) e^{(n+1)\tau} / n + e^{(n+1)\tau}$$

$$= n + 1 / 1 + n e^{-(n+1)\tau}$$

Epidemic curve is $dy / d\tau = - dx / d\tau$

$$W = - dx / d\tau = xy = n (n+ 1)^2 e^{-(n+1)\tau} / (n + e^{-(n+1)\tau})^2$$

The epidemic curve at attains its maximum

When $\tau = \log n / (n + 1)$

When $x = y = ½ (n + 1)$, $w = ¼ (n + 1)^2$

Stochastic model

Let us now consider the simplest probability version of the deterministic model. As before, let us assume a homogeneously mixing group of (n + 1) individuals and suppose for simplicity that the epidemic starts at time t = 0 with one infective and n susceptibles. Let us take the random variables X(t) and Y(t) to represent the number of susceptible and infectives respectively at time t

Where X(t) + Y(t) = n + 1 .

Then the chance of a contact between any two specified individuals in an interval Δt is $\beta\Delta t + o(\Delta t)$. When β is the contact rate and β = constant.

It follows that the chance of one new infection in the whole group in Δt is $\beta xy\Delta t$ to order Δt . When the transition occurs, x decreases by one unit and Y increases by one unit. Suppose if we take the possibility of removal then the chance of one removal in Δt can be taken as $\gamma Y\Delta t$ where γ is the removal rate. The variable Y decreases by one unit after the transition, but X remains unchanged.

Let $p_n(\tau)$ be the probability that there are still r susceptible remaining uninfected at time τ. The probability of r susceptibles remaining at time $\tau + \Delta\tau$ can be expressed as

$$\Pr(\tau + \Delta\tau) = (r+1)(n-r)\,\tau\, p_{r+1}(\tau) + \{1 - r(n-r+1)\Delta\tau\}\, pr(\tau) \quad (1.1)$$

$$\left.\begin{aligned} dp_n / d\tau &= (r+1)(n-r)\, p_{r+1} - r(n-r+1)\, pr, \\ 0 &\le r \le n-1 \end{aligned}\right\} \quad (1.2)$$

$$dp_n / d\tau = -n\, p_n$$

with initial condition $p_n(0) = 1$ (1.3)

Laplace transform and its inverse with respect to time given by

$$\varphi^*(s) = \int_0^\infty e^{-s\tau}\varphi(\tau)d\tau \ , R(s) > 0 \quad (1.4)$$

$$\varphi(\tau) = 1/2\,\pi i \int_{c-i\infty}^{c+i\infty} e^{-s\tau}\varphi^*(s)ds \quad (1.5)$$

When C is positive and greater than the real parts of all the singularities of $\varphi^*(s)$.

Applying the equation (1.1) to (1.5)

$$\left.\begin{aligned} p_r^* &= (r+1)(n-r)/s + r(n-r+1)p_{n+1}^*, 0 \le r \le n-1 \\ p_n^* &= 1/s + n \end{aligned}\right\} \quad (1.6)$$

The Epidemic Curve

Let k cases out of n occur in the interval (τ, $\tau + \delta\tau$). Let $f(\tau)$ be the frequency function for the time of occurrence of new cases then

$$F(\tau)d\tau = E\left(\frac{k}{n}\right) = 1/n[\mu_1'(\tau + \delta\tau) - \mu'(\tau)]$$

$$= -1/n\, d\mu_1'/d\tau d\tau \qquad (1.7)$$

When $\mu_1'(\tau)$ is the average number of susceptibles at time τ.

$$W = d\mu_1'/d\tau \qquad (1.8)$$

The normalized epidemic curve is

$$W = w/n = -1/n\, d\mu_1'/d\tau \qquad (1.9)$$

The probability of one new infective in Δτ is r (n – r + a) Δτ.

$$\therefore\ p_r^* = (r+1)(n-r+a-1\ )p_{r+1}^*, 0 \le r \le n-1$$

$$p_n^* = 1/s + na$$

The Laplace transform of W is

$$W^* = \int_0^\infty e^{-s\tau} w d\tau$$

$$= -1/n \int_0^\infty e^{-s\tau} d\mu_1'/d\tau d\tau \qquad \text{(using 1.9)}$$

$$= 1 - s/n \int_0^\infty e^{-s\tau} \mu_1' d\tau$$

$\mu_1' = \pi$ when τ = 0 and is exponentially small as $\tau \to \infty$

$$\mu_1'(\tau) = \sum_{r=0}^{n} rpr(\tau)$$

$$W^* = 1 - s/n \sum_{r=1}^{n} rpr^*$$

$$= 1 - s/n \sum_{r=a}^{n+a-1} 1/r \prod j = n - r + an\{1 + s/j(n - j + a)\}^{-1}$$

(1.10)

General Epidemic

Let us now turn to a more realistic and generally applicable representation of an epidemic basic parameters in the model are therefore the infection rate and the removal rate. This type of process is called general epidemic.

Deterministic model

Suppose let us have a community of total size n, comprising time t, x susceptibles y infectives in circulation and z individuals who are isolated, d dead or recovered and immune.

$$x + y + z = n \qquad (1.11)$$

β – infection rate and γ – removal rate. In time Δt, there are βxyΔt new infectors and γyΔt removals.

The basic differential equations are

$$\left.\begin{aligned} dx / dt &= -\beta xy \\ dy / dt &= \beta xy - \gamma y \\ dz / dt &= \gamma y \end{aligned}\right\} \qquad (1.12)$$

ρ = γ / β , is the relative removal rate. Eliminating y from the first and third of these equations. By division gives after integration.

$$x = x_0 e^{-z/p}$$

$$dz/dt = \gamma(n - x - z) \quad \text{using x + y + z = n} \tag{1.13}$$

$$dz/dt = \gamma(n - z - x_0 e^{-z/p}) \tag{1.14}$$

$$dz/dt = \gamma(n - x_0 + (x_0/\rho - 1)z - x_0 z^2/2\rho^2) \tag{1.15}$$

Assume that, z / ρ is small and ($x_0/\rho - 1$) is small

$$\therefore z = \rho^2/x_0(x_0/\rho - 1 + \alpha \tan h\,(\tfrac{1}{2}\alpha\gamma t - \varphi))$$

Where $$\alpha = \{(x_0/\rho - 1)^2 + 2x_0 y_0/\rho^2\}^{1/2} \tag{1.16}$$

And $\varphi = \tan h^{-1} 1/\alpha\ (x_0/\rho - 1)$

∴ The epidemic curve is therefore

$$dz/dt = \gamma\alpha^2\rho^2/2x_0 \sec h^2\ (1/2\ \alpha\gamma t - \varphi) \tag{1.17}$$

It is in general a symmetrical bell shaped curve.

The total number of removals after the allows of a very long, ideally infinite period of time.

Let t $\rightarrow \infty$, $z_\infty = \rho^2/x_0\ (x_0/\rho - 1 + \alpha)$

$$z_\infty \sim 2\rho\ (1 - \ \rho/x_0)$$

(1.18)

Let us now turn to a more mathematically precise treatment of the foregoing analysis based on the discussion of Kendall[22].

Suppose , let us assume that the infection rate is a function β (z) of z then (1.13) is changed by

$$x = x_0 \exp[-1/\gamma\ \int_0^z \beta(w)dw] \tag{1.19}$$

Which together (1.14) gives

$$dz/dt\ = \gamma[n - z - x_0 \exp[-1/\gamma\ \int_0^z \beta(w)dw]] \tag{1.20}$$

$$\beta(z) = 2\beta/(1 - z/\rho) + (1 - z/\rho)^{-1} \tag{1.21}$$

Then β (0) = β and β (z) < β when 0 < z < ρ.

Consider $n - z - x_0 e^{-z/p}$=0 (1.22)

Let the unique negative and positive roots of (1.22) be $-\eta_1$ and η_2 respectively.

$$\therefore t = 1/\gamma \int_0^z dw/n - w - x_0\ e^{-zw/p} \quad 0 \leq z < \eta_2$$

(1.23)

Which when taken in conjunction with (1.14) gives a formal solution for that epidemic curve dz / dt in terms of a pair of parametric equations. The whole of the curve for $0 \leq t < \infty$ is involved since the integral in (1.23) diverges when z $\rightarrow \eta_2$ and therefore $z_\infty = \eta_2$.

Stochastic model

Let X(t) and Y(t) be representing the number of susceptibles and infectives respectively. The chance of one new infection in Δt as $\beta XY\Delta t$ where β is the infection rate. The chance of one removal in Δt is $\gamma Y\Delta t$ where γ is the removal rate. The variable Y decreases by one unit after the transition but X remains unchanged.

At t = 0, there are n susceptibles and a infectives. Let $p_{rs}(t)$ be the probability that at time t there are r susceptibles still uninfected and s infectives in circulation. The chance of one new infection in time Δt is $\beta rs\Delta t$ and the chance of one removal $\gamma s\Delta t$.

$\gamma / \beta = \rho$, the ratio of removal rate of infection rate which is called as relative removal rate.

$$\left.\begin{aligned} dp_{rs}/d\tau &= (r+1)(s-1)p_{r+1,s-1} \\ &\quad -s(r+\rho)p_{rs} + \rho(s+1)p_{r,s+1} \end{aligned}\right\} \quad \text{and} \qquad (1.24)$$

$$dp_{na}/d\tau = -a(n+\rho)p_{na}$$

$$0 \le r+s \le n+a, 0 \le r \le n, 0 \le s \le n+a$$

$$p_{na}(0) = 1 \qquad \Big\} \qquad (1.25)$$

If let us introduce the probability generating function given by

$$P(z,w,\tau) = \sum p_{rs}(\tau) z^r w^s$$

Which satisfies

$$\partial\rho/\partial t = (w^2 - zw)\,\partial^2 p/\partial z \partial\, w + \rho(1-w)\,\partial\rho/\partial w$$

(1.26)

With initial condition p(z,w,0) = $z^n w^a$.

Total Size of Epidemic

$$P_w = \lim_{t\to\infty} p_{n-w}, 0$$

$$= \lim_{\lambda\to 0} \lambda q_{n-w}, 0 \qquad (1.27)$$

$$= \lim_{\lambda\to 0} \rho q_{n-w}, 1.$$

Put r = n – w and s = 0 in the following equation

$$(r+1)(s-1)q_{r+1,s-1} - \{s(r+\rho)+\lambda\}q_{rs} + \rho(s+1)q_{r,s+1}$$

and $-\{a(n+\rho)+\lambda\}q_{na} + 1 = 0$ (1.28)

$$p_w = \rho f_{n-w}, 1 \qquad ,0 \le w \le n$$

Where $f_{rs} = \lim_{\lambda \to 0} q_{rs}$. (1.29)

$1 \leq r + s \leq n + a$, $0 \leq r \leq n$, $1 \leq s \leq n + a$

Putting $\lambda = 0$,

$$(r+1)(s-1)f_{r+1,s-1} - \{s(r+\rho) + \lambda\}f_{rs} + \rho(s+1)f_{r,s+1} = 0$$

$$-\{a(n+\rho) + \lambda\}f_{na} + 1 = 0 \quad (1.30)$$

$$\therefore f_{rs} = n!\,(r+\rho-1)\rho^{n+a-r-s}/sr!\,n! + \rho g_{rs} \quad (1.31)$$

$$\left.\begin{array}{c} g_{r+1,s-1} - g_{rs} + (r\rho\rho)^{-1} g_{r,s+1} = 0 \\ g_{na} = 1 \end{array}\right\} \quad (1.32)$$

$$g_{rs} = \sum_{i=s-1}^{n+a-r-1} (r+\rho)^{s-i-1} g_{r+1,i}$$

$$g_{r1} = (r+\rho)^{-1} g_{r2}$$

$$g_{na} = 1 \quad (1.33)$$

Carrier Models

Carrier are individual who although apparently healthy themselves, harbor infection which can be transmitted to others. Diseases such the poliomyelitis, tubes, culosis, or typhoid are typical examples some carrier may be infectives for a very long long time, others becomes clean of infections are quickly in either case the carriers are effectively removal from circulation, but

as they are not ill and exhibit no removal symptoms of diseases, they are no themselves usually recognized as actual cases. On the other hands, carriers may be suspected because of the existence of on other wise inexplicable occurrence of scatted cases. This may lead to a deliberate search for carrier and some or all of them may be identified through the use of special test.

Basic Deterministic Model

In this model, let us concentrate attention only two types of individuals. Susceptible and carriers. It is assumed that only carrier are responsible for the actual spread of infection. When a susceptible is infected, he is supposed to exhibit symptoms sufficiently quickly to be effectively recognized and removal from circulation before he can transmit the diseases others.

The elimination of carrier proceeds at some finite rate which depends on both spontaneous recovery and public dedication. Let us suppose that at time t, we have x susceptibles and y carriers. The number of new infectives in time Δt is $\beta XY\Delta t$ where β is the infection rate, while the number of carriers removed in Δt is assumed be $\gamma Y\Delta t$ where γ is the removal rate for carriers.

The deterministic process is characterized by the equation

$$\left.\begin{aligned} dx / dt &= -\beta xy \\ dy / dt &= -\gamma y \end{aligned}\right\} \qquad (1.34)$$

with $x = n, y = b, t = 0$. If we start with n susceptibles and b carriers at time $t = 0$.

$$\therefore \quad \left.\begin{aligned} x &= n \exp\left[\frac{\beta b}{\gamma(e^{-\gamma t}-1)}\right) \\ y &= be^{-\gamma t} \end{aligned}\right\} \tag{1.35}$$

The ultimate number of unaffected susceptibles as t $\rightarrow \infty$ is $x_\infty = ne^{-\beta b/\gamma}$ and the total size W of the observed epidemic is

$$W = n(1 - e^{-\beta b/\gamma}) \tag{1.36}$$

In this model let us take the number of susceptibles and carriers at time t are represented by the random variable X(t) and U(t). The chance of one new infection occurring in time Δt is βXUΔt. When this event happens X decreases by one unit and U remains unchanged. Again, let us assume that the chance of one carrier being removal is γU Δt. In this case U is decreased by one unit but X is unchanged.

$$\rho = \gamma/\beta \text{ and } \tau = \beta t.$$

Let the probability of being r susceptibles and u carriers at time τ be $p_{ru}(\tau)$.

Let the point probability generating function p(x, y, τ) defined by

$$p(x, y, \tau) = \sum p_{ru}(\tau) x^r y^u$$

$$\partial p/\partial t = (x^{-1} - 1)xy\,\partial^2 p/\partial x\partial y + \rho(y^{-1} - 1)\,y\,\partial p/\partial y$$

(1.37)

$$= (1 - x)y\,\partial^2 p/\partial x\partial y + \rho(1 - y)\,\partial p/\partial y$$

With initial condition assuming

$$\left.\begin{aligned} p(x, y, 0) &= x^n u^b \\ p(x, y, \tau) &= X(x)Y(y)\Gamma(\tau) \end{aligned}\right\} \quad (1.38)$$

$$T_1/T = (1 - x)y\,X'Y'/XY + \rho(1 - y)\,Y'/Y = -\lambda \quad (1.39)$$

Where λ is a suitable constant

$$\left.\begin{aligned} T &= e^{-\lambda\tau} \\ (1 - x)y\,X'/X &= \rho(1 - y)/y - \lambda \end{aligned}\right\} \quad (1.40)$$

Where j is some suitable constants

$$\left.\begin{aligned} X &\propto (1 - x)j \\ Y &\propto (y - \rho/\rho + j)^{\lambda/\rho + j} \end{aligned}\right\} \quad (1.41)$$

Time Dependent Parameters

Working in τ time, let us f replace by

$$\partial p/\partial t = (1 - x)y\,\partial^2 p/\partial x\partial y + \rho(\tau)(1 - y)\,\partial p/\partial y \quad (1.42)$$

subject to the some initial condition as before.

Let us write the probability generating function

$$P(x, y, \tau) = \sum_{r=0}^{n} \sum_{u=0}^{b} P_{ru}(\tau) x^r y^u \tag{1.43}$$

$$= \sum_{j=0}^{n} \binom{n}{j} (x-1)^j f_j(y, \tau) \tag{1.44}$$

Where $f_j(y, \tau)$ are to be determined.

Substituting (1.43) in (1.41) and equating coefficients of $(x-1)^j$ gives a simple linear first order partial differential equation for $f_j(y, \tau)$.

$$\partial f_j / \partial \tau + \{(j+\rho)y - \rho\} \partial f_j / \partial y = 0 \tag{1.45}$$

$$d\tau/\rho = dy/(j+\rho)y - \rho = df_j/0 \tag{1.46}$$

Let us find two independent integrals of

One solution is f_j = constant (1.47)

and another solution is $dy/d\tau = (j+\rho)y - \rho$ (1.48)

Multiplying through (1.47) by the integrating factor

$$\theta_j(\tau) = \exp\left(-j\tau - \int_0^\tau \rho(v) dv\right) \tag{1.49}$$

Leads to the second integral

$$y\theta_j(\tau) + \int_0^\tau \rho(z)\theta_j(z)\, dz = constant \tag{1.50}$$

The general solution of (1.41) and (1.49).

The general solution of (1.44) as

$$f_j = \varphi(y\theta_j(\tau) + \int_0^\tau \rho\theta_j\, dz) \tag{1.51}$$

Where ϕ is an arbitrary function that can be determined from the initial conditions

$P(x, y, 0) = x^n y^b$ in (1.37)

$$P(x, y, 0) = x^n y^b$$

$$= \{1 + (x - 1)\}^n y^b$$

$$= \sum_{j=0}^{n} \binom{n}{j} (x - 1)^j y^b$$

$$f_j(y, 0) = y^b$$

$\tau = 0 \Rightarrow \phi(y) = f_j(y, 0) = y^b$

$$\therefore\ f_j(y, \tau) = \left(y\theta_j(\tau) + \int_0^\tau \rho(z)\theta_j\,(z)dz\right)^b \tag{1.52}$$

When $\theta_j(\tau)$ is defined in (1.48)

Immigration of Susceptible and carriers:

Suppose that new susceptibles appear at a constant rate μ_1 and that new carriers are introduced at a constant rate γ.

The deterministic equations are

$$\left.\begin{aligned} dx/dt &= -\beta xy + \mu \\ dx/dt &= -\gamma y + \delta \end{aligned}\right\} \tag{1.53}$$

With initial condition x = n , y = b , t = 0.

Setting the differential coefficients equal to zero gives

$$x_0 = \gamma u/\beta\delta \ , y_0 = \ \delta/\gamma.$$

Getting $y = \ \delta/\gamma \ + (\ b - \delta/\gamma)e^{-\gamma t}$ (1.54)

$$\Rightarrow exp[-\beta v/\gamma t - \beta/\gamma(b - \delta/\gamma)e^{-\gamma t}]$$

$$+\mu/\gamma \ exp[-\beta\delta/\gamma t - \beta/\gamma(b - \delta/\gamma)e^{-\gamma t}]$$

$$\int_1^{e^{-\gamma t}} [-\beta\delta/\gamma^2 - 1e^{-\beta/\gamma(b-\delta/\gamma)}\xi \ d\xi]$$

(1.55)

Also $\partial p/\partial t = \beta(1 - x)y\partial^2 p/\partial x\partial y \ + \alpha(1 - y)\ \partial p/\partial y$

$$+[\mu(x - 1) + \delta(y - 1)]P$$

(1.56)

When

$$\left.\begin{aligned} P(x, y, t) &= \sum P_{ru}(t)x^r y^u \\ P(x, y, 0) &= x^n u^b \end{aligned}\right\} \tag{1.57}$$

Suppose

$$P(x,y,t) = \sum_{j=0}^{\infty}(x-1)^j f_j(y,t) \tag{1.58}$$

Substituting (1.56) in (1.54) and equating coefficients of $(x-1)^j$ given.

$$\partial f_j/\partial t + \{j\beta + \gamma)y - \gamma\}\partial f_j/\partial y + \delta(1-y)f_j = \mu f_{j-1}. \tag{1.59}$$

The marginal probability generating function of the number of carriers is

$$P(1,y,t) = f_0(y,t) \tag{1.60}$$

and the relevant partial differential equation with j = 0 is

$$\partial f_0/\partial t + \gamma(y-1)\partial f_0/\partial y = \delta(y-1)f_0 \tag{1.61}$$

$$\left.\begin{array}{ll}(y-1)e^{-\gamma t} & = constant\\ f_0 e^{-\delta y/\gamma} & = constant\end{array}\right\} \tag{1.62}$$

$$f_0(y,t) = e^{\delta y/\gamma}\phi\{(y-1)e^{-\gamma t}\} \tag{1.63}$$

When ϕ is an arbitrary function to be determined from the initial condition

$$f_0(y,0) = y^b \tag{1.64}$$

Using (1.55) and (1.58)

Putting t = 0 and (y – 1) = η in (1.61), and using (1.62)

$$\phi(\eta) = (1+\eta)^b e^{-\delta(1+\eta)/\gamma} \tag{1.65}$$

$$\therefore\ f_0(y,t) = (1+(y-1)e^{-\gamma t})^b \exp(\delta/\gamma(y-1)(1-e^{-\gamma t})) \tag{1.66}$$

The average number of carriers π is

$$\pi = \delta/\gamma + (b - \delta/\gamma)e^{-\gamma t} \tag{1.67}$$

As t → ∞ (1.64) ⇒

$$f_0(y, \infty) = \exp(\delta/\gamma(y - 1)) \tag{1.68}$$

So that the carrier distribution tends to a Poisson distribution with parameter δ / γ.

CHAPTER II

A CONTRIBUTION TO THE MATHEMATICAL THEORY OF EPIDEMICS

Introduction

If one consider two population identical in respect of their densities their recovery and death rates but differing in respect of their infectivity rates it will appear that epidemic in the population with the higher infectivity rate may be great as compared with those in the population with the lower infectivity rate. If the density of the former population is in the neighbourhood of the threshold value.

The density of a particular population is normally very close to its threshold density it will be comparatively free from epidemic but if this state is upset either by a slight increase in population density or by a slight increase in the infectivity rate a large epidemic may break out.

It will appear that a similar stable of affairs holds with respect to diseases with are transmitted through an intermediate host. The product of the two population densities is the determining factor and no epidemic can occur when the product falls below a certain threshold value.

Assume that a certain number y_0 of the population have just been infected although this infection is naturally dependent on some process outside that defined by equation. Thus

$$v_{0.0} = v_0 + y_0 \tag{2.1}$$

If $\psi_\theta$denote the rate of removal he sum of recovery and death rates, then the number who are removed from each θ group at the end of the interval t is $\psi_\theta, v_{t,\theta}$ and this is clearly equal to $v_{t,\theta} - v_{t+1,\theta+1}$. Thus

$$\begin{aligned} v_{t,\theta} &= v_{t-1,\theta-1}\big(1-\psi(\theta-1)\big) \\ &= v_{t-2,\theta-2}\Big(1-\psi(\theta-1)\big(1-\psi(\theta-2)\big)\Big) \\ &= v_{t-\theta,0}B_\theta \end{aligned} \tag{2.2}$$

Where B_θ is the product $\big(1-\psi(\theta-1)\big)\big(1-\psi(\theta-2),\ldots\ldots\ldots.1-\psi(0)\big)$.

Now v_t denotes the number of persons in unit area infected at the interval t and this must be equal to $x_t \sum_1^t \phi_\theta v_{t,\theta}$ where $x_t$denote the number of individuals still unaffected and ϕ_θ is the rate of infectivity at age θ.

It clear that,

$$\begin{aligned} x_t &= N - \sum_0^t v_{t,0} \\ &= N - \sum_0^t v_t - y_0 \end{aligned} \tag{2.3}$$

N is the initial population density.

If z_t denotes the number who have been removed by recovery and death then

$$x_t + y_t + z_t = N \tag{2.4}$$

Then,

$$v_t = x_t \sum_{1}^{t} \phi_\theta \, v_{t,\theta} = x_t \sum_{1}^{t} \phi_\theta \, B_\theta v_{t-\theta,0}$$

$$= x_t \left(\sum_{1}^{t} A_\theta \, v_{t-\theta} + A_t y_0 \right) \tag{2.5}$$

Also,

$$y_t = \sum_{0}^{t} v_{t,\theta} = \sum_{0}^{t} B_\theta v_{t-\theta} + B_t y_0 \tag{2.6}$$

By definition,

$$-v_t = x_{t+1} - x_t \tag{2.7}$$

$$x_t - x_{t+1} = x_t \left(\sum_{1}^{t} A_\theta \, v_{t-\theta} + A_t y_0 \right) \tag{2.8}$$

Also $z_{t+1} - z_t$ is the number of person. The interval of time t and this is equal to $x_t \sum_{1}^{t} \psi_\theta v_{t,\theta}$ to $x_t \sum_{1}^{t} \psi_\theta B_\theta v_{t-\theta} + \psi_t B_t y_0$

$$z_{t+1} - z_t = \sum_{1}^{t} C_\theta \, v_{t-\theta} + C_t y_0 \tag{2.9}$$

$$y_{t+1} - y_t = x_t \left[\sum_{1}^{t} A_\theta \, v_{t-\theta} + A_t y_0 \right] - \left[\sum_{1}^{t} C_\theta \, v_{t-\theta} + C_t y_0 \right]$$

Then in the limit the above equation becomes

$$x_t + y_t + z_t = N \tag{2.10}$$

$$v_t = -\frac{dx_t}{dt} \tag{2.11}$$

$$\frac{dx_t}{dt} = -x_t \left[\int_0^t A_\theta v_{t-\theta} d\theta + A_t y_0 \right] \tag{2.12}$$

$$\frac{dz_t}{dt} = \int_0^t C_\theta v_{t-\theta} d\theta + C_t y_0 \tag{2.13}$$

$$y_t = \int_0^t B_\theta v_{t-\theta} d\theta + B_t y_0 \tag{2.14}$$

where $B_\theta = e^{-\int_0^\theta \psi(a) da}, A_\theta = \phi_\theta B_\theta$ and $C_\theta = \psi_\theta B_\theta$. By equation (2.13) dropping the suffix t except when necessary in the analysis

$$\frac{dx}{dt} = -x\left[\int_0^t A_\theta v_{t-\theta} d\theta + A_t y_0\right]$$

$$= -x\left[\int_0^t A_{t-\theta} v_\theta d\theta + A_t y_0\right]$$

$$= -x\left[\int_0^t A_{t-\theta} \frac{dx_\theta}{d\theta} d\theta + A_t y_0\right] \qquad (2.15)$$

Therefore,

$$\frac{dlogx}{dt} = A_{t-\theta} x_\theta|_0^t - \int_0^t x_\theta \frac{dA_{t-\theta}}{d\theta} d\theta - A_t y_0$$

$$= A_0 x_t - A_t x_0 + \int_0^t x_\theta A'_{t-\theta}\, d\theta - A_t y_0$$

Where $A'_{t-\theta} = \frac{dA_{t-\theta}}{d(t-\theta)} = -\frac{dA_{t-\theta}}{d\theta}$.

But $A_0 = \phi_0, B_0 = \phi_0 = 0$. Since A_n individual at the moment of bocoming infected cannot transmit infection.

Hence,

$$\frac{dlogx}{dt} = \left.\begin{matrix} -A_t(x_0 + y_0) + \int_0^t x_\theta A'_{t-\theta}\, d\theta \\ -A_t N + \int_0^t A'_\theta x_{t-\theta}\, d\theta \end{matrix}\right\} \qquad (2.16)$$

An integral equation similar to Volterra's equation,

$$f(t) = \phi(t) + \int_0^t N(t,\theta)\phi(\theta)d\theta$$

$$\frac{dlogx}{dt} = A_t + \lambda \int_0^t N(t,0)x(\theta)d\theta$$

Used in resolving Volterra equation

$$x = f_0(t) + \lambda f_1(t) + \lambda^2 f_2(t) + \ldots\ldots\ldots$$

Substituting this expression in the equation

$$\frac{dx}{dt} = x\left[A_t + \lambda \int_0^t N(t,\theta)x(\theta)d\theta\right]$$

and equating the coefficient of the power of λ.

$$\frac{d}{dt} f_n(t) = f_n(t)A_t + f_{n-1}(t)\int_0^t N(t,\theta)f_0(\theta)d\theta + f_{n-2}(t)\int_0^t N(t,\theta)f_1(\theta)d\theta$$

$$+\ldots\ldots\ldots\ldots + f_0(t)\int_0^t N(t,\theta)f_{n-1}(\theta)d\theta$$

$$= L_{n-1}(t)$$

This is a differential equation for $f_n(t)$ of which the solution's

$$f_n(t)e^{-\int_0^t A_t dt} = \int_0^t L_{n-1}(t)\, e^{-\int_0^t A_t dt} dt + constant$$

Also $f_n(0)$ is zero $(n > 0)$. Since the initial condition are presumably independent of λ. Hence the constants of integration are all zero except $f_0(0)$.

$$\frac{df_0(t)}{dt} = f_0(t)A_t$$

$$f_0(t) = f_0(0)e^{\int_0^t A_t dt}$$

So that $f_0(0) = x_0$. The integral equation

$$x = x_0E_t + \sum_{n=1}^{\infty} \lambda^n E_t \int_0^t \frac{L_{n-1}(t)}{E_t}\, dt$$

$$= E_t\left[x_0 + \sum_{n=1}^{\infty} \lambda^n \int_0^t \frac{L_{n-1}(t)}{E_t}\, dt\right]$$

$$x = E_t\left[x_0 + \sum_{n=1}^{\infty} \int_0^t \frac{L_{n-1}(t)}{E_t}\, dt\right] \qquad (2.17)$$

$$\frac{dlogx}{dt} = A_t + \int_0^t Q_{t-\theta}x_\theta d\theta$$

Multiplying both side by e^{-zt} where the real part of z is positive and integrating with respect to t between the limits zero and infinity

$$\int_0^{\infty} e^{-zt}\, \frac{dlogx}{dt} dt = \int_0^{\infty} e^{-zt}A_t\, dt + \int_0^{\infty} e^{-zt} \int_0^{\infty} Q_{t-\theta}x_\theta d\theta\ dt$$

Therefore

$$-log\ x_0 + \int_0^\infty z\, e^{-zt}\ log\ x\, dt = F(z) + \int_0^\infty e^{-zt} Q_\theta d\theta \int_0^\infty e^{-zt}\ x_t\ dt$$

$$= F(z) + F_1(z) \int_0^\infty e^{-zt}\ x_t\ dt \qquad (2.18)$$

where $F(z)$ is written for $\int_0^\infty e^{-zt} A_t\, dt$ and $F_1(z)$ for $\int_0^\infty e^{-z\theta} Q_\theta d\theta$.

Thus,

$$\int_0^\infty e^{-zt}(z\ log\ x - F(z)x)dt = F(z) + log\ x_0$$

$$\int_0^\infty \phi(x,z)\psi(z,t)dt = \chi(z) \qquad (2.19)$$

where the functions ϕ, ψ and χ are known and x is a function of t. z may have any value provided that its real part is positive.

$$-\int_0^\infty \frac{dlogx}{dt} dt = \int_0^\infty \int_0^t A_\theta v_{t-\theta} d\theta\, dt + y_0 \int_0^\infty A_t\, dt$$

$$log\ \frac{x_0}{x_\infty} = \int_0^\infty A_\theta d\theta \int_0^\infty v_t\, dt + y_0 \int_0^\infty A_t\, d\theta$$

Put A for $\int_0^\infty A_t\,dt$ and use the relation,

$$\int_0^\theta v_t\,dt = -\int_0^\infty \frac{dx}{dt}\,dt = x_0 - x_\infty$$

$$log\,\frac{x_0}{x_\infty} = A(x_0 - x_\infty) + Ay_0 = A(N - x_\infty)$$

Let us introduce the value $p = \frac{N-x_\infty}{N}$, Then $x_\infty = N(1-p)$ and

$$log\,\frac{1-p}{1-y_0/N} = AN_p \qquad (2.20)$$

This equation determines the size of the epidemic in terms of A, N and y_0. The equation (2.15) in a similar manner,

$$\int_0^\infty y_t\,dt = Np\int_0^\infty B_\theta d\theta$$

Thus $\int_0^\infty B_\theta d\theta$ is the average case duration.

$$-\int_0^\infty e^{-zt}\,\frac{dlogx}{dt}dt = \int_0^\infty e^{-zt}\int_0^t A_\theta v_{t-\theta}d\theta\,dt + y_0\int_0^\infty e^{-zt}A_t\,dt$$

$$= \int_0^\infty e^{-zt}\,A_\theta d\theta\int_0^\infty e^{-zt}v_t\,dt + y_0\int_0^\infty e^{-zt}A_t\,dt$$

Therefore,

$$\int_0^{\infty} e^{-zt} A_t dt = \frac{-\int_0^{\infty} e^{-zt} \frac{dlogx}{dt} dt}{y_0 + \int_0^{\infty} e^{-zt} v_t dt} \tag{2.21}$$

$$A_\theta = \frac{1}{2\pi i} \int_{a-i\infty}^{a+i\infty} e^{zt} F_2(z) dt \tag{2.22}$$

By Equation (2.15)

$$\int_0^{\infty} e^{-zt} y_t dt = \int_0^{\infty} e^{-zt} \int_0^{t} B_\theta v_{t-\theta} d\theta \, dt + y_0 \int_0^{\infty} e^{-zt} B_t dt$$

$$\int_0^{\infty} e^{-zt} B_t dt = \frac{\int_0^{\infty} e^{-zt} y_t \, dt}{y_0 + \int_0^{t} e^{-zt} v_t dt} \tag{2.23}$$

$$B_\theta = \frac{1}{2\pi i} \int_{a-i\infty}^{a+i\infty} e^{zt} F_3(z) dt \tag{2.24}$$

If $F_2(z)$ and $F_3(z)$ can be expressed as rational function of z, then in place of Laplace's transformation.

Special Cases:

The earlier stage of an epidemic in a large population:

During an earlier stage of an epidemic in a large population, the number of unaffected persons may be considered to be constant. Since any alteration is small in comparison with total number.

$$-\frac{dx}{dt} = v_t = N\left[\int_0^\infty A_\theta v_{t-\theta} d\theta + A_t y_0\right]$$

Where N is this constant population per unit area using Fock's method.

$$\int_0^\infty e^{-zt} v_t dt = \frac{N y_0 \int_0^\infty e^{-zt}\, A_t\, dt}{1 - N\int_0^\infty e^{-zt} A_t dt} \tag{2.25}$$

$$v_t = \frac{1}{2\pi i}\int_{a-i\infty}^{a+i\infty} e^{zt}\, F_4(z) dt \tag{2.26}$$

$$\int_0^\infty e^{-zt}\, y_t\, dt = \int_0^\infty e^{-zt} \int_0^t B_\theta v_{t-\theta} d\theta\, dt + y_0 \int_0^\infty e^{-zt} B_t\, dt$$

$$= \int_0^\infty e^{-zt} v_t\, dt \int_0^\infty e^{-z\theta}\, B_\theta d\theta + y_0 \int_0^\infty e^{-zt} B_t\, dt$$

$$= \frac{N y_0 \int_0^\infty e^{-zt}\, A_t\, dt \int_0^\infty e^{-zt}\, B_t\, dt}{1 - N\int_0^\infty e^{-zt} A_t dt} + y_0 \int_0^\infty e^{-zt}\, B_t\, dt$$

$$= \frac{y_0 \int_0^{\infty} e^{-zt}\, B_t\, dt}{1 - N \int_0^{\infty} e^{-zt} A_t dt} \tag{2.27}$$

Thus,

$$y_t = \frac{1}{2\pi i} \int_{a-i\infty}^{a+i\infty} e^{zt}\, F_5(z) dt \tag{2.28}$$

$$y_t = \int_0^t B_{t-\theta} v_\theta d\theta + B_t y_0$$

$$= N \int_0^t B_{\theta-t} \left(\int_0^\theta A_{\theta-z} v_z dz + A_\theta y_0 \right) d\theta + B_t y_0$$

$$y_t = N \int_0^t B_{t-\theta} \int_0^\theta A_{\theta-z} v_z dz d\theta + N y_0 \int_0^t B_{t-\theta} A_\theta d\theta + B_t y_0$$

$$= N \int_0^t A_{t-\theta} \int_0^\theta B_{\theta-z} v_z dz d\theta + N y_0 \int_0^t A_{t-\theta} B_\theta d\theta + B_t y_0$$

$$= N \int_0^t A_{t-\theta} (y_0 - B_\theta y_0 + B_\theta y_0)\, d\theta + B_t y_0$$

$$= N \int_0^t A_{t-\theta} y_0\, d\theta + B_t y_0 \tag{2.29}$$

The equation for $v_{t,0}$ was given as,

$$v_{t,0} = \int_0^t A_\theta v_{t-\theta,0} d\theta$$

$$v_{t,0} = \frac{1}{2\pi i} \int_{a-i\infty}^{a+i\infty} e^{zt} \frac{N_0}{1 - \int_0^\infty e^{-z\theta} A_\theta d\theta} dz$$

Thus $v_{t,0} = v_t$ except in the short interval of time 0 to $\in$ and during this interval the integral equation does not hold. But instead $\int_0^\in v_{t,0}\, dt$ is equal to y_0.

Thus, $v_{t,0} = v_{t,0} - v_{\in,0} + v_{\in,0}$

$$= \int_\in^t A_{t-\theta}\, v_{\theta,0} d\theta + \int_0^\in A_{t-\theta}\, v_{\theta,0} d\theta$$

$$= \int_0^t A_{t-\theta}\, v_\theta d\theta + A_{t-\in'} \int_0^\in v_{\theta,0}\, d\theta \;\; where\; 0 < \in' < \in$$

$$= \int_0^t A_{t-\theta}\, v_{\theta,0} d\theta + A_t y_0 \theta$$

Then,

$$v_{t,0} = \frac{1}{2\pi i} \int_{a-i\infty}^{a+i\infty} e^{zt}\, F(z) dz$$

Where

$$F(z) = \frac{y_0}{1 - \int_0^{\infty} e^{-z\theta} A_\theta d\theta}$$

Let us denote this by $\frac{y_0}{1-A}$.

In the new form,

$$F_4(z) = -y_0 + \frac{y_0}{1-A} = \frac{Ay_0}{1-A}$$

Now if v_t has no singularities, the Laplacian solution of $F_4(z)$ is a function with no singularities and so the Laplacian of y_0 corresponds to the singularity.

The Laplacian solution $\frac{1}{2\pi i}\int_{a-i\infty}^{a+i\infty} e^{zt}\,(-y_0)dz$ corresponds to a function at the origin that $\int_0^{\in} \phi(t)dt$ tends to y_0 as $\in$ tends to zero.

The expression $\frac{1}{2\pi i}\int_{a-i\infty}^{a+i\infty} e^{zt}\,(-y_0)dz$ may be taken as representing a function with same properties as $v_t - v_{t,0}$.

$$\int_0^{\in} \left(v_t - v_{t,0}\right) dt = -y_0$$

when $\in$ becomes very small.

The values A_θ and B_θ from observed values of v_i and y_t

$$A_\theta = \frac{1}{2\pi i}\int_{a-i\infty}^{a+i\infty} e^{zt}\ \frac{\int_0^\infty e^{-zt}v_t dt}{Ny_0 + N\int_0^\infty e^{-zt}v_t dt}\,dz \qquad (2.30)$$

and

$$B_\theta = \frac{1}{2\pi i}\int_{a-i\infty}^{a+i\infty} e^{zt}\ \frac{\int_0^\infty e^{-zt}y_t dt}{y_0 + N\int_0^\infty e^{-zt}v_t dt}\,dz \qquad (2.31)$$

If $F(z)$ can be expressed as a rational function of the form $\frac{\psi_n(z)}{\psi_m(z)}$ where ψ_n and ψ_m are polynomials of degree n and m respectively and n is less than m. Then it is always possible to express $F(z)$ in the form $\sum\sum \frac{A_{r,s}}{(z-\alpha_r)^s}$ where r and s vary from unity to a and b respectively and a and b have finite values.

But $\int_0^\infty e^{-zt}e^{at}t^c dt = \frac{c!}{(z-\alpha)^{c+1}}$

$$\int_0^\infty e^{-zt}\phi(t)dt = \sum\sum \frac{A_{r,s}}{(z-\alpha_r)^s}$$

$$\phi(t) = \sum\sum \frac{A_{r,s}}{(s-1)!}t^{s-1}e^{a,t}$$

Constant Rates:

The special case in which ϕ and ψ are constants k and l respectively.

The equations are,

$$\left.\begin{aligned}\frac{dx}{dt} &= -kxy \\ \frac{dy}{dt} &= kxy - ly \\ \frac{dz}{dt} &= ly\end{aligned}\right\} \tag{2.32}$$

and $x + y + z = N$

Then $\frac{dz}{dt} = l(N - x - z)$ and $\frac{dx}{dz} = -\frac{k}{l}x, log\ \frac{x_0}{x} = \frac{k}{l}z.$

Assume that z_0 is zero.

$$\frac{dz}{dt} = l\left(N - x_0 e^{-k/lz} - z\right)$$

Assume that $k/l\,z$ is small compared with unity.

$$\frac{dz}{dt} = l\left\{N - x_0 + (k/l\,x_0 - 1)z - \frac{x_0 k^2 z^2}{2l^2}\right\}$$

But $N - x_0 = y_0$ where y_0 is small. The solution of this equation is,

$$z = \frac{l^2}{k^2 x_0}\left\{\frac{k}{l}x_0 - 1 + \sqrt{-q}\ \tanh\frac{\sqrt{-q}}{2}lt - \phi\right\} \tag{2.33}$$

where $\phi = \tanh^{-1}\frac{\frac{k}{l}x_0 - 1}{\sqrt{-q}}$ and $\sqrt{-q} = \left\{\left(\frac{k}{l}x_0 - 1\right)^2 + 2x_0 y_0\ \frac{k^2}{l^2}\right\}^{\frac{1}{2}}$

CHAPTER III

A SIMPLE STOCHASTIC EPIDEMIC

Introduction

The usual deterministic epidemic curve gives the rate of change with respect to time of the total number of cases. While the most appropriate stochastic analogues is probably the curve of the rate of change with respect to time of the stochastic mean. In some process stochastic means are identical with deterministic values but this is not the case is epidemic process. It is worth remarking in parsing that the rather unexpected smoothness of observed epidemic curve is most likely to be due to the partial ironing out of statistical variations by summation over finite periods of time and by summation over relatively isolated epidemic occurring simultaneously is subgroup of the main population.

In which none of the infected individuals is removed from circulation by death recovery or isolated. This is admittedly on over – simplification but apart from providing a possible basis for more extensive investigations.

The analytical difficulties present in the treatment of the simple epidemic appear here in a more from through it has proved possible to compute the frequency distribution of the total size of the epidemic for moderate group given the ratio of removal to infected rate. An important result is the problem of the of the distribution of multiple cases of disease in a household and a method is

given for obtaining maximum – likelihood estimates of the ratio of the removal to infection rate.

The Importance of Stochastic Means in Epidemics

Let us assume that the probability of a new case occurring in a small interval of time is proportional to both the number of susceptible and the number of infectious individual.

These original epidemic are not necessarily in phase and often interact with each other. Consider a single town or district. Each here it is obvious that a given infectious individual has not the same change of infecting each inhabitant. In close contact with a small number of people only perhaps of the order of 10 – 50 depending on the nature of his activities. The whole district will there be built from epidemic taking place in several relatively small group of associates and acquaintance.

The co – efficient of variation of the total number of cases will be $\frac{1}{\sqrt{k}}$ times the co – efficient of variation of any one of the groups. The larger the value of k. The more nearly will the curve of the total number of cases approach in shape the curve of the stochastic mean for a population of size n and expect the overall epidemic curve to approach in shape the curve of the rate of change with respect to time of the stochastic mean.

Deterministic treatment of a simple epidemic

Let y be the number of susceptibles at time t and let β be the infection rate. Then the number of new infections in time dt is $py(n-y+1)dt$ replace t by βt. The deterministic differential equation is

$$\frac{dy}{dt} = -y(n-y+1)$$

Initial condition $y = n$ when $t = 0$. The solution is

$$y = n(n+1)/\{n + e^{(n+1)t}\}$$

Thus the deterministic epidemic curve is,

$$Z = -\frac{dy}{dt} = y(n-y+1)$$

$$= \frac{n(n+1)^2 e^{(n+1)t}}{\{n + e^{(n+1)t}\}^2} \qquad (3.1)$$

The curve reaches a maximum. When,

$$t = log\ n/(n+1), \quad y = 1/2\,(n+1) \ \ \&\ z = 1/4\,(n+1)^2$$

It is clearly symmetrical about $t = log\ n/(n+1)$.

The latter does not seem to satisfy the apparent initial condition there must be misprint.

Stochastic treatment of a simple epidemic

(a) Solution of stochastic differential difference equation

Let us replacing t by βt on the assumption of homogeneous mixing the probability of one now infection take the interval dt is $y(n-y+1)dt$.

Suppose that $p_r(t)$ is the probability that there are r susceptibles still uninfected at time t.

The stochastic differential – difference equation

$$\left.\begin{aligned} &\frac{dp_r(t)}{dt} = (r+1)(n-r)p_{r+1}(t) - r(n-r+1)p_r(t), \quad r = 0,1,\dots\dots \\ &and \qquad\qquad \frac{dp_n(t)}{dt} = -np_n(t) \end{aligned}\right\} \quad (3.2)$$

Let us now use the Laplace transform and its inverse with respect to time given by

$$\left.\begin{aligned} \phi^*(\lambda) &= \int_0^\infty e^{-\lambda t}\phi(t)dt, \qquad\qquad R(\lambda) > 0, \\ \phi(t) &= \frac{1}{2\pi i}\int_{c-i\infty}^{c+i\infty} e^{\lambda t}\phi^*(\lambda)d\lambda, \end{aligned}\right\} \quad (3.3)$$

where $\int_{c-i\infty}^{c+i\infty} \equiv \lim_{w\to\infty} \int_{c-i\omega}^{c+i\omega}$,and c is positive and greater than the abscissae of all the residues. Using the boundary condition

$$\begin{aligned} p_r(0) &= 1, \quad (r = n) \\ &= 0 \quad (r < n) \end{aligned}$$

The recurrence relation

$$q_r = \frac{(r+1)(n-r)}{\lambda + r(n-r+1)}q_{r+1}, \quad r = (0,1,\dots\dots\dots\dots\dots.(n-1))$$

and

$$q_n = \frac{1}{\lambda + n}$$

where $q_r = p_r^* = \int_0^\infty e^{-\lambda t}p_r(t)dt$

$$q_r = \frac{n!\,(n-r)!}{r!} \Big/ \prod_{j=1}^{n-r+1} \big(\lambda + j(n-j+1)\big) \qquad 0 \le r \le n$$

If $r \geq 1/2\,(n+1)$ then the factor in the denominator are all different while if $r < 1/2\,(n+1)$ some of the are repeated.

$$(\lambda+n)\{\lambda+2(n-1)\}\{\lambda+3(n-2)\}\ldots\ldots\ldots.\{\lambda+r(n-r+1)\}^2$$

$$\{\lambda+(r+1)(n-r)\}^2\ldots\ldots\ldots\times\{\lambda+(1/2\ n-1)(1/2\ n+2)\}^2$$

$$\{\lambda+1/2\ n(1/2\ n+1)\}^2 \text{ for } n \text{ even}$$

and

$$(\lambda+n)\{\lambda+2(n-1)\}\{\lambda+3(n-2)\}\ldots\ldots\ldots.\{\lambda+r(n-r+1)\}^2$$

$$\{\lambda+(r+1)(n-r)\}^2\ldots\ldots\ldots\times\left\{\lambda+\frac{(n-1)}{2}\frac{(n-3)}{2}\right\}^2$$

$$\left\{\lambda+\tfrac{(n+1)^2}{4}\right\} \text{ for } n \text{ odd}$$

Thus all terms after the $(r-1)th$ are squared unless 'n' is odd in which case the least term is not squared.

The denominator like $\{\lambda+r(n-r+1)\}$ and $\{\lambda+r(n-r+1)\}^2$ will give rise to, $exp\{-r(n-r+1)t\}$ and $t\,exp\{-r(n-r+1)t\}$ respectively. The coefficient of the latter terms are simply the coefficient of the corresponding terms in the expansion of q_r in partial fractions.

$$q_0 = \frac{(n!)^2}{[\lambda\,(\lambda+n)^2\,\{\lambda+2(n-1)\}^2\ldots\ldots\ldots\ldots.]} \tag{3.4}$$

$$= \frac{1}{\lambda} + \sum_{r=1}\left\{\frac{kr}{\{\lambda+r(n-r+1)\}^2} + \frac{lr}{\{\lambda+r(n-r+1)\}^2}\right\} \tag{3.5}$$

where

$$kr = q_0\{\lambda + r(n-r+1)\}^2|_{\lambda=-r(n-r+1)} = \frac{-(n!)^2(n-2r+1)^2}{r!\,(r-1)!\,(n-r)!\,(n-r+1)!} \tag{3.6}$$

Now if the probability generating function is,

$$\pi(x,t) = \sum_{r=0}^{n} x^r p_r(t) \tag{3.7}$$

Then it can seen from (3.7) that $\pi(x,t)$ satisfies the partial differential equation

$$\frac{\partial \pi}{\partial t} = (1-x)\left\{n\frac{\partial \pi}{\partial x} - x\frac{\partial^2 \pi}{\partial x^2}\right\} \tag{3.8}$$

The boundary condition

$$\pi(x,0) = x^n \tag{3.9}$$

The equation for the moment generating function $M(\theta,t)$ are derived (3.8) & (3.9) writing $x = e^{\theta}$, Then

$$\frac{\partial M}{\partial t} = \left(e^{-\theta} - 1\right)\left\{(n+1)\frac{\partial M}{\partial \theta} - x\frac{\partial^2 M}{\partial \theta^2}\right\} \tag{3.10}$$

The boundary condition, $M(\theta,0) = e^{n\theta}$ (3.11)

Suppose that the rth moment of the distribution of y is m_r' then,

$$M(\theta) = 1 + m_1'\theta + m_2'\frac{\theta^2}{2!} + \cdots \ldots\ldots\ldots\ldots \tag{3.12}$$

In (3.10) and equate coefficients of θ to give the following set of differential equation

$$\left.\begin{aligned}\frac{dm_1'}{dt} &= -\{(n+1)m_1' - m_2'\} \\ \frac{dm_2'}{dt} &= +\{(n+1)m_1' - m_2'\} - 2\{(n+1)m_2' - m_3'\} \\ \frac{dm_3'}{dt} &= -\{(n+1)m_1' - m_2'\} + 3\{(n+1)m_2' - m_3'\} - 3\{(n+1)m_3' - m_4'\}\end{aligned}\right\} \quad (3.13)$$

These equation while capable of giving the higher moment in term of m_1' when the latter has been found.

$$m_2' = (n+1)m_1' + \frac{dm_1'}{dt} \quad (3.14)$$

are not so convenient for finding m_1' itself. Since all the moment are known when $t = 0$. In fact,

$$m_1' = n - nt - \frac{n(n-2)}{2!}t^2 - \frac{n(n^2-8n+8)}{3!}t^3 + \ldots\ldots\ldots \quad (3.15)$$

The coefficient of θ in the partial differential equation for the moment generating function for the simple differential equation for atleast the early moments, fails to be of service in the case of stochastic epidemic processes.

(b) Stochastic Mean Values

Let the transform of the probability – generating function be,

$$\pi^*(x,\lambda) = \sum_{r=0}^{n} x^r q_r \quad (3.16)$$

The equation

$$\pi^*(x,\lambda) = \frac{1}{\lambda} + \sum_{r=1} \left\{ \frac{f_r(x)}{\{\lambda + r(n-r+1)\}^2} + \frac{g_r(x)}{\{\lambda + r(n-r+1)\}^2} \right\} \quad (3.17)$$

where $f_r(x)$ and $g_r(x)$ are polynomial in x.Then,

$$\pi(x,t) = 1 + \sum_{r=1} \{t f_r(x) + g_r(x)\} e^{-r(n-r+1)t} \tag{3.18}$$

Therefore,

$$m_1'(t) = \frac{\partial \pi}{\partial x}|_{x=1} = \sum_{r=1} \{t f_r'(1) + g_r'(1)\} e^{-r(n-r+1)t} \tag{3.19}$$

Now the transform of (3.8) show that $\pi^*(x,\lambda)$ satisfies the differential equation

$$x(1-x)\frac{\partial^2 \pi}{\partial x^2} - n(1-x)\frac{\partial \pi^*}{\partial x} + \lambda \pi^* = x^n \tag{3.20}$$

Substitute (3.17) in (3.20)

$\{\lambda + r(n-r+1)\}^2$ and put $\lambda = -r(n-r+1)$

$$x(1-x)f_r'' - n(1-x)f_r' - r(n-r+1)f_r = 0 \tag{3.21}$$

$$f_r(x) = CF\{-r, -n+r-1, -n, x\} \tag{3.22}$$

where F is a terminating hypergeometric series and C an arbitrary constant. Substituting this value in (3.22) differentiating with respect to x and then putting $x = 1$, gives

$$f_r'(1) = k_r \frac{dF}{dx}|_{x=1}$$

$$= -k_r \frac{r(n-r+1)}{n} F\{-r+1, -n+r; -n+1, 1\}$$

Therefore,

$$f_r'(1) = \frac{n!\,(n-2r+1)^2}{(n-r)!\,(r-1)!} \tag{3.23}$$

Specimen values of these co – efficient occurring in the expression for $m_1'(t)$ given by (3.19) are

$$\left.\begin{array}{cc} r & f_r'(1) \\ 1 & n(n-1)^2 \\ 2 & n\,(n-1)(n-3)^2/1! \\ 3 & n\,(n-1)(n-2)(n-5)^2/2! \\ 4 & n\,(n-1)(n-2)(n-3)(n-7)^2/3! \\ \vdots & \vdots \end{array}\right\} \tag{3.24}$$

Substitute and multiply by $\{\lambda + r(n-r+1)\}^2$ differentiate with respect to λ and then put $\lambda = -r(n-r+1)$

$$x(1-x)g_r'' - n(1-x)g_r' - r(n-r+1)g_r = -f_r \tag{3.25}$$

Let us derive the series solution for $g_r(x)$ in terms of the known $f_r(x)$

$$g_1'(1) = n - n(n-1)\left(1 + \frac{1}{2} + \frac{1}{3} + \cdots \ldots \ldots + \frac{1}{n-2}\right) \tag{3.26}$$

Completion times

Let us call an epidemic complete when all the available susceptibles have been exhausted. Now $P_0(\tau)$ is the probability that the epidemic is complete at time τ. Since the number of susceptibles is a noon – increasing function. $P_0(\tau)$ is also the change that the epidemic has been completed in the interval from 0 to τ.

Thus $P_0(\tau)$ is the distribution function and $\frac{dP_0}{d\tau}$ the frequency function for the completion time τ.

The moment generating function for the completion time is, $M_r(\theta) = Ee^{-\theta r}$

$$= \int_0^\infty \frac{dP_0}{d\tau}\ e^{\theta r}\ d\tau$$

$$= \left[P_0 e^{\theta r}\right]_0^\infty - \theta \int_0^\infty P_0\ e^{\theta r}\ d\tau$$

$$= -\theta q_0(-\theta) \text{ for } \theta < 0$$

Since $P_0(0) = 0, P_0(\infty) = 1$

Therefore $M_\tau(\theta) = -\theta q_0(-\theta)$ (3.29)

Substitute for q_0 in (3.4) then,

$$M_\tau(\theta)$$

$$= \frac{(n!)^2}{\prod_{j=1}^{n}\{-\theta + j(n-j+1)\}}$$

$$= \prod_{j=1}^{n}\left\{1 - \frac{\theta}{j(n-j+1)}\right\}^{-1} \quad (3.30)$$

The cumulate – generating function is then given by,

$$K_\tau(\theta) = -\sum_{j=1}^{n} log\ \left\{1 - \frac{\theta}{j(n-j+1)}\right\} \quad (3.31)$$

The rth cummulant is evidently,

$$K_r = (r-1)! \sum_{j=1}^{n} \frac{1}{j^r (n-j+1)^r} \quad (3.32)$$

Each term on the right – hand side of (3.32) can be expanded in a series of partial fractions.

$$\left.\begin{aligned} K_r &= 2(r-1)!\sum_{p=1}^{r} a_p s_p \\ where\ a_p &= r\,(r+1)\,\ldots\ldots(2r-p+1)/(r-p)!\,(n+1)^{2r-p}\ (p<r) \\ a_r &= \frac{1}{(n+1)^r} \\ and\ s_p &= \sum_{u=1}^{n}\frac{1}{u_p} \end{aligned}\right\} \quad (3.33)$$

The first four cumulants are,

$$\left.\begin{aligned} K_1 &= \tfrac{2}{n+1}\,S_1 \\ K_2 &= \tfrac{4}{(n+1)^3}\,S_1 + \tfrac{2}{(n+1)^2}\,S_2 \\ K_3 &= \tfrac{24}{(n+1)^5}\,S_1 + \tfrac{12}{(n+1)^4}\,S_2 + \tfrac{4}{(n+1)^3}\,S_3 \\ K_4 &= \tfrac{240}{(n+1)^7}\,S_1 + \tfrac{120}{(n+1)^6}\,S_2 + \tfrac{48}{(n+1)^5}\,S_3 + \tfrac{12}{(n+1)^4}\,S_4 \end{aligned}\right\} \quad (3.34)$$

Then,

$$\left.\begin{aligned} S_1(n) &= \psi(n+1) - \psi(1) \\ S_p(n) &= \frac{(-1)^{p-1}}{(p-1)!}\left\{\psi^{(p-1)}(n+1) - \psi^{(p-1)}(1)\right\}\ \ (p>1) \end{aligned}\right\} \quad (3.35)$$

The asymptotic formula by using the well – known expansions

$$S_1(n) \sim log\ n + \gamma + \frac{1}{2n} - \frac{B_2}{2}\frac{1}{n^2} - \frac{B_4}{4}\frac{1}{n^4} \dots \dots \dots \dots$$

$$S_p(n) \sim \left\{\xi(p) - \frac{1}{(p-1)n^{p-1}}\right\} + \frac{1}{n^p}\left\{\frac{1}{2} - \frac{B_2}{2}\binom{p}{1}\frac{1}{n} - \frac{B_4}{4}\binom{p+2}{3}\frac{1}{n^3} \dots \dots \dots .\right\}$$

(3.36)

It is evident from (3.34) , (3.35) and (3.36) that for large n

$$\left.\begin{aligned} K_1 &= \frac{2}{(n+1)}\{\log n + \gamma + O(n^{-1})\} \\ K_r &= \frac{2\ (r-1)!}{(n+1)^r}\zeta(r)\ \{1 + O(n^{-1})\}\ (r > 1) \end{aligned}\right\} \qquad (3.37)$$

Thus the co – efficient of variation is asymptotically equal to

$$\pi/2\ \sqrt{3}\log n \qquad (3.38)$$

CHAPTER IV

THE TOTAL SIZE OF A GENERAL STOCHASTIC EPIDEMIC

Stochastic models have a special importance in this context due to the fact that for epidemic processes stochastic means are not the same as the corresponding deterministic values. Although for large homogeneously mixing groups deterministic methods might be fairly adequate, it seems likely that in practice epidemics actually occur in several relatively small groups of friends and acquaintances, the epidemiological returns for an administrative unit being compounded of many such comparatively distinct processes.

Deterministic treatment

Let us consider a homogeneously mixing community of n individuals, of whom at time t there are x susceptibles, y infectious cases in circulation and z individuals who are isolated, dead, or recovered and immune. $x + y + z = n$.

Now suppose that there is a constant infection rate β and a constant removal rate γ, so that the number of new infections in time dt is $\beta xydt$ and the number of removals from circulation is γydt. Let us choose our time scale so that t is replaced by βt. Then it is easy to see that the course of the epidemic is represented by the differential equations

$$\left.\begin{aligned} \frac{dx}{dt} &= -xy, \\ \frac{dy}{dt} &= xy - \rho y, \\ \frac{dz}{dt} &= \rho y, \end{aligned}\right\} \tag{4.1}$$

where $\rho = \gamma/\beta$, the ratio of the removal to infection rate. Initially, when $t = 0$, let us assume that x is approximately equal to n. It is then clear from (4.1) that unless $\rho < n$ no epidemic can start to build up as this requires $[dy/dt]_{t=0} > 0$.

If $\rho = n - v$ where v is small compared with n an epidemic of total size $2v$ will occur. If the initial density of susceptibles is $n = \rho + v$ then the introduction of a few infected persons will give rise to an epidemic after which the density of susceptibles is reduced of $\rho - v$ a value as for below the threshold ρ as originally it was above it.

Stochastic treatment:

The assumption of homogeneous mixing of the susceptibles and infectious individuals in circulation the probability of one new infection taking place in time dt is $xydt$, while the probability of one infected person being removed from circulation in time dt is ρydt.

Let $p_{rs}(t)$ be the probability that at time t there are r susceptibles still uninfected and s infectious individuals in circulation.

The partial differential equation for the probability generating function II :

$$\frac{\partial \Pi}{\partial t} = (v^2 - uv)\frac{\partial^2 \Pi}{\partial u \partial v} + \rho(1 - v)\frac{\partial \Pi}{\partial v} \tag{4.2}$$

where

$$\Pi = \sum_{r,s} u^r v^s p_{rs,} \tag{4.3}$$

with limits $0 \leq r + s \leq n + a, \quad 0 \leq r \leq n, \quad 0 \leq s \leq n + a$

Let us now use the Laplace transform and its inverse with respect to time given by

$$\left.\begin{aligned} \phi^*(\lambda) &= \int_0^\infty e^{-\lambda t}\phi(t)dt, \qquad R(\lambda) > 0, \\ \phi(t) &= \frac{1}{2\pi i}\int_{c-i\infty}^{c+i\infty} e^{\lambda t}\phi^*(\lambda)d\lambda, \end{aligned}\right\} \tag{4.4}$$

Taking transforms of (4.2) and (4.3),and using the boundary condition

$$p_{na}(0) = 1, \tag{4.5}$$

Let us obtain

$$(v^2 - uv)\frac{\partial^2 \Pi^*}{\partial u \partial v} + \rho(1 - v)\frac{\partial \Pi^*}{\partial v} - \lambda\Pi^* + u^n v^a = 0, \tag{4.6}$$

and

$$\Pi^* = \sum_{r,s} u^r v^s p_{rs}^* = \sum_{r,s} u^r v^s q_{rs,} \tag{4.7}$$

where

$$q_{rs} = p_{rs}^* = \int_0^\infty e^{-\lambda t} p_{rs}(t)dt \tag{4.8}$$

Substituting (4.7) in (4.6), and equating coefficients of $u^r v^s$, yields the recurrence relations

$$\left.\begin{array}{rl} & (r+1)(s-1)q_{r+1,s-1} - \{s(r+\rho)+\lambda\}q_{rs} + \rho(s+1)q_{rs} = 0 \\ and & -\{a(n+\rho)+\lambda\}q_{na} + 1 = 0, \\ with & 0 \le r+s \le n+a,\ \ 0 \le r \le n, \quad 0 \le s \le n+a. \end{array}\right\} \quad (4.9)$$

Any q_{rs} whose suffix falls outside the prescribed ranges is taken to be identically zero. Using the inverse of the Laplace transformation then arrive at the required p_{rs} exhibiting them as sums of exponential terms like $e^{-i(j+\rho)t}$.

Now the epidemic ceases to spread to fresh susceptibles as soon as $s = 0$. Thus the probability of an epidemic of total size ω is

$$P_w = \lim_{t\to\infty} p_{n-w,0}(t) \qquad (0 \le w \le n),$$

$$= \lim_{\lambda\to 0} \lambda q_{n-w,0}$$

$$= \lim_{\lambda\to 0} \rho q_{n-w,1},$$

$$putting\ r = n - w\ and\ s = 0 \quad (4.10)$$

$$= \rho f_{n-w,1}, \quad (4.11)$$

where

$$\left.\begin{array}{rl} & f_{rs} = \lim_{\lambda\to 0} q_{rs}, \\ for & 1 \le r+s \le n+a,\ \ 0 \le r \le n, \qquad 0 \le s \le n+a \end{array}\right\} \quad (4.12)$$

The quantities f_{rs} evidently satisfy the following recurrence relations obtained from (4.9) by writing f_{rs} for q_{rs} and putting $\lambda = 0$,

$$\left.\begin{array}{rl} & (r+1)(s-1)f_{r+1,s-1} - s(r+\rho)f_{rs} + \rho(s+1)f_{r,s+1} = 0 \\ and & -a(n+\rho)f_{na} + 1 = 0, \end{array}\right\} \quad (4.13)$$

$$f_{rs} = \frac{n!\,(r+\rho-1)!\,\rho^{n+a-r-s}}{sr!\,(n+\rho)!}\ g_{rs} \quad (4.14)$$

Substituting in (4.13) gives

$$\left.\begin{aligned} g_{r+1,s-1} - g_{rs} + (r+\rho)^{-1} g_{r,s+1} &= 0 \\ g_{na} &= 1 \end{aligned}\right\} \tag{4.15}$$

Thus the progress of the epidemic can be regarded as a random walk from the point (n, a) to the points $(n-w, 0), w = 0,1, \ldots\ldots\ldots, n$ with an absorbing barrier at $r = 0$ and where the possible transitions from (r, s) are $(r, s) \rightarrow (r-1, s+1)$, occurring with probability $r/(r+\rho)$ and $(r, s) \rightarrow (r, s-1)$, occurring with probability $\rho/(r+\rho)$

Thus,

$$P_w = \frac{\rho^{a+w}}{\rho + n - w} \frac{\binom{n}{w}}{\binom{n+\rho}{w}} \sum_{\alpha} (\rho+n)^{-\alpha_0} (\rho+n-1)^{-\alpha_1} \ldots\ldots (\rho+n-w)^{-\alpha_w}$$

(4.16)

where the summation is over all compositions of $a + w - 1$ into $w + 1$ parts such that $0 \leq \alpha_i \leq a + i - 1$ for $0 \leq i \leq w - 1$ and $1 \leq \alpha_w \leq a + w - 1$. The purposes of computation there appears to be some advantage especially if n is at all large in calculating the quantities p_w from (4.11), (4.14), and (4.15) instead of from (4.16). The relative removal rate ρ is large epidemic tend to be small and conversely,

Household distribution of cases:

The first case in a family would arise from an outside contact while subsequent cases would occur through contacts within the family. The frequencies of the final number of cases observed can then be found in terms of a parameter p such a model is quite adequate for measles and satisfactory tests of goodness – of – fit were obtained for the data available, merely by equating observed and expected means. Equation (4.11), (4.14) and (4.15) can be used as before to calculate the quantities p_w for small values of n.

In partially solving the recurrence relation to give g_{rs} as a linear function of $g_{r+1,i}$ $i = (s-1), \ldots\ldots (n-r)$. The requisite formula are easily found to be,

$$\left.\begin{aligned} g_{rs} &= \sum_{i=s-1}^{n-r} (r+\rho)^{s-i-1}\, g_{r+1,i} \quad (s>1) \\ with\ g_{r1} &= \frac{g_{r2}}{(r+\rho)} \\ g_{n1} &= 1 \end{aligned}\right\} \qquad (4.17)$$

$n = 1$:

$$p_0 = \rho/(\rho+1) \quad \hat{\rho} = a_0/a_1 \qquad I_\rho = N/\rho(\rho+1)^2$$

$$p_1 = 1/(\rho+1)$$

$n = 2$:

$$p_0 = \rho/(\rho + 2)$$

$$p_1 = 2\rho^2/(\rho + 2)(\rho + 1)^2$$

$$p_2 = 2(2\rho + 1)/(\rho + 2)(\rho + 1)^2$$

$$\frac{dL}{dp} = \frac{a_0 + a_1}{\rho} + \frac{2a_2}{2\rho + 1} - \frac{2(a_1 + a_2)}{\rho + 1} - \frac{N}{\rho + 2}$$

$n = 3$:

$$p_0 = \rho/(\rho + 3)$$

$$p_1 = 3\rho^2/(\rho + 3)(\rho + 2)^2$$

$$p_2 = 6\rho^3(2\rho + 3)/(\rho + 3)(\rho + 2)^2(\rho + 1)^3$$

$$p_3 = 6(5\rho^3 + 12\rho^2 + 8\rho + 2)/(\rho + 3)(\rho + 2)^2(\rho + 1)^3$$

$$\frac{dL}{dp} = \frac{a_0 + 2a_1 + 3a_2}{\rho} + \frac{2a_2}{2\rho + 3} + \frac{(15\rho^2 + 24\rho + 8\ )a_3}{5\rho^3 + 12\rho^2 + 8\rho + 2}$$

$$- \frac{3(a_2 + a_3)}{\rho + 1} - \frac{2(a_1 + a_2 - a_3)}{\rho + 2} - \frac{N}{\rho + 3}$$

$n = 4$:

$$p_0 = \rho/(\rho + 4)$$

$$p_1 = 4\rho^2/(\rho + 4)(\rho + 3)^2$$

$$p_2 = 12\rho^3(2\rho+5)/(\rho+4)(\rho+3)^2(\rho+2)^3$$

$$p_3 = 24\rho^4(5\rho^3+27\rho^2+47\rho+27)/(\rho+4)(\rho+3)^2(\rho+2)^3(\rho+1)^4$$

$$p_4 = 24(14\rho^6+93\rho^5+235\rho^4+293\rho^3+197\rho^2+74\rho+12)/(\rho+4)$$

$$(\rho+3)^2(\rho+2)^3(\rho+1)^4$$

$$\frac{dL}{dp} = \frac{a_0+2a_1+3a_2+4a_3}{\rho} + \frac{2a_2}{2\rho+5} + \frac{(15\rho^2+54\rho+47\,)a_3}{5\rho^3+12\rho^2+47\rho+27}$$

$$+\frac{(84\rho^5+465\rho^4+940\rho^3+879\rho^2+394\rho+74)a_4}{14\rho^6+93\rho^5+235\rho^4+293\rho^3+197\rho^2+74\rho+12}$$

$$-\frac{4(a_3+a_4)}{\rho+1} \; -\frac{3(a_2+a_3+a_4)}{\rho+2} - \frac{2(a_1+a_2+a_3+a_4)}{\rho+3}$$

$$-\frac{N}{\rho+4}$$

$n = 5$:

$$p_0 = \rho/(\rho+5)$$

$$p_1 = 5\rho^2/(\rho+5)(\rho+4)^2$$

$$p_2 = 20\rho^3(2\rho+7)/(\rho+5)(\rho+4)^2(\rho+3)^3$$

$$p_3 = 60\rho^4(5\rho^3+42\rho^2+116\rho+106)/(\rho+5)(\rho+4)^2(\rho+3)^3(\rho+2)^4$$

$$p_4 = \frac{120\rho^5(14\rho^6+177\rho^5+910\rho^4+2443\rho^3+3626\rho^2+2836\rho+918)}{(\rho+5)(\rho+4)^2(\rho+3)^3(\rho+2)^4(\rho+1)^5}$$

$$\frac{dL}{dp} = \frac{a_0 + 2a_1 + 3a_2 + 4a_3 + 5a_4}{\rho} + \frac{2a_2}{2\rho + 7} + \frac{(15\rho^2 + 84\rho + 116\,)a_3}{5\rho^3 + 42\rho^2 + 116\rho + 106}$$

$$+ \frac{(84\rho^5 + 885\rho^4 + 3640\rho^3 + 7329\rho^2 + 7252\rho + 2836)a_4}{14\rho^6 + 177\rho^5 + 910\rho^4 + 2443\rho^3 + 3626\rho^2 + 2836\rho + 918}$$

$$+ \frac{\begin{matrix}(420\rho^9 + 5364\rho^8 + 28832\rho^7 + 85680\rho^6 + 155646\rho^5 \\ +180720\rho^4 + 136244\rho^3 + 65856\rho^2 + 18912\rho + 2448)\,a_5\end{matrix}}{14\rho^6 + 177\rho^5 + 910\rho^4 + 2443\rho^3 + 3626\rho^2 + 2836\rho + 918}$$

$$- \frac{5(a_4 + a_5)}{\rho + 1} - \frac{4(a_3 + a_4 + a_5)}{\rho + 2} - \frac{3(a_2 + a_3 + a_4 + a_5)}{\rho + 3}$$

$$- \frac{2(a_1 + a_2 + a_3 + a_4 + a_5)}{\rho + 4} - \frac{N}{\rho + 5}$$

The values of n as small as 1 to 5,it is probably just derive the p_w straight from Foster's formula (4.16).

CHAPTER V

THE OUTCOME OF STOCHASTIC EPIDEMICS

Introduction

Bailey has considered a Stochastic Epidemic model of the type set up by Barlett and shows that the probability distribution function $\{P_n\}$ of the ultimate number of infected individuals is calculated by solving a set of doubly recurrent relation . These same probabilities are obtained by the solution of a set of singly recurrent relations by Whittle in this chapter [39].

The growth of a stochastic epidemic in a closed population is a very challenging one. A temporally homogeneous Markov process having a finite number of states and yet there is great difficult in finding out anything useful about the sample "epidemic curve".

Let $Bs\Delta t$ be the probability that an infectious individual is removed in the infinitesimal time interval $(t, t+\Delta t)$ and let $A_r s\Delta t$ be the corresponding probability that a new infection takes place. No particular form is assumed for the function A_r at the moment.

The development of the probabilities p_{rs} is then governed by the relations

$$\frac{\partial}{\partial t}\, p_{rs} = A_{r+1}(s-1)p_{r+1,s-1} + B(s+1)p_{r,s+1} - (A_r s - Bs)p_{rs} \quad (5.1)$$

$$(\lambda + A_r s + Bs)q_{rs} = A_{r+1}(s-1)q_{r+1,s-1} + B(s+1)q_{r,s+1} + \delta_{n,r}\delta \tag{5.2}$$

If the transformation,

$$q_{rs} = \int_0^\infty e^{-\lambda t}\ p_{rs}(t)dt \tag{5.3}$$

is performed. As Bailey observes, the probability of an epidemic of total size w is then

$$P_w = Bf_{n-w,1} \tag{5.4}$$

$$f_{rs} = \lim_{\lambda \to 0} q_{rs} \tag{5.5}$$

Establishment of the recurrence relations

$$h_{r0} = 0 \qquad h_{rs} = sf_{rs} \quad (s = 1,2,\dots\dots) \tag{5.6}$$

$$\alpha_r = \frac{B}{A_r + B} \tag{5.7}$$

$$\beta_r = \frac{A_{r+1}}{A_r + B} \tag{5.8}$$

Then the equation for the f_{rs} take the form

$$h_{rs} = \alpha_r h_{r,s+1} + \beta_r h_{r+1,s-1} \tag{5.9}$$

$$h_{ns} = \alpha_n h_{n,s+1} + \beta_n \left(\frac{\delta_{as}}{A_{n+1}}\right) \quad (r = n-1, n-2, \dots\dots, s = 1,2,) \tag{5.10}$$

$$Let\ H_r(x) = \sum_{s=1}^{\infty} h_{rs}\ \alpha^{s+1}$$

$$H_r(x) = \frac{x^2}{x - \alpha_r}\ [\beta_r H_{r+1}(x) - \alpha_r h_{r1}] \tag{5.11}$$

The direct solution (5.9) show that

$$h_{r1} = \frac{\beta_r}{\alpha_r}\ H_{r+1}(\alpha_r) \tag{5.12}$$

as indeed it must if the expression (5.11) for H_r is to constitute a finite series in x.

$$H_r(x) = \frac{\beta_r x^2}{x - \alpha_r}\ [H_{r+1}(x) - H_{r+1}(\alpha_r)] \tag{5.13}$$

A relation with certainly holds for $r = n - 1, n - 2, \ldots \ldots$ and also for $r = n$ if introduce a function.

$$H_{n+1}(x) = \frac{x^a}{A_{n+1}} \tag{5.14}$$

$$P_w = B\ \frac{\beta_{n-w}}{\alpha_{n-w}}\ H_{n-w+1}\ [\alpha_n - w] \tag{5.15}$$

The equation (5.13) and (5.14) $H_{n-w+1}(x)$ can be expressed in terms of $H_{n-w+2}(\alpha_{n-w+1}), \ldots\ldots H_n(\alpha_{n-1}), H_{n+1}(x)$. $x = \alpha_{n-w}$ in this expression and substituting for the $H_{r+1}(\alpha_r)$ from (5.15)

$$\sum_{w=0}^{u} K_{n-u+1,n-u}\,, K_{n-u+2,n-u}, \dots\dots\dots\dots\dots\dots . K_{n-w,n-u}\ \frac{\alpha_{n-w}}{\beta_{n-w}}\ p_w$$

$$= K_{n-u+1,n-u}\,, K_{n-u+2,n-u}, \dots\dots\dots\dots\dots\dots . K_{n,n-u}\ \left(\frac{B}{A_{n+1}}\right)\ \alpha_{n-u}^{\alpha} \quad (5.16)$$

where $K_{rr} = 1, K_{rs} = \frac{\alpha_s^2\ \beta_r}{\alpha_s - \alpha_r} \quad (r \neq s)$ (5.17)

for $u = n$ reduces to

$$\sum_{0}^{n} P_w = 1 \quad (5.18)$$

complications arise if any of the $A_r's$ are equal. When this happens P_w involves not only $H_{n+1}(x)$ but also its derivatives. In this direction is that for which A_r is constant for $r > 0$.

$$\left.\begin{aligned} A_r &= A\ \ (r = 1,2, \dots\dots\dots) \\ A_0 &= 0 \end{aligned}\right\} \quad (5.19)$$

The appropriate modification of (5.17) may be derived by a repeated application of de L'Hospital rule and may be shown by induction to have a solution,

$$\left.\begin{aligned} P_w &= \frac{A^w\ B^{\alpha+w}}{(A+B)^{\alpha+2w}}\ \ \frac{a(a+2w-1)!}{w!\ (a+w)!} \\ P_n &= 1 - \sum_{0}^{n-1} P_w \end{aligned}\right\} \quad (5.20)$$

$$A_r = C_r \tag{5.21}$$

where C is constant,

$$\left.\begin{aligned} \alpha_r &= \frac{B}{B + C_r} \ , \qquad \beta_r = \frac{C(r+1)}{B + C_r} \\ K_{rs} &= \frac{B(r+1)}{(B + Cs)(r - s)} = \frac{\alpha_s (r+1)}{r - s} \end{aligned}\right\} \tag{5.22}$$

$$\sum_{w=0}^{u} \binom{n-w}{n-u} \alpha_{n-u}^{-w} \ P_w = \binom{n}{u} \ \alpha_{n-u}^{\alpha} \ (u = 0,1,2, \dots \dots, n) \tag{5.23}$$

For computational purposes it is convenient to consider instead of P_w the quantity.

$$Q_w = \frac{(n-w)!}{n!} \ P_w \tag{5.24}$$

$$\sum_{w=0}^{n} \frac{\alpha_{n-u}^{-w} \ Q_w}{(u-w)!} = \frac{\alpha_{n-u}^{\alpha}}{u!} \tag{5.25}$$

The Probability of Epidemic

A comparison formula for establishing behaviour of more refined models. The model upon which it is based is a perfectly valid one which for quite large ranges of w is more realistic then that corresponding to assumption (5.22). Since this assumption requires that the population mix homogeneously.

The case $a = 2, n = 30, \rho = B/C = 30B/A = 10$

	w	0	1	2	3
P_w	$A_r = 3$	0.0625	0.0235	0.0110	0.0058
	$A_r = 0.1r$	0.0625	0.0251	0.0122	0.0078

An epidemic has taken place if the total proportion of susceptibles which become infected exceeds a predetermined fraction γ. With this definition the probability of no epidemic is

$$\pi_\gamma = \sum_{w=0}^{n\gamma} P_w \tag{5.26}$$

Assume that in all three cases the infection intensity is non – decreasing with increasing

$$\left.\begin{aligned} A_{r+1} &\geq A_r \\ A'_{r+1} &\geq A'_r \\ A''_{r+1} &\geq A''_r \end{aligned}\right\} \quad (r = 0,1,2, \dots \dots \dots .,) \tag{5.27}$$

The range $n \geq r \geq n(1-\gamma)$ the intensity for the first model lies uniformly between those for the other two

$$A'_r \geq A_r \geq A''_r \tag{5.28}$$

It is then intuitively evident that

$$\sum_{0}^{n\gamma} P'_w \leq \sum_{0}^{n\gamma} P_w \leq \sum_{0}^{n\gamma} P_w^n \tag{5.29}$$

Suppose now that the intensities for those two comparison models have the constant values

$$\left.\begin{aligned} A'_r &= A_n \\ A''_r &= A_{n(1-\gamma)} \end{aligned}\right\} \quad (r > 0) \tag{5.30}$$

$A'_0 = A''_0 = 0$ condition (5.29) is thus fulfilled and the inequality (5.30) becomes

$$\sum_{0}^{n\gamma} S_w(A_n) \gtrless \pi_r \gtrless \sum_{0}^{n\gamma} S_w\left(A_{n(1-\gamma)}\right) \tag{5.31}$$

Consider now that partial sum $\sum_0^{n\gamma} S_w(A)$ as n becomes large

$$\frac{S_{w+1}}{S_w} = \frac{AB}{(A+B)^2} \frac{(a+2w+1)\,(a+2w)}{(w+1)\,(a+w+1)} < \frac{5AB}{(A+B)^2}$$

$$If\ w > \frac{(a+1)(a-5)}{6} \tag{5.32}$$

The quantity $5k$ will be less than unity except for the case $A = B$. It exclude for the moment

$$\sum_{0}^{n\gamma} S_w(A) = \sum_{0}^{\infty} S_w(A) - R_{n\gamma}(A) \tag{5.33}$$

where,

$$R_{n\gamma}(A) = \sum_{n\gamma+1}^{\infty} S_w(A) < S_{n\gamma+1}(A)\,[1 + (5k) + (5k)^2 + \ldots\ldots\ldots] = O[(5k)^{n\gamma}]$$

(5.34)

$$\sum_{0}^{\infty} S_w(A) = \left[\frac{1 - \sqrt{(1-5k)}}{2k}\right]^a \left(\frac{B}{A+B}\right)^a$$

$$= \left[\frac{A + B - [|A - B|]}{2A}\right]^a \tag{5.35}$$

Combining (5.32), (5.34), (5.35) and (5.36)

$$\left[\frac{A_n + B - [|A_n - B|]}{2A_n}\right]^a + O[(5k)^{n\gamma}] \lesseqgtr \pi_\gamma$$

$$\lesseqgtr \left[\frac{A_{n(1-\gamma)} + B - \left[\left|A_{n(1-\gamma)} - B\right|\right]}{2A_{n(1-\gamma)}}\right]^a \tag{5.36}$$

$$\left.\begin{array}{l} A_n > B, A_{n(1-\gamma)} > B;\ (B/A_n)^a \lesseqgtr \pi_\gamma \lesseqgtr \left(B/A_{n(1-\gamma)}\right)^a \\ A_n > B, A_{n(1-\gamma)} < B;\ (B/A_n)^a \lesseqgtr \pi_\gamma \lesseqgtr 1 \\ A_n < B, A_{n(1-\gamma)} < B;\ \pi_\gamma = 1 \end{array}\right\} \tag{5.37}$$

$$\rho_n = B/C = nB/A_n \tag{5.38}$$

The ratio of removal and infection rates for a population of size n:

$$\left.\begin{array}{c} For\ \rho_n < n\ and\ \rho_{n(1-\gamma)} < n(1-\gamma), the\ probability\ of\ epidemic\ lies\ between \\ 1-\left(\frac{\rho_n}{n}\right)^a\ and\ 1-\left(\frac{\rho_{n(1-\gamma)}}{n(1-\gamma)}\right)^a \\ For\ \rho_n < n\ and\ \rho_{n(1-\gamma)} > n(1-\gamma), the\ probability\ of\ epidemic\ lies\ between \\ zero\ and\ 1-\left(\frac{\rho_n}{n}\right)^a \\ For\ \rho_n > n\ and\ \rho_{n(1-\gamma)} > n(1-\gamma), the\ probability\ of\ epidemic\ is\ zero \end{array}\right\} \quad (5.39)$$

Since for large n the ratio $\rho_n/n = B/A_n$ will tend to an almost constant value statement (5.50) roughly condensed to,

$$\left.\begin{array}{c} For\ \rho_n < n\ the\ probability\ of\ epidemic\ is\ 1-(\rho_n/n)^q \\ For\ \rho_n > n\ the\ probability\ of\ epidemic\ is\ zero \end{array}\right\} \quad (5.40)$$

The probability completion is of fairly constant magnitude for small w, roughly of order $(1/2)^a$. As the number of susceptibles diminish, however the critical value of ρ with full and it seems likely that the epidemic will eventually be halted although only after having made appreciable inroads on the population.

The probability distribution P_w of (5.25) presents two different forms according as A is less than or greater than B. In both cases P_w dwindles with increasing w and if the population size is large enough to permit w to take large value P_w will finally approach zero. In the case $A < B$ the sum of the P_w up to this stage will approach unity.

In this case $A > B$ this sum will have some value less than unity $(1 - \alpha)$. So that P_n must have a finite value α if relation is to be fulfilled.

For large n the probability of no epidemic

$$\pi_\gamma = \sum_{0}^{n\gamma} S_w(A) \tag{5.41}$$

will be equal to the area under the initial part of the curve: Unity if $A < B, \alpha$ if $A > B$.

The fact that all probability mass which does not fall in the first J – shaped part of the curve falls at $w = n$ indicates that either the epidemic keeps with in bounds or else it infects the entire population.

Models with varying A show a similar, although less extreme behaviour. Thus the distribution curves calculated by Bailey are either J – shaped or U – shaped, depending upon the relative value of the removal ratio and the population size.

The J – shaped curve corresponds to cases in which the infection is almost certainly confined to small proportion of the population and so $\beta(z) = \beta$ when $z = 0$ and $\beta\ (z) < \beta$ when $0 \leqq z \leqq \rho$. From this we infer that the K and K approximation consistently underestimates the infection-rate and so it will underestimate the total size $z(\infty)$ of the epidemic.

CHAPTER VI

THE DISTRIBUTION OF THE TOTAL SIZE OF AN EPIDEMIC

The distribution of the total number of cases in an epidemic of the general stochastic type for a closed population. The recurrence relation from which the required probabilities were computed numerically. This calculations reveled a gradual transition from j – shaped distribution containing only small epidemics for population size below the threshold to u – shaped distributions containing either large or small epidemics but practically no epidemics of intermediate size when the threshold is exceeded. There is also an transitional form of distribution near the threshold value. The main object is to arrive at approximate formula for the distribution of the total epidemic size with are appropriate for large population given by [8].

The Deterministic Model

Suppose that at time t there are x susceptibles, y infectives and z recovered or dead in the population.

Initially take $x = \xi, y = \eta, z = 0$, so that,

$$x + y + z = \xi + \eta$$

The deterministic equations are

$$\frac{dx}{dt} = -xy, \frac{dy}{dt} = xy - \rho y, \frac{dz}{dt} = \rho y \qquad (6.1)$$

where ρ is called relative rate.

Then $\frac{dx}{dz} = -\frac{x}{\rho}$ and $x = \xi\ exp(-z/\rho)$ for all t. At the end of the epidemic $y = 0, z = \xi + \eta - x$ and the number x of individual remaining uninfected satisfies the equation

$$x\ exp(-x/\rho) = \xi\ exp[-(\xi + \eta)/\rho] \tag{6.2}$$

Suppose that ξ and ρ large and η/ρ is small. There are two values of x satisfying near the respective roots $\xi, \xi'\ of\ x\ exp(-x/\rho) = \xi\ exp(-\xi/\rho)$. A first approximation

$$x = \xi - {}^{\eta\xi}\Big/_{(\rho - \xi)} \tag{6.3}$$

where $\xi > \rho$the required root is near $\xi' < \rho$ and approximately,

$$x = \xi' - {}^{\eta\xi'}\Big/_{(\rho - \xi')} \tag{6.4}$$

then $\xi \gg \rho$ and ξ'/ρ is small.

$$x \sim \xi' \sim \xi e^{-{}^{\xi}/_{\rho}} \tag{6.5}$$

The Stochastic Model

The transition in $(t, t + \delta t)$ are $(x, y) \longrightarrow (x - 1, y + 1)$ with probability $xy\ \delta t + O(\delta t)$ and $(x, y) \longrightarrow (x, y - 1)$ with probability $\rho y\ \delta t + O(\delta t)$

$$\left.\begin{aligned} P\{(x,y) \longrightarrow (x-1,y+1)\} &= {}^{x}/_{(\rho+x)} \\ P\{(x,y) \longrightarrow (x,y-1)\} &= {}^{\rho}/_{(\rho+x)} \end{aligned}\right\} \tag{6.6}$$

where initially $x = \xi, y = \eta$ and absorption occur on $y = 0$. An alternative formulation of the random walk in terms of new cases $w = \xi - x$ and removals z is some interest.

$$\left.\begin{aligned} P\{(w,z) \longrightarrow (w+1,z)\} &= {}^{(\xi-w)}\big/_{(\rho+\xi-w)} \\ P\{(w,z) \longrightarrow (w,z+1)\} &= {}^{\rho}/_{(\rho+\xi-w)} \end{aligned}\right\} \tag{6.7}$$

The game stops when the player is ruined $(w + \eta = z)$ or when he has drawn all real pennies $(w = \xi)$.

Let $P(x/\xi,\eta)$ be the probability that there are ultimately x uninfected individuals. When initially there were ξ susceptibles and η infectives.

$$\xi\, P\left({}^{x}/_{\xi-1,\eta+1}\right) + \rho\, P\left({}^{x}/_{\xi,\eta-1}\right) - (\rho+\xi)P\left({}^{x}/_{\xi,\eta}\right) = 0$$

$$\xi > x, \eta \geqq 1 \text{ and} \tag{6.8}$$

$$\rho P\left({}^{x}/_{x,\eta-1}\right) - (\rho+x)P\left({}^{x}/_{x,\eta}\right) = 0 \tag{6.9}$$

with the condition

$$P\left({}^{x}/_{\xi,0}\right) = \delta(\xi - x) \tag{6.10}$$

where $\delta(\xi - x) = 0, \xi \neq x$ and $\delta(0) = 1$.

$$P\left(x/x, \eta\right) = \left[\rho/(\rho + x)\right] P\left(x/x, \eta - 1\right) = \ldots\ldots\ldots\ldots\ldots = \left[\rho/(\rho + x)\right]^{\eta} \quad (6.11)$$

$$\binom{\xi}{x + s}\left(\frac{\rho}{\rho + x + s}\right)^{\xi - x + \eta} \quad (6.12)$$

$$P\left(x/\xi, \eta\right) = \sum_{s=0}^{\xi - x} A_s \binom{\xi}{x + s}\left(\frac{\rho}{\rho + x + s}\right)^{\xi - x + \eta} \quad (6.13)$$

If $A_0 = 1$, let us have

$$\delta(\xi - x) = \sum_{s=0}^{\xi - x} A_s \binom{\xi}{x + s}\left(\frac{\rho}{\rho + x + s}\right)^{\xi - x + \eta} \quad (6.14)$$

The coefficient A_s can be determined recursively and hence $P(x/\xi, \eta)$ can be found provided A_s is independent of ξ

$$A_s = (-)^s \binom{x + s}{s} H_s \quad (6.15)$$

$$\binom{\xi}{x + s}\binom{x + s}{\xi} = \binom{\xi}{x}\binom{\xi - x}{s} \quad (6.16)$$

Then,

$$P\left(x/\xi, \eta\right) = \binom{\xi}{x} \sum_{s=0}^{\xi - x} (-)^s H_s \binom{\xi - x}{s}\left(\frac{\rho}{\rho + x + s}\right)^{\xi - x + \eta} \quad (6.17)$$

$$\delta(\xi - x) = \sum_{s=0}^{\xi-x} (-)^s H_s \binom{\xi - x}{s} \left(\frac{\rho}{\rho + x + s}\right)^{\xi-x} \tag{6.18}$$

Their coefficient H_s dependent only on x and ρ. Their value lies in the fact that a technique is available for obtaining an asymptotic approximation. When ξ is large.

Some Exact Results

Since the left side of (6.18) is zero except when $\xi = x$, it can equally well be put in the form

$$\delta(\xi - x) = \sum_{s=0}^{\xi-x} (-)^s H_s \binom{\xi - x}{s} \left(\frac{\rho}{\rho + x + s}\right)^{\xi-x} \tag{6.19}$$

then $H_s = H_s(x, \rho)$ and $P(x/\xi, \eta) = P(x/\xi, \eta\,, \rho)$ to show their dependence on ρ it appears that.

$H_s \equiv H_s(x, \rho)$ and $P(x/\xi, \eta) = P(x/\xi, \eta\,, \rho)$ to show their dependence on ρ it appears that.

$$H_s(x, \rho) = H_s(0, \rho + x) \tag{6.20}$$

The exact relation,

$$P\left({}^{x}/_{\xi, \eta\,, \rho}\right) = \left(\frac{\rho}{\rho + x + s}\right)^{\xi - x + \eta} \binom{\xi}{x} P\left({}^{0}/_{\xi\, -\, x\,, \eta, \rho + x}\right) \tag{6.21}$$

The equations are with H_s for $H_s(0, \rho)$

$$P\left(0/_{\xi,\eta},\rho\right)=\sum_{s=0}^{\xi}(-)^{s}\,H_{s}\binom{\xi}{s}\left(\frac{\rho}{\rho+s}\right)^{\xi+\eta} \tag{6.22}$$

$$\delta(\xi)=\sum_{s=0}^{\xi}(-)^{s}\,H_{s}\binom{\xi}{s}\left(\frac{\rho}{\rho+s}\right)^{\xi} \tag{6.23}$$

$$H_{s}=\frac{s!}{C_{s}^{s}}\begin{vmatrix} C_0 & 1 & 0 & & 0 & 0 & \dots\dots & \dots\dots & 0 & 0 \\ \frac{C_0^2}{2!} & \frac{C_1}{1!} & 1 & & 0 & 0 & & & 0 & 0 \\ \frac{C_0^3}{3!} & \frac{C_1^2}{2!} & C_1 & & & & & & 0 & 0 \\ \vdots & & & & 1 & 0 & & & & \\ \frac{C_0^{s-1}}{(s-1)!} & \frac{C_1^{s-2}}{(s-2)!} & \frac{C_2^{s-3}}{(s-3)!} & & & & & & C_{s-2} & 1 \\ \frac{C_0^{s}}{s!} & \frac{C_0^{s-1}}{(s-1)!} & \frac{C_2^{s-2}}{(s-2)!} & & & & & & \frac{C_s^2-2}{2!} & C_{s-1} \end{vmatrix}$$

where $C_s=\rho/(\rho+s)$ and $H_0=1$. Substitution is (6.22) give an explicit solution for $P(0/\xi,\eta,\rho)$.

Approximation below the Threshold

The problem that H_s can also be expressed in the form $H_s=C_s^{-s}C_s(0)$.

where

$$C_s(z)=s!\int_{z}^{C_0}dz_1\int_{z_1}^{C_1}dz_2\,\dots\dots\dots\dots\int_{z_{s-1}}^{C_{s-1}}dz_s \tag{6.24}$$

is called Gontcharoff polynomial. j[th] derivative vanishes at $z = C_j$. It can be discovered about the asymptotic behaviour of these expression by using a technique originally developed for a related problem. But there is an essential difference here which complicates matters.

In the application mentioned C_s is an increasing positive sequence and this ensures that $C_s(0)$ is always positive.

In this problem C_s is a decreasing positive sequence and beyond a certain value of s. H_s begins to oscillate with increasing amplitude and alternating sign.

In (6.23) replace ξ by m multiply it by $(-\lambda)^m \binom{\xi}{m}$ and sum from $m = 0$ to ξ.

$$I = \sum_{s=0}^{\xi} H_s \binom{\xi}{s} (\lambda C_s)^s (1 - \lambda C_s)^{\xi - s}, C_s = {}^{\rho}/_{(\rho + s)} \tag{6.25}$$

where λ is an arbitrary parameter.

$$T_s(\lambda) = \binom{\xi}{s} (\lambda C_s)^s (1 - \lambda C_s)^{\xi - s} \tag{6.26}$$

for large ξ. The range $0 < \lambda < 1$ ensures that $T_s(\lambda)$ is positive. But λ can be allowed to exceed unity provided $T_s(\lambda)$ remains positive near the root S_0.

Assume ξ and ρ are large and write $z = s/\xi$, $dz = 1/\xi$, $C(z) = C_s$, $T_s(\lambda) = T(z,\lambda)dz$.

$$T(z,\lambda) \sim \left[\frac{\xi}{2\pi z(1-z)}\right]^{1/2} \left[\frac{\lambda C(z)}{z}\right]^{\xi z} \left[\frac{1-\lambda C(z)}{1-z}\right]^{\xi(1-z)}$$

$$= \left[\frac{\xi}{2\pi z(1-z)}\right]^{1/2} \left\{1 - \frac{[z-\lambda C(z)]}{z}\right\}^{\xi z} \left\{1 + \frac{[z-\lambda C(z)]}{1-z}\right\}^{\xi(1-z)}$$

$$= \left[\frac{\xi}{2\pi z(1-z)}\right]^{1/2} exp\left\{-\frac{\xi[z-\lambda C(z)]^2}{2z(1-z)} + \begin{matrix} terms\ involving \\ higher\ powers \\ of\ z-\lambda C(z) \end{matrix}\right\}$$

(6.27)

The maximum of $T(z,\lambda)$ is at the unique root of $z - \lambda C(z) = 0$. z_0 is written us, $z - \lambda C(z) = (z - z_0)\,[1 - \lambda C'(z_0)]$ and because $z - z_0$ is $O\left(\xi^{1/2}\right)$ over its effective.

The normal approximation,

$$T(z,\lambda) \sim \left[\frac{\xi}{2\pi z_0(1-z_0)}\right]^{1/2} exp\left\{-\frac{\xi\,[1-\lambda C'(z_0)]^2}{2z_0(1-z_0)}(z-z_0)^2\right\} \quad (6.28)$$

where $z_0 = \lambda C(z_0)$ (6.29)

Assumed that $H(z) = H_{\xi z}$

$$1 \sim \int_0^1 H(z)\,T(z,\lambda)dz \sim H(z_0) \int_0^1 T(z,\lambda)dz$$

$$\sim H(z_0)/\,[1-\lambda C'(z_0)] = H(z_0)/\big[\,[1-z_0C'(z_0)/C(z_0)]\big] \qquad (6.30)$$

$$H(z)\sim 1-{}^{zC'(z)}\Big/_{C(z)}$$

Then $C'(z)/C(z) = -\xi/(\rho+s)$ and approximation

$$Hs\sim 1+s/(\rho+s) = 2-\rho/(\rho+s) \qquad (6.31)$$

It depends on the assumption that $H(z)$ varies slowly. It fail for large value of s corresponding to roots for which λ causes $T_s(\lambda)$ to oscillate. Also, small value of s have been excluded by the argument. The approximation value of s upto about ρ. An approximation for $P(x/\xi,\eta,\rho)$ when ξ is less than the threshold ρ.

Let us substitute (6.30) in the right side of (5.28). It is satisfied for $\xi > 0$.

$$\sum_{s=0}^{\xi}(-)^s\,H_s\binom{\xi}{s}\left(\frac{\rho}{\rho+s}\right)^{\xi} \sim \sum_{s=0}^{\xi}(-)^s\binom{\xi}{s}\left[2\left(\frac{\rho}{\rho+s}\right)^{\xi} - \left(\frac{\rho}{\rho+s}\right)^{\xi+1}\right]$$

$$= \frac{1}{(\xi-1)!}\int_0^{\infty}\left(2u^{\xi-1} - {}^{u^{\xi}}\Big/_{\xi}\right)$$

$$= \frac{1}{(\xi-1)!}\int_0^{\infty} e^{-u}\left[\left[2u^{-2\xi-1}\Big/\rho^{\xi}\right] - \left[\frac{1}{\xi}+\frac{\xi}{\rho}\right]u^{2\xi}\Big/\rho^{\xi} + \ldots\ldots\right] du$$

The term in $\rho^{-\xi}$ vanishes and the loading term is,

$$-\xi(2\xi)!/\rho^{\xi+1}/(\xi-1)! \tag{6.32}$$

For large ρ is small even at $\xi = 1$. As ξ increases approximately,

$$-\left[\rho\, e^2/8(2)^{1/2}\right][4\xi/\rho e]^{\xi+2} \tag{6.33}$$

which decreases to a minimum at about $\xi = \rho/4$.

$$P\left(0/\xi,\eta,\rho\right) \sim \frac{1}{(\xi+n-1)!}\int_0^{\infty}\left[2u^{\xi+\eta-1} - u^{\xi+\eta}\Big/(\xi+\eta)\right]$$

$$\left(1-e^{-u/\rho}\right)^{\xi} e^{-u}\, du$$

$$\sim \frac{\eta(2\xi+\eta-1)}{(\xi+\eta)!\,\rho^{\xi}} + O\left(\rho^{-\xi-1}\right) \tag{6.34}$$

Then from (6.23) the value of ξ below the threshold ρ.

$$P\left(x/\xi,\eta,\rho\right) \sim \frac{\eta\rho^{\xi-x+\eta}}{(\rho+x)^{2\xi-2x+\eta}}\binom{\xi}{x}\frac{(2\xi-2x+\eta-1)!}{(\xi-x+\eta)!}$$

$$P\left(x/\xi,\eta,\rho\right) \sim \frac{\eta\rho^{w+\eta}}{(\rho+\xi-w)^{2w+\eta}}\binom{\xi}{w}\frac{(2w+\eta-1)!}{(w+\eta)!}$$

Since ξ is large a further approximation leads to the result.

$$P \sim \frac{\eta \rho^{w+\eta\xi w}}{(\rho+\xi)^{2w+\eta}} \frac{(2w+\eta-1)!}{w!\,(w+\eta)!} \tag{6.35}$$

Approximation above the Threshold

The range of ξ above the threshold ρ. It is necessary to study the behaviour of H_s at values of s beyond these which can be reached by the previous method. It has been mentioned that H_s begins to oscillate violently when a exceeds a certain value.

$$\lambda = -v/(1-v)$$

and

$$H_s = (-)^s[1-(s)^s/C_s^s] \qquad K_s = (-)^s(s/\rho)^s\, L_s \tag{6.36}$$

Then,

$$(1-v)^{\xi} = \sum_{s=0}^{\xi} K_s \binom{\xi}{s} [v(1-C_s)]^s\, [1-v(1-C_s)]^{\xi-s} \tag{6.37}$$

$T_s(\lambda)$ replaced by

$$U_s(\lambda) = \binom{\xi}{s} [v(1-C_s)]^s\, [1-v(1-C_s)]^{\xi-s} \tag{6.38}$$

which has peaks at the root of

$$s = v\xi(1-C_s) = vs\ \xi/(\rho+s)$$

The lower root $s = 0$ is irrelevant the upper root is $S_0 = v\xi - \rho$.

Let $H_s = 1 * s/(\rho + s) + (-)^s (s/\rho)^s \, L_s$ (6.39)

Substituting (5.39) in (5.23)

$$\delta(\xi - x) \sim \sum_{s=0}^{\xi} \left(1 + \frac{s}{\rho + s}\right) (-)^s \binom{\xi}{s} \left(\frac{\rho}{\rho + s}\right)^{\xi} \sum_{s=0}^{\xi} L_s \binom{\xi}{s} \left(\frac{s}{\rho + s}\right)^s \left(\frac{\rho}{\rho + s}\right)^{\xi - s}$$

(6.40)

$$= A + B$$

The second term B can be expressed as $\sum L_s U_s(1)$ put $z = s/\xi$ and $U_s(1) = U(z, 1)dz$. The upper root (5.38) is $S_0 = \xi - \rho$ and provided that is for from zero.$U(z, 1)$ will have an isolated peak $z_0 = 1 - \rho/\xi$ near which

$$U(z, 1) \sim \left[\frac{\xi}{2\pi z_0 (1 - z_0)}\right]^{1/2} exp\left\{-\frac{\xi \, [1 - \lambda C'(z_0)]^2}{2 z_0 (1 - z_0)} (z - z_0)^2\right\} \qquad (6.41)$$

Assume that $L_s = L(z)$.

$$B \sim L(z_0)/[1 - C'(z_0)] = \rho L_{\xi - \rho}/(\xi - \rho) \qquad (6.42)$$

where ξ is much greater than ρ which is itself large under these condition there is a remarkable simple approximation for $P(x/\xi, \eta, \rho)$ in the region of large epidemics. The term in A die any away rapidly and their sum approximates to,

$$\sum_{s=0}^{\infty} \left(-\xi \, e^{-\xi/\rho}\right)^s \Big/ s! = exp\left(-\xi^{-\xi/\rho}\right) \qquad (6.43)$$

Hence,

$$\rho L_{\xi/\rho}/(\xi-\rho) \sim -\exp\left(-\xi\, e^{-\xi/\rho}\right) \tag{6.44}$$

The formula for $P(0/\xi,\eta,\rho)$ corresponding to (6.40) is

$$P\left({}^{0}/_{\xi,\eta,\rho}\right) \sim \sum_{s=0}^{\xi}\left(1+\frac{s}{\rho+s}\right)(-)^{s}\binom{\xi}{s}\left(\frac{\rho}{\rho+s}\right)^{\xi+\eta}$$

$$+\sum_{s=0}^{\xi} L_s\binom{\xi}{s}\left(\frac{s}{\rho+s}\right)\ \left(\frac{\rho}{\rho+s}\right)^{\xi-x+\eta}$$

Suppose that η is small. Compared with (6.40) to the order of approximation considered the effect of the extra factor $[\rho/(\rho+s)]^{\eta}$ is to leave the first term unaltered and to multiply the second term by $[\rho/(\rho+s_0)]^{\eta} = (\rho/\xi)^{\eta}$. It follows that,

$$P(0/\xi,\eta,\rho) \sim [1-(\rho/\xi)^{\eta}]\ exp\left(-\xi^{-\xi/\rho}\right) \tag{6.45}$$

then from () for small values of x

$$P\left({}^{x}/_{\xi,\eta,\rho}\right) \sim \left[1-\left({}^{\rho}/_{\xi}\right)^{\eta}\right]\frac{\left(\xi e^{-\xi/\rho}\right)^{x}}{x!}\ exp\left(-\xi^{-\xi/\rho}\right) \tag{6.46}$$

The threshold is large but the population size is much larger the distribution of the number remaining uninfected in a large epidemic has approximately the Poisson form with the deterministic mean $\xi e^{-\xi/\rho}$.

$$\rho \sim \left(\rho/\xi\right)^{\eta} \frac{\eta \rho^{w} \xi^{w+\eta}}{(\rho+w)^{2w+\eta}} \frac{(2w+\eta-1)!}{w!\,(w+\eta)!}$$

A More Refined Approximation:

When ξ is not much larger then ρ.

$$A = \frac{1}{(\xi-1)!} \int_{0}^{\infty} u^{\xi-1} (2-u/\xi) \left(1-e^{-u/\rho}\right)^{\xi} e^{-u}\, du$$

$$A = \frac{\xi^{\xi}}{(\xi-1)!} \int_{0}^{\infty} v^{\xi-1} (2-v) \left(1-e^{-v\xi/\rho}\right)^{\xi} e^{-\xi v}\, dv \qquad (6.48)$$

Threshold theorems

Rajarshi [34] gives a simpler proofs of two threshold theorems for a general stochastic epidemic using reflection principle.

A fairly elementary proof for the threshold theorems due to, Williams and Whittle, simpler than Bailey[3] is given. The proofs are based on an application of the reflection principle through the ballot problem.

Some important definitions

One dimensional random walk

It is a Markov Chain whose state space is a finite or infinite subset a, a+1,……b of the integers in which the particle if it is in state i can in a single transition either stay i or move to one of the adjacent states i – 1 , i + 1.

Total size of the Epidemic

It is the total number of removals after the elapse of a very long, ideally infinite period of time.

Intensity of the epidemic

It is the proportion of the total number of susceptibles that finally contracts the disease and is denotes by i.

Relative removal rate

The ratio of removal rate to infection rate is known as the relative removal rate and is denoted by $= \gamma/\beta$.

Relative removal rate per susceptible

The ratio of removal rate to the number of susceptible is called the relative removal rate per susceptible and is denoted by $\theta = \rho/n$.

Reflection principle

This principle relates to the fact that there is a one to one correspondence between all paths from A(a1,a2) to B(b1,b2) which touch or cross the X – axis and all paths from $A'(a1, -a2)$ to B.

Ballot problem

Suppose that in a ballot candidate P scores p votes and candidate Q scores q votes where p > q. The probability that throughout the counting there are always more votes for P than for $Q = \frac{p-q}{p+q}$.

Ballot Theorem 6.1

Let n and x be positive integers. There are exactly $x/n\ Nn, x$ paths $(S1, \ldots \ldots Sn = x)$ from the origin to (n, x) such that $S1 > 0 \ldots . Sn > 0$.

Proof

Clearly there exists exactly as many admissible paths as there are paths from $(1,1)$ to (n, x) which neither touch or cross the t axis.

The number of such paths equals

$$N_{n-1,x-1} - N_{n-1,x+1} = \binom{p+q-1}{p-1} - \binom{p+q-1}{p}$$

$$\text{R.H.S} = N_{n,x}\binom{p-q}{p+q}$$

Recently a more direct algebraic proof of the threshold theorem for large n has been obtained by William. Also an ingenious method of investigating limiting behaviour more fully has been found by Whittle.

William's Threshold Theorem 6.2

If n is sufficiently large then $P(\theta)$ the probability of a finite epidemic size is given by $P(\theta) = \begin{cases} \theta^a \ if \ \theta < 1 \\ 1 \ if \ \theta \ \geq 1 \end{cases}$

Proof

Let $\{X(t), Y(t), Z(t), t \geq 0\}$ be a general stochastic epidemic with β and γ as the infection and removal rates respectively. Where $X(t)$ is the number of susceptibles at t, $Y(t)$ is the number of infectious persons at t and $Z(t)$ the number of removal in $(0, t)$ we assume that

$$P[x(0) = n, y(0) = a, z(0) = 0] = 1$$

Let the intensity of an epidemic be denoted by i.

Let $W = \lim_{t\to\infty} Z(t) - a$ be the size of an epidemic.

Then with $P(\omega) = P(W = \omega) = \pi_i = \sum_{W=0}^{n_i} P(\omega)$ gives the probability of an epidemic with intensity not greater than i.

Let us regard the progress of the epidemic interms of the succession of population states represented by the points (r, s). The process is thus seen as a random walk starting from the point (n, a) and ending at one of the points $(n - w, 0)$.

$0 \leq w \leq n$, with an absorbing barrier along the line s = 0.

The transitional probabilities are

$$P_r[(r,s) \to (r-1, s+1)] = r/r+\rho$$

and $P_r[(r,s) \to (r, s-1)] = \rho/r+\rho$

The formula required can be written down more or less directly by considering the sum of the probabilities of all possible paths from (n,a) to $(n-w,0)$. One way of doing this is to take all paths to the point $(n-w,1)$ which do not go below the line s = 1 followed by the final step to $(n-w,0)$ with probability $\rho/n+\rho-w$

Let us obtain

$$P(W) = \frac{\lfloor n\rho^{a+w}}{\lfloor (n-w)(n+\rho).....(n+\rho-w)} \alpha^{\sum (n+\rho)^{\alpha_0}(n+\rho-1)^{\alpha_1}.....(n+\rho-w)^{\alpha_w}}$$

Where the summation is over all compositions $\boldsymbol{a+w-1}$ into $\boldsymbol{w+1}$ parts such that

$$0 \leq \sum_{j=0}^{i} \alpha_j < a+i-1$$

for $0 \leq i < w-1$ and $1 \leq \alpha_w \leq a+w-1$.

Let A be the collection of all $\bar{\alpha} = (\alpha_0, \alpha_1, \dots\dots \alpha_w)$ such that α_i is a non negative integer for every i.

$$\alpha_0 + \alpha_1 + \cdots \ldots . \alpha_j < a + j \text{ for j = 0,1,2,.....w -1}$$

$$\alpha_w \geq 1 \; and \; \alpha_0 + \alpha_1 + \cdots \ldots . + \alpha_w = a + w$$

Then

$$P(w) = \frac{n(n-1) \ldots \ldots \ldots (n-(w-1))}{(n+\rho)(n+\rho-1) \ldots . (n+\rho-(w-1))} \rho^{a+w} \sum_{\alpha \in A} \prod_{r=0}^{w} (n+\rho-r)^{-\alpha_n}$$

For a fixed w, (and a sufficiently large n),

$$\frac{\mathrm{n(n-1) \ldots \ldots \ldots (n-(w-1))}}{\mathrm{(n+\rho)(n+\rho-1) \ldots . (n+\rho-(w-1))}} \backsimeq \frac{\mathrm{n^w}}{\mathrm{(n+\rho)^w}}$$

$$\prod_{r=0}^{w} (n+\rho-r)^{-\alpha_n} = \prod_{r=0}^{w} \frac{1}{(n+\rho-r)^{\alpha_n}}$$

$$= \frac{1}{(n+\rho-r)^{\alpha_0}} \cdot \frac{1}{(n+\rho-r)^{\alpha_1}} \cdots \cdot \frac{1}{(n+\rho-r)^{\alpha_w}} \ldots \ldots$$

$$= \frac{1}{(n+\rho)^{\alpha_0}\left[1-\frac{r}{n+\rho}\right]^{\alpha_0}} \cdot \frac{1}{(n+\rho)^{\alpha_1}\left[1-\frac{r}{n+\rho}\right]^{\alpha_1}} \ldots \ldots \ldots \ldots \ldots$$

$$\frac{1}{(n+\rho)^{\alpha_w}\left[1-\frac{r}{n+\rho}\right]^{\alpha_w}} . \ldots$$

$$= \frac{1}{(n+\rho)^{\alpha_0}(n+\rho)^{\alpha_1} \ldots \ldots . . (n+\rho)^{\alpha_w}}$$

$$= \frac{1}{(n+\rho)^{\alpha_0+\alpha_1+\cdots \ldots \ldots +\alpha_w}} = \frac{1}{(n+\rho)^{a+w}}$$

$$= \left(\frac{1}{n+\rho}\right)^{a+w}$$

Lemma 6.3

Let x and y be two positive integers. Suppose on a two dimensional plane, we allow only the two types of transition: (x', y') to $(x'-1, y'-1)$ (to the north west) and (x', y') to $(x', y'-1)$ (to the south). Where x' and y' are non negative integers. Then the total number of ways of reaching (0,0) from (x,y) without touching or crossing the x axis is given by

$$\binom{2x+y-1}{x}.\frac{y}{x+y}$$

To arrive at (0,0) we first observe that there have to be x transitions of the type I and x + y transitions of the type II. To every transition of the north west type we associate a south east transition and to every transition to the south we associate a north east transition. In this new walk, the condition of not touching or crossing the x axis in naturally retained. The situation is similar to the ballot problem.

Out of 2x + y total votes, the winner wins by y votes. The total number of ways in which he maintains the lead throughout the counting is

$$\left(N_{2x+y,y}\right).\frac{y}{x+y}$$

Where

$$Nm,r = \binom{m}{1/2\ (m-r)}$$

$$N_{2x+y,y} = \binom{2x+y}{1/2\ (2x+y-y)} = \binom{2x+y}{x}\frac{y}{x+y}$$

Going back to the general stochastic epidemic we imbed a discrete time process and plot the number of susceptibles and the number of infectives on the (x,y) plane. Let us notice that the north west transition is a new infection and the transition to the south corresponds to a removal of a case. Thus in a two dimensional random walk, subjected to the above conditions, we are looking for the number of paths reaching (n – w , 0) from (n , a) .

$$P(w) = \left(\frac{n}{n+\rho}\right)^{w} \rho^{a+w} \left(\frac{1}{n+\rho}\right)^{a+w}$$

Taking x = w , y = a

$$= \left(\frac{n}{n(1+\rho/n)}\right)^{w} \frac{\rho^{a+w}}{\rho^{a+w}(1+\rho/n)^{a+w}} \binom{2x+y}{x}.\frac{y}{2x+y}$$

$$= \left(\frac{1}{1+\theta}\right)^{w} \frac{1}{(1+1/\theta)^{a+w}} \binom{2w+a}{w}.\frac{a}{2w+a}$$

$$= \frac{\lfloor 2w+a}{\lfloor w \cdot \lfloor w+a}\, a \left(\frac{1}{1+\theta}\right)^{w} \left(\frac{\theta}{1+\theta}\right)^{a+w} \frac{a}{2w+a}$$

$$= \frac{\lfloor 2w+a-1}{\lfloor \underline{w} \cdot \lfloor \underline{w+a}} a \left(\frac{1}{1+\theta}\right)^{w} \left(\frac{\theta}{1+\theta}\right)^{a+w}$$

$$p = \frac{\theta}{1+\theta}, q = 1-p, \qquad q = 1 - \frac{\theta}{1+\theta} = \frac{1}{1+\theta}$$

$$P(W) = \frac{a\lfloor 2w+a-1}{\lfloor \underline{w} \cdot \lfloor \underline{w+a}} p^{a+w} q^{w}$$

P(w) is wth term in the expansion $\left(1 - \frac{|p-q|}{2q}\right)^{a}$

$$\sum_{w=0}^{\infty} P(w) = \left[\frac{1 - \left|\frac{\theta}{1+\theta} - \left(1 - \frac{\theta}{1+\theta}\right)\right|}{2\left(\frac{1}{1+\theta}\right)}\right]^{a}$$

$$= \frac{[1+\theta-|\theta-1|]^{a}}{2} = [\min(\theta,1)]^{a}$$

$$= \left[\frac{(1+\theta)+(\theta-1)}{2}\right]^{a} = \theta^{a} \quad \begin{matrix} if\ \theta < 1 \rightarrow \theta - 1 < 0 \\ \theta > 1, \theta - 1 > 0 \end{matrix}$$

$$= \frac{(1+\theta)-(\theta-1)}{2} = \frac{2}{2} = 1$$

Therefore $P(\theta) = \theta^{a}$ if $\theta < 1$, if $\theta \geq 1$.

(i.e) when the relative removal rate per susceptible θ is greater than or equal to unity there is no true epidemic, while if it is less than unity a true epidemic can occur with probability $1 - \theta$.

Whittle's Threshold Theorem 6.4

For an epidemic with intensity i, we have

$$[\min(\theta, 1)]^a < \pi_i < \left[\min\left(\frac{\theta}{1-i}, 1\right)\right]^a$$

Proof:-

Let us consider an epidemic $\{X(t), Y(t), Z(t); \lambda, \mu, t > 0\}$ for which the conditional probability of a new infection in $(t, t+h)$ is $\lambda y(t)h + o(h)$ and the same for a removal is $\mu y(t)h + o(h)$.

Then the epidemic with intensity is faster than the epidemic with $\lambda = \beta n(1-i)$ $\mu = \gamma$ and it is slower than the epidemic with $= \beta n$ $\mu = \gamma$.

Let $P(w, \lambda, \mu)$ denotes the probability that $W = w$ for $\{x(t), y(t), z(t); \lambda, \mu, t > 0\}$

$$P(w, \lambda, \mu)$$

$$= \frac{\lfloor 2w + a - 1}{\lfloor w \cdot \lfloor w + a} a \left(\frac{\theta}{1+\theta}\right)^{a+w} \left(\frac{1}{1+\theta}\right)^{w}$$

$$= \frac{\lfloor 2w + a - 1}{\lfloor w \cdot \lfloor w + a} a \left(\frac{\rho/n}{1+\rho/n}\right)^{a+w} \left(\frac{1}{1+\rho/n}\right)^{w}$$

$$= \frac{\lfloor 2w+a-1}{\lfloor w \cdot \lfloor w+a} a \left(\frac{\rho}{1+\rho} \right)^{a+w} \left(\frac{1}{1+\mu/\lambda} \right)^{w}$$

$$= \frac{\lfloor 2w+a-1}{\lfloor w \cdot \lfloor w+a} a \left(\frac{\mu/\lambda}{1+\mu/\lambda} \right)^{a+w} \left(\frac{1}{1+\mu/\lambda} \right)^{w}$$

$$= \frac{\lfloor 2w+a-1}{\lfloor w \cdot \lfloor w+a} a \left(\frac{\mu}{\lambda+\mu} \right)^{a+w} \left(\frac{1}{1+\mu/\lambda} \right)^{w}$$

$$= \frac{\lfloor 2w+a-1}{\lfloor w \cdot \lfloor w+a} a \left(\frac{\mu}{\lambda+\mu} \right)^{a+w} \left(\frac{\lambda}{\lambda+\mu} \right)^{w}$$

$$P[n,\lambda,\mu] = 1 - \sum_{w=0}^{n-1} P(w,\lambda,\mu)$$

$$\sum_{w=0}^{\infty} P(w,\lambda,\mu) = [(min\{(\lambda/\mu)^{-1},1\})]^{a}$$

and comparing the epidemic with intensity i

$$\rho = \mu/\lambda \quad , \pi_i = \sum_{w=0}^{n_i} P_w$$

(i) $\rho < n(1-i), (\rho/n)^a < \pi_i < (\rho/n(1-i))^a$

(ii) $n(1-i) \leq \rho < n, (\rho/n)^a \leq \pi_i < 1$

(iii) $\rho < n(1-i), (\rho/n)^a < \pi_i < (\rho/n(1-i))^a$

Therefore $\rho \geq n$, there is zero probability of an epidemic exceeding any pre assigned intensity i. While $\rho < n$, the probability of an epidemic is approximately $1-(\rho/n)^a$ for small i. Returning to the fast and slow processes with $\lambda = \beta n$ and $\lambda = \beta n(1-i)$ respectively.

$$\sum_{0}^{n_i} P_w(\beta n) \leq \pi_i = \sum_{0}^{n_i} P_w \leq \sum_{0}^{n_i} P_w(\beta n - \beta n_i)$$

For sufficiently large n,

$$[min(\rho/n, 1)]^a \leq \pi_i \leq [min(\rho/n(1-i), 1)]^a \quad ()$$

Where $\rho = \mu/\lambda$.

Slower process $\mu/\lambda = \gamma/\beta n(1-i) = \rho/n(1-i)$.

Faster process $\mu/\lambda = \gamma/\beta n = \rho/n$.

Three main cases follow from ()

(i) $\rho < n(1-i), (\rho/n) < \pi_i < (\rho/n(1-i))^a$

(ii) $n(1-i) \leq \rho < n, (\rho/n)^a \leq \pi_i \leq 1$

(iii) $n < \rho, \pi_i = 1$

CHAPTER VII

SIMPLER PROOFS OF TWO THRESHOLD THEOREMS FOR A GENERAL STOCHASTIC EPIDEMIC

Threshold theorems

A fairly elementary proof for the threshold theorems due to, Williams and Whittle, simpler than Bailey[3] is given. The proofs are based on an application of the reflection principle through the ballot problem and the exact distribution of the size of the epidemic as derived by Foster [14]. William's threshold theorem is extended to an epidemic with multiple introduction of cases.

Introduction

Let $\{(X(t), Y(t), Z(t), t \geqq 0)\}$ be a general stochastic epidemic with β and γ as the infection and removal rates respectively, where $X(t)$ = number of susceptibles at t, $Y(t)$ = number of infectious persons at t and $Z(t)$ = number of removals in $(0, t)$.

$$P[X(0) = n; Y(0) = a; Z(0) = 0] = 1.$$

Let the intensity of an epidemic be denoted by i . Let $W = lim_{t\to\infty} Z(t) - a$ be the size of the epidemic. Then with $P(w) = P[W = w\}, \pi_i = P(w)$ gives the probability of an epidemic with intensity not greater than i.

Let $\rho = \gamma/\beta$ be the relative removal rate and $\theta = \rho/n$ be the relative removal rate per susceptible.

William's Threshold Theorem 7.1

If n is sufficiently large then $P(\theta)$ the probability of a finite epidemic size is given by

$$P(\theta) = \begin{cases} \theta^a \; if \; \theta < 1 \\ 1 \; if \; \theta \geq 1 \end{cases}$$

Let A be the collection of all $\bar{\alpha} = (\alpha_0, \alpha_1, \ldots\ldots \alpha_w)$ such that α_i is a non negative integer for every i.

$$\alpha_0 + \alpha_1 + \cdots \ldots \alpha_j < a + j \text{ for j = 0,1,2,.....w -1}$$

$$\alpha_w \geq 1 \; and \; \alpha_0 + \alpha_1 + \cdots \ldots + \alpha_w = a + w$$

Then

$$P(w) = \frac{n(n-1) \ldots\ldots\ldots (n-(w-1))}{(n+\rho)(n+\rho-1) \ldots . (n+\rho-(w-1))} \rho^{a+w} \sum_{\alpha \in A} \prod_{r=0}^{w} (n+\rho-r)^{-\alpha_n} \tag{7.1}$$

For a fixed w, (and a sufficiently large n),

$$\frac{n(n-1) \ldots\ldots\ldots (n-(w-1))}{(n+\rho)(n+\rho-1) \ldots . (n+\rho-(w-1))} \approx \left(\frac{n}{n+\rho}\right)^w \tag{7.2}$$

and

$$\prod_{r=0}^{w}(n+\rho-r)^{-\alpha_r} \approx \left(\frac{1}{n+\rho}\right)^{a+w} \tag{7.3}$$

Lemma 7.2

Let x and y be two positive integers. Suppose on a two dimensional plane, we allow only the two types of transition: (x', y') to $(x'-1, y'-1)$ (to the north west) and (x', y') to $(x', y'-1)$ (to the south). Where x' and y' are non negative integers. Then the total number of ways of reaching (0,0) from (x, y) without touching or crossing the x axis is given by

$$\binom{2x+y-1}{x}.\frac{y}{x+y} \tag{7.4}$$

To arrive at (0,0) we first observe that there have to be x transitions of the type I and $x + y$ transitions of the type II. To every transition of the north west type let us associate a south east transition and to every transition to the south we associate a north east transition. In this new walk, the condition of not touching or crossing the x axis in naturally retained. The situation is similar to the ballot problem.

Out of $2x + y$ total votes, the winner wins by y votes. The total number of ways in which he maintains the lead throughout the counting is

$$\left(N_{2x+y,y}\right).\frac{y}{x+y}$$

Where

$$Nm,r = \binom{m}{1/2\ (m-r)}$$

$$N_{2x+y,y} = \binom{2x+y}{1/2\ (2x+y-y)} = \binom{2x+y}{x}\frac{y}{x+y}$$

Going back to the general stochastic epidemic we imbed a discrete time process and plot the number of susceptibles and the number of infectives on the (x, y) plane. Then we notice that the north west transition is a new infection and the transition to the south corresponds to a removal of a case. Thus in a two dimensional random walk, subjected to the above conditions, we are looking for the number of paths reaching $(n - w, 0)$ from (n, a) .Taking $x = w, y = a$

$$P(w) = \frac{(2w+a-1)!\,a}{w!\,(w+a)!}\ \left(\frac{\theta}{\theta+1}\right)^{a+w}\ \left(\frac{1}{1+\theta}\right)^{w} \tag{7.5}$$

Let $p = \theta/(1+\theta)$ and $q = 1-p$. Let us seen that $P(w)$ is the w the term in the expansion $\{(1-|p-q|/2q)\}^a$. Thus

$$\sum_{w=0}^{\infty} P(w) = (min\{\theta, 1\})^a \tag{7.6}$$

This completes the proof for William's Theorem.

Whittle's Threshold Theorem 7.3

For an epidemic with intensity i, we have

$$[min(\theta, 1)]^a < \pi_i < \left[min\left(\frac{\theta}{1-i}, 1\right)\right]^a$$

provided n is sufficiently large.

Proof

Let us consider an epidemic $\{X(t), Y(t), Z(t); \lambda, \mu, t > 0\}$ for which the conditional probability of a new infection in $(t, t+h)$ is $\lambda y(t)h + o(h)$ and the same for a removal is $\mu y(t)h + o(h)$.

Then the epidemic with intensity is faster than the epidemic with $\lambda = \beta n(1-i)$ $\mu = \gamma$ and it is slower than the epidemic with $\lambda = \beta n, \quad \mu = \gamma$.

Let $P(w, \lambda, \mu)$ denotes the probability that $W = w$ for $\{x(t), y(t), z(t); \lambda, \mu, t > 0\}$

$$P(w; \lambda, \mu) = \frac{(2w + a - 1)!\, a}{w!\,(w+a)!} \left(\frac{\lambda}{\lambda+\mu}\right)^w \left(\frac{\mu}{\lambda+\mu}\right)^{w+a};$$

$$w = 0,1,2, \ldots\ldots, n-1$$

$$P[n; \lambda, \mu] = 1 - \sum_{w=0}^{n-1} P(w; \lambda, \mu) \tag{7.7}$$

$$\sum_{w=0}^{\infty} P(w,\lambda,\mu) = [(min\{(\lambda/\mu)^{-1},1\})]^{a}$$

and comparing the epidemic with intensity i, with the faster and slower epidemics, the proof is complete.

CHAPTER VIII

ON THE ASYMPTOTIC DISTRIBUTION OF THE SIZE OF A STOCHASTIC EPIDEMIC

Introduction

For a stochastic epidemic of the type it was shown that when the threshold is large but the population sign in much larger, the distribution of this number remaining un infected in a large epidemic has approximately the Poisson form. A sample proof is given without use of Daniel's assumption that the original number of infectives is small, based on a construction of the epidemic process which is more explicit then the usual description are given by [39].

Let a population which at time $t = 0$, consist of $X(0) = n$ healthy individuals and $Y(0) = m$ individual with a contagious infection. An epidemic in such a population is often modeled by a continuous time Markov process as follows.

If $X(t)$ and $Y(t)$ are the number of healthy individual and infectious individual respectively, present at time t then the transition probabilities are given by

$$P\{X\,(t+\delta), Y(r+\delta) \;=\; (\,x', y'\,)/(\,X(t), Y(t) \;=\; (x, y))\}$$

$$= \; xy\delta + o(\delta)\; for\; \{(x', y') = \; (x-1, y+1)\}$$

$$= \; \rho y\delta \; + \; o(\delta)\; for\; (x', y') = \; (x, y-1)$$

$$= \; 1 - xy\delta - \rho y\delta + o(\delta)\; for\; (x', y') = (x, y)$$

(8.1)

The transitions listed represent the infection of a healthy individual, the removal of an infectious individual from the population and no change respectively. All other possible transition in $[t\,, t+\,\delta]$ are assumed to have collective probability$o(\delta)$. The positive constant ρ is called thresholds on the relative removal rate of the epidemic.

The starts of the form (x ,0) are absorbing so that no more transition occur after the last infectious individuals has been removed.

Absorption at ($x, 0$) means that x individuals have escaped infection at end of the epidemic and that $X(\infty) \;=\; x$, when $(\infty) = \lim_{t\to\infty} X(t)$.

Construction of the Epidemic Process

Let the n originally healthy individuals be indexed by $i,\; 1 \leqq \; i \leqq \; n$ and let m originally infectious individuals be indexed by $j, 1 \;\leqq\; j \leqq \; m$.

Let $(\hat{r}_j)_{j=1}^{m}$ and $(r_j)_{j=1}^{n}$ be i.i.d random variables unit density $\rho e^{-\rho t}$ on $[0, \infty]$.

Individual j in the original infectious group will remain infectious group will remain infectious for r_j time units before removal from the population. Individual I in the original healthy group will remain infectious for r_i time unit of an individual becomes infected.

Let $\{ I_i \}_{i=1}^{n}$ be i.i.d random variables with density e^{-1} on $[0, \infty]$ independent of $\tilde{r}_j's$ and $r_i's$.

The variable I_i is resistance of infection of an individual i in the original healthy group. Let $\{ I_{(k)} \}_{k=1}^{n}$ be the associated order varieties so that $l_{(1)} < l_{(2)} < \ldots\ldots\ldots\ldots\ldots < l_{(n)}$. Let $r^{(k)} = r$ if $I_{(k)} = 1$.

The originally infected individual j remains in the population for r_j time units after which infected individuals is removed. The healthy individual i accumulates exposure to infection at a rate equal to the number of infected individuals present.

When the total exposure to infection of healthy individuals i reaches I_i, individual i become infected and then remain the population for an additional r_i time units before removal.

Suppose $(X(t), Y(t) = (x, y))$ the probability that the particular infected individual is removed in the time interval $[t, t + \delta]$ is $\rho\delta + o(\delta)$ because the distribution of the $r_j's$ and $r_i's$ has constant hazard rate ρ.

The probability that exactly one of the y infected individuals is removed in $[\, t, t + \delta \,]$ is therefore $\rho\, y\, \delta + o(\delta)$.

The probability that a particular one of these healthy individuals become infected in $[\, t, t + \delta \,]$ is $\rho y\delta + o(\delta)$. So that the probability that exactly one of the healthy individuals become infected is $x\, y\, \delta + o(\delta)$.

The Markov property follows from the memory less property of the exponential distribution.

Let v be the number of new infectious occurring during the course of the epidemic.

If $l_{(1)} > \sum_{j=1}^{m} \hat{r}_j$ then all originally infectious individuals are removed before the resistance to infectious of any healthy individuals has been exceeded so that $v = 0$.

Otherwise the originally healthy individuals associated with $l_{(1)}$, becomes the first new infections and $v \geqq 1$.

An easy induction argument shows that $v+1$ is the smallest k, $1 \leqq k \leqq n$ for which

$$l_{(k)} > \sum_{j=1}^{m} \hat{r}_j + \sum_{i=1}^{k-1} r^{(i)} \tag{8.2}$$

in this inequality does not hold for any $k, 1 \leqq k \leqq n$ then $v = n$.

Let us define $R = \sum_{j=1}^{m} \hat{r}_j + \sum_{i=1}^{v} r^{(i)}$ then R is the amount of exposure to infection with stood by those individuals who remain healthy at the end of the epidemic and $X(\infty) = n - v$ is the number of $l_{(i)}$'s greater then R.

Theorem 8.1

If $n_k \to \infty$ *and* $\rho_k \to \infty$ and

$$n_k \, exp\left\{ - \frac{n_k + m_k}{\rho_k} \right\} \to b, \quad 0 < b < \infty \tag{8.3}$$

Then $X_k(\infty)$ converges distribution to a Poisson random variable with mean b.

Proof

The subscript k will again be suppressed

Taking logarithms in $ne^{-(m+n)/\rho} \to b$ yields

$$\Longrightarrow log\, n - \frac{n+m}{\rho} \to log\, b, \text{ so that}$$

$$\rho \sim m + n \,/\, log\, n$$

This ρ is $o(m+n)$ *but* $(m+n)^{\gamma}$ *is* $o(\rho)$ *for* $0 < \gamma < 1$.

Lemma 8.2

Let $0 < \in < 1$ be given if $\rho < \in^{2}(m+n)$ then

$$P\{x(\infty) > \in (m+n)\} < \left[\frac{\rho}{\in(m+n)}\right]^{m} < \in^{m} \leqq \in$$

Proof

The population of infected individuals as a continuous time birth and death process with a variable birth rate. The ratio of death rate to birth rate is $\rho/\, X(t)$ which is less than $\rho/\in (m+n)$, until $X(t) \leq \in (m+n)$.

The probability that a birth and death process starting at m and with a death rate to birth rate ratio $q < 1$ is even absorbed 0 is q^{m}.

Lemma 8.3

Let $0 < \in < 1$ for n sufficiently large

$$\rho\left\{R < \frac{(1-2\in)(m+n)}{\rho}\right\} < 2 \in. \qquad (8.4)$$

Proof

Using lemma (8.2) , R is greater than the sum of the first $(1-\in)(m+n)$ terms of $\{\tilde{r}_1, \tilde{r}_2, \ldots, \tilde{r}_m, \tilde{r}^{(1)}, \tilde{r}^{(2)}, \ldots\ldots, \tilde{r}^{(n)}\}$ with probability greater then $(1-\in)$

for sufficiently larger n.

The sum of the first $(1-\in)(m+n)$ first terms has mean $(1-\in)(m+n)/\rho$ and variance $(1-\in)(m+n)/\rho^2$.

Lemma 8.4

The number of $l_i's$ which are greater than $(1-\in)(m+n)/\rho$ is binomial $(n, e^{-(1-2\in)m+n/\rho})$ this distribution has mean $ne^{-(1-2\epsilon)m+n/\rho} \sim n\left(\frac{b}{n}\right)^{1-2\in}$

$$= b^{1-2\in} n^{2\in} \qquad (8.5)$$

Proof

It is easy to see that $X(\infty)$ in $o(1/n)$ in probability. Thus except on a set of small probability R is greater than the sum of the first $m+n-1/n$ terms of $\{\tilde{r}_1, \tilde{r}_2, \ldots, \tilde{r}_m, r^{(1)}, r^{(2)}, \ldots\ldots, r^{(n)}\}$.

R is of course less than or equal to the sum of all the terms. The probability approaching,

$$\frac{m+n}{\rho} - \frac{(m+n)^{2/3}}{\rho} < R < \frac{m+n}{\rho} + \frac{(m+n)^{2/3}}{\rho}$$

The number of l_i's greater than

$$\frac{m+n}{\rho} \pm \frac{(m+n)^{2/3}}{\rho}$$

is distributed as a binomial

$$\left(n, exp\left\{\frac{m+n}{\rho} - \frac{(m+n)^{2/3}}{\rho}\right\}\right)$$

which has mean

$$n\ exp\left\{-\frac{m+n}{\rho} \mp \frac{(m+n)^{2/3}}{\rho}\right\} \sim b\ exp\left\{\mp \frac{(m+n)^{2/3}}{\rho}\right\} \to b.$$

Thus with probability approaching $1, X(\infty)$, is less than a

Binomial $\left(n, exp\left\{-\frac{m+n}{\rho} + \frac{(m+n)^{2/3}}{\rho}\right\}\right)$ random variables and greater than a

Binomial $\left(n, exp\left\{-\frac{m+n}{\rho} - \frac{(m+n)^{2/3}}{\rho}\right\}\right)$ random variables.

Since both of these distribution that converge in law to a Poisson unit mean b.

CHAPTER IX

REPRODUCTION NUMBERS AND THRESHOLDS IN STOCHASTIC EPIDEMIC MODELS HOMOGENEOUS POPULATION

Introduction:

Let us compare threshold results for the deterministic and stochastic versions of the homogeneous SI model with recruitment death due to the disease, a background death rate, and transmission rate $\beta cXY/N$. If an infective is introduced into a population of susceptibles, the basic reproduction number, R_0 plays a fundamental role for both, though the threshold results differ somewhat. For the deterministic model, no epidemic can occur if $R_0 \leq 1$ and an epidemic occurs if $R_0 > 1$ For the stochastic model we find that on average, no epidemic will occur if $R_0 \leq 1$. If $R_0 > 1$, there is a finite probability, but less than 1, that an epidemic will develop and eventuate in an endemic quasi-equilibrium. However, there is also a finite probability of extinction of the infection, and the probability of extinction decreases as R, increases above 1 is given by [21].

The basic reproduction number is defined as follows. Let c be the average number of persons contacted per person per unit time, and let β be the probability of transmission per contact between a susceptible and an infected. The combined parameter $\lambda = c\beta$ has units $time^{-1}$ and is called the number of

effective contacts per person per unit time. Let D be the mean duration of the infectious period. Then the number of contacts effective in transmission per infective if all contacts are with susceptible is R_0, the basic or initial reproduction number where $R_0 = c\beta D$. R_0 is a dimonsionless number.

If the population is a large population of susceptibles and let us introduce one infective who is just beginning the infectious period, R_0 must be greater than 1 for an epidemic to take off.

$$c\beta D - 1 > 0.$$

Let us consider the concept of a threshold for epidemic takeoff directly related to the basic reproduction number. If $R_0 > 1$, an epidemic starts; then as the fraction of susceptibles decreases the epidemic slows, more so if those recover are immune to the disease. If new susceptibles are introduced at a constant rate, an endemic steady state can occur when

$$R = R_0 S = 1.$$

Here S is the fraction of susceptibles in the population. R has also been called the reproductive number or replacement number. Let R changes as the fraction of susceptibles changes.

In this chapter let us examine the deterministic and stochastic formulations for SI, SIS, SIR and $SIRS$ models for homogeneous populations.

The Homogeneous SI models

The Deterministic Model

Let

X, Y The number of susceptibles and infectives respectively. Both are continuous, non negative variables

U A constant rate of recruitment of new susceptibles into the population.

μ The rate constant for competing deaths, assumed to be the same for susceptibles and infecteds. Thus, the rate at which susceptibles die due to all causes is μX.

k The rate constant for deaths due to the disease.

c The mean number of persons contacted per person unit time. These contacts are, by definition, the type of contacts that can potentially transmit the disease.

β The probability of transmission of the disease for a contact of a susceptible with an infected.

The Deterministic Equations:

The total number of persons contacted per unit time by all susceptibles is cX. Assuming that the contacts are randomly distributed over susceptibles and infecteds in the population, the fraction $Y/(X + Y - 1)$ of these contacts is with infecteds. Let us use $Y/(X + Y)$ in place of $Y/(X + Y - 1)$ because X

and Y are continuous variables. It makes little difference for $X + Y$ large, and the use of $Y/(X + Y - 1)$ leads to difficulties for $X + Y \leq 1$. For comparison with the stochastic model in which X and Y are counted in integral units, let us use $Y/(X + Y - 1)$ in the deterministic model and avoid the region $X + Y \leq 1$. Then, since β is the fraction of contacts between susceptibles and infecteds in which there is transmission, the rate at which susceptibles are infected must be

$$c\beta \frac{XY}{X + Y - 1}$$

Thus the differential equations for X and Y are

$$\frac{dX}{dt} = -c\beta \frac{XY}{X + Y - 1} - \mu X + U \tag{9.1}$$

$$\frac{dY}{dt} = c\beta \frac{XY}{X + Y - 1} - (k + \mu)Y \tag{9.2}$$

Global Stability and the Basic Reproduction Number

Put $X + Y$ for $X + Y - 1$ in the denominators of the first terms in (9.1) and (9.2), Equation (9.2) becomes

$$\frac{dY}{dt} = c\beta \frac{XY}{X + Y} - (k + \mu)Y \tag{9.3}$$

Then if

$$R_0 = \frac{c\beta}{k+\mu} < 1 \tag{9.4}$$

the disease – free equilibrium is globally stable. That result is obtained directly by factoring (9.3) as in

$$\frac{dY}{dt} = \left[c\beta \frac{X}{X+Y-1} - (k+\mu)\right] Y \tag{9.5}$$

and noting that since $X/(X+Y) < 1$ for $Y > 0$, if $c\beta - (k+\mu) \leq 0$, the derivative of Y is always negative except at $Y = 0$.

The result for Equation (9.2) is slightly different. Factoring (9.2)

$$\frac{dY}{dt} = \left[c\beta \frac{X}{X+Y-1} - (k+\mu)\right] Y \tag{9.6}$$

At the disease – free equilibrium, $X = U/\mu, Y = 0$, and

$$\frac{X}{X+Y-1} = \frac{\mu}{U-\mu}$$

Now, one obtains

$$R_0 = \left(\frac{c\beta}{k+\mu}\right)\left(\frac{U}{U-\mu}\right) < 1 \tag{9.7}$$

as the condition for global stability of the disease – free equilibrium. Usually $U \gg \mu$, so there is little difference between the $R_0's$ obtained from (9.4) and from (9.7). Let us continue to use the notation $R_0 = c\beta/(k+\mu)$ and point out that the first factor in (9.6) gives R_0 when $Y = 1$.

The Stochastic Model

$[c\beta xy/(x+y-1)]\Delta t$ is the probability that a susceptible is converted to an infected in t. In that transition x decreases by 1 and y increases by 1.This

transition probability is zero if $x = 0$ and $y = 0$. Also if $x + y \leqq 1$, there is no transmission.

The Stochastic Equation

$U\Delta t$ is the probability that x increases by 1 in Δt, by recruitment.

$\mu x\Delta t$ is the probability of losing one susceptible to a competing cause of death in $\Delta t, x$ decreases by 1.

$\mu y\Delta t$ is the probability of losing one infective to a competing cause of death in $\Delta t, y$ decreases by 1

$ky\Delta t$ is the probability of losing an infective due to the disease in Δt; y decreases by 1.

Define $p_{xy}(t)$ as the probability that the population has x susceptibles and y infectives at time t. The expression for $p_{xy}(t + \Delta t)$, following the approach of Bailey [4], to show the derivation of the differential equation for $p_{xy}(t)$ is

$$p_{xy}(t + \Delta t) = p_{x+1,y-1}\frac{c\beta(x+1)(y-1)}{x+y-1}\,\Delta t + p_{x,y+1}(k+\mu)(y+1)t$$

$$+p_{x-1,y}U\,\Delta t + p_{x+1,y}\,\mu\,(x+1)\Delta t$$

$$+p_{x,y}1 - \frac{c\beta xy}{x+y-1}\,\Delta t - (k+\mu)y\Delta t - U\Delta t - \mu x\Delta t \quad (9.8)$$

Rearranging and taking limits gives the differential equation for p_{xy},

$$\frac{dp}{dt} = c\beta\left[\frac{(x+1)(y-1)}{x+y-1}\, p_{x+1,y-1} - \frac{xy}{x+y-1} p_{x,y}\right] + U\left[p_{x-1,y} - p_{xy}\right]$$

$$+(k+\mu)\left[(y+1)p_{x,y+1} - yp_{xy}\right] + \mu\left[(x+1)p_{x+1,y} - xp_{xy}\right] \tag{9.9}$$

If $i < 0$ and $j < 0$ then $P_{ij} = 0$.

Initial Conditions.

If no infectives are present, the number of susceptibles is given by a linear death process with immigration Let us assume that process is at equilibrium when the infectives are introduced. At that point $E(x) = m_x = U/\mu$.

Let us choose that initially there are n susceptibles , where n is the integer closest to U/μ. To such a population, let us take m infecteds. That gives for initial conditions,

$$p_{nm}(0) = 1, p_{xy}(0) = 0, x \neq n \; or \; y \neq m$$

Let us to be most interested in the case $m = 1$.

The Mean Number of Infecteds

Next let us compare the time courses of the mean number of infecteds from the stochastic model with the time courses of the number of infecteds from the deterministic model.

By definition the expected values are given by

$$m_y(t) = E[y] = \sum_{x=0}^{\infty}\sum_{y=0}^{\infty} y p_{xy}(t) \tag{9.10}$$

and $m_x(t) = E[x]$

$$= \sum_{x=0}^{\infty}\sum_{y=0}^{\infty} x p_{xy}(t) \tag{9.11}$$

The generating function approach to find equations for the mean values but have failed with it. However, one can generate the differential equations for the mean values,

$$\frac{dm_x}{dt} = \sum_{x=0}^{\infty}\sum_{y=0}^{\infty} \frac{dp_{xy}}{dt} \tag{9.12}$$

and $$\frac{dm_y}{dt} = \sum_{x=0}^{\infty}\sum_{y=0}^{\infty} y\,\frac{dp_{xy}}{dt} \tag{9.13}$$

Starting with the system in state (x, y) let us calculate the expected value of $y(t + \Delta t) - y(t)$

$E[y(t + \Delta t) - y(t)|x, y]$

$$= c\beta \frac{xy}{x + y - 1}\,\Delta t - (k + \mu)y\,\Delta t + o(\Delta t) \tag{9.14}$$

Taking expected values and using the usual limit process as $\Delta t \to 0$ gives

$$\frac{dE[y]}{dt} = E\left[\frac{c\beta xy}{x + y - 1}\right] - E[(k + \mu)y] \tag{9.15}$$

Hence

$$\frac{dm_y}{dt} = c\beta \sum_{x=0}^{\infty}\sum_{y=0}^{\infty} \frac{xy}{x+y-1} p_{xy} \; - (k+\mu) \sum_{x=0}^{\infty}\sum_{y=0}^{\infty} y\, p_{xy} \tag{9.16}$$

Similarly

$$\frac{dm_x}{dt} = -c\beta \sum_{x=0}^{\infty}\sum_{y=0}^{\infty} \frac{xy}{x+y-1} p_{xy} \; - \mu \sum_{x=0}^{\infty}\sum_{y=0}^{\infty} x\, p_{xy} + U \tag{9.17}$$

Equations (9.16) and (9.17) can also be obtained directly by substituting (9.9) into (9.12) and (9.13), though with somewhat more effort.

Relations between Stochastic means and deterministic variables:

1.Reproduction number and Global stability : $\boldsymbol{R_0} < 1$

$$\frac{dm_y}{dt} = (k+\mu) \left[\sum_{x=0}^{\infty}\sum_{y=0}^{\infty} \frac{\beta c}{k+\mu} \; \frac{xy}{x+y-1} p_{xy} \; - 1 \right] y p_{xy} \tag{9.18}$$

Assume that $R_0 - 1 = [\beta c/(k+\mu) - 1] < 0$. The initial value, $m_y(0)$, is finite. To show that the derivative of $m_y(t)$ is negative for all $t < \infty$ and that its asymptotic steady value is zero.

The derivative of m_y is always negative. Consider Equation (9.18) for $t \geq 0$. All terms for which $y = 0$ are equal to zero, so in the summations consider the terms in y for $y \geq 1$. For all $y \geq 1$ and all $x > 0$,

$$\frac{x}{x+y-1} \leq 1 \tag{9.19}$$

and the equality sign holds only when $y = 1$ and $x \neq 0$. Hence, if $R_0 - 1 < 0$, all coefficients of yp_{xy} in (9.18) must be negative for $y \geq 1$. Therefore the derivative of m_y is always negative and m_y must always decrease.

The Equilibrium State Value of $\mathbf{m_y}$ is Zero.

The equilibrium state solution for Equation (9.16), m_y^e for which

$$\frac{dm_y}{dt} = 0 \tag{9.20}$$

when $R_0 < 1$. For the equilibrium state, Equation (9.18) can be written us

$$R_0 \sum_{x=0}^{\infty}\sum_{y=0}^{\infty} \frac{xy}{x+y-1} p_{xy} = \sum_{x=0}^{\infty}\sum_{y=0}^{\infty} y\, p_{xy} = m_y^e \tag{9.21}$$

The double sum on the left-hand side may be written

$$\sum_{x=0}^{\infty}\sum_{y=1}^{\infty} \xi_{xy}\, yp_{xy} \tag{9.22}$$

where

$$0 \leq \ \xi_{xy} \leq 1 \tag{9.23}$$

Hence there exists $\xi^e, 0 \leq \xi^e \leq 1$, such that

$$\sum_{x=0}^{\infty}\sum_{y=0}^{\infty} \xi_{xy}\, y\, p_{xy} = \xi^e \sum_{x=0}^{\infty}\sum_{y=1}^{\infty} y\, p_{xy} \tag{9.24}$$

Thus, equation (9.21) becomes

$$(R_0\xi^e - 1)m_y^e = 0 \tag{9.25}$$

By hypothesis, $R_0 < 1$, so the first factor in (9.25) cannot be zero. Hence, $m_y^e = 0$.

If $R_0 - 1 < 0$, the equilibrium state for Equation (9.16) has for solution $m_y^e = 0$ and the derivative of m_y is always negative. Since y is a nonnegative variable, if its expected value goes to zero, all probabilities p_{xy} for $y > 0$ must go to zero, and hence all higher moments must also go to zero. Hence, the disease – free equilibrium is globally stable for the stochastic model.

Case i: $R_0 = 1$

For $x = 0$, $\xi_{xy} = 0$, and for $y = 1$, $\xi_{xy} = 1$; for all other x and y, $0 < \xi_{xy} < 1$. Hence, some of the coefficients in (9.18) are negative and others are zero. And, except for the unusual circumstance $p_{xy}(t) = 0$ for $y \neq 1$, there exists ξ^e, $0 \leq \xi^e < 1$, such that (9.24) holds, so that the conclusion $m_y^e = 0$ still holds.

The Equilibrium State Value of m_x. From (9.17), at the steady state let us obtain

$$c\beta\xi^e m_y^e + \lambda m_x^e = U \tag{9.26}$$

For $R_0 < 1, m_y^e = 0$, so

$$m_x^e = U/\mu \tag{9.27}$$

2. Initial Time Course of the Epidemic

In previous case $y \ll x,\ p_{xy}$ will be negligible for large y. Then, for all terms in (9.16) for which p_{xy} is significant,

$$\frac{x}{x+y-1} = 1 \tag{9.28}$$

Under that constraint, Equation (9.16) reduces to

$$\frac{dm_y}{dt} = [\beta c - (k+\mu)] \sum_{x=0}^{\infty} \sum_{y=0}^{\infty} y\, p_{xy} = [\beta c - (k+\mu)\ \ ] m_y \tag{9.29}$$

Initially, m_y grows or decays exponentially; it grows if $R_0 > 1$, it decreases if $R_0 < 1$, and it is stationary for a time if $R_0 = 1$. The relation (9.28) is satisfied. The larger the initial size of the population, the longer relation (9.29) will be valid.

With the approximation of (9.28) and (9.29), the epidemic becomes a birth – and – death process. For the general epidemic, the birth – and – death approximation holds until about $n^{1/2}$ of the susceptibles become infected. For is model in which the size of the population decreases as the epidemic spreads.

3. *Endemic Equilibrium State:* $R_0 > 1$

In Equation (9.24), let us define a mean value $\xi, 0 < \xi(t) < 1$, as in (9.30) and explicitly show its dependence on t.

$$\xi(t) = \frac{\sum_{x=0}\sum_{y=1}[x/(x+y-1)]\, yp_{xy}}{\sum_{x=0}\sum_{y=1}\, yp_{xy}} \tag{9.30}$$

$\xi(t)$ is a weighted average of $x/(x + y - 1)$ with weights $yp_{xy}(t)$. Using (9.30), rewrite (9.16) and (9.17) as in

$$\frac{dm_y}{dt} = (k+\mu)[R_0\xi(t) - 1]m_y \tag{9.31}$$

and

$$\frac{dm_x}{dt} = -c\beta\xi(t)m_y - \mu m_x + U \tag{9.32}$$

At the equilibrium state,

$$(R_0\xi^e - 1)m_y^e = 0 \tag{9.33}$$

and

$$m_x^e = \frac{U - (k+\mu)R_0\xi^e m_y^e}{\mu} \tag{9.34}$$

With $R_0 > 1$, Equation (9.33) can in general have two solutions, but now $m_y^e \neq 0$.

Let us note that Equation (9.31) has a solution for $\frac{dm_y}{dt}$ at which $\frac{dm_x}{dt} \neq 0$.

$$\xi^e = 1/R_0 \tag{9.35}$$

$$m_x^e = \frac{U - (k+\mu)m_y^e}{\mu} \tag{9.36}$$

These can be compared with results on the deterministic system,

$$\frac{X^s}{X^s + Y^s} = \frac{1}{R_0} \tag{9.37}$$

$$X^s = \frac{U - (k+\mu)Y^s}{\mu} \tag{9.38}$$

Avian Influenza

Let us present a highly pathogenic Avian influenza epidemic model with saturated contact rate. According to study of the dynamics, we calculated the basic reproduction number of the model. Through the analysis of this model, we have the following conclusion: if $R_0 \leq 1$, there is only one disease-free equilibrium which is globally stable, the disease will die; if $R_0 > 1$, there is only one endemic equilibrium which is globally stable, disease will be popular.

Avian influenza virus belongs to the influenza A virus. According to the difference of the pathogenic Avian influenza virus in chicken and turkey, we divided it into three levels: high, medium, low/non pathogenic. Because of the bird flu virus hemagglutinin structure characteristics, general infected birds,

when the virus genetic reassortment during replication, causing structural changes. The Avian influenza virus which acquires the ability to infect people, can make adult infect the Avian influenza disease. The highly pathogenic Avian influenza has a high death rate, which is about 100 percent for birds and more than 70 percent for humans.

At present, some authors have researched some Avian influenza model, they had constructed a mathematical model which interprets the spread of Avian influenza from the bird world to the human world. Literature has introduced a piecewise treatment function. When the number of the infective had not exceeded the maximum treatment capacity, the treatment rate was proportional to the number of the infective. When the number of the infective had exceeded the maximum treatment capacity, it took maximum saturation treatment value. Literature have studied of SIR model with saturated treatment rate. In the literature, the saturated treatment rate is $\frac{rI}{1+\alpha I}$, where r is the cure rate and α is the parameters of infection which is due to delayed treatment. The conclusion had indicated that in the prevention and treatment of Avian flu drugs under the condition of limited, culling of infected poultry was the most effective way to control the spread of Avian flu in humans

Avian influenza model with saturated contact rate is given by,

$$\begin{cases} X' = c - \dfrac{\omega XY}{1+\delta Y} - dX, \\ Y' = \dfrac{\omega XY}{1+\delta Y} - (d+m)Y \\ S' = b - \dfrac{\beta SY}{1+\delta Y} - \alpha S \\ I' = \dfrac{\beta SY}{1+\delta Y} - (\varepsilon + \alpha + \gamma)I \\ R' = \gamma I - \alpha R \end{cases} \tag{9.39}$$

In system (9.39), the human is divided into three compartments: Susceptible (*S*), infected (*I*), recovery (*R*). The birds are divided into susceptible poultry (*X*) and infected poultry (*Y*). The parameters *c* and *b* are respectively the natural birth rate of Avian and human. *d* and α are respectively the natural mortality of poultry and human. *m* and ε are respectively the poultry and human mortality due to illness. ω stands for infectious rate of susceptible poultry to infected poultry. β stands for infected poultry of the infection rate of susceptible individuals.

γ is the recovery rate that infects individuals through treatment. When *Y* is small, the contact ratio, infected poultry and susceptible poultry, is approximatively proportional to the *Y*; With the increase of *Y*, the contact rate gradually reaches saturation. When *Y* is very large, it is close to a constant $\frac{\omega}{\delta}$. The same way to explain $\frac{\beta}{1+\delta Y}$, that is to say, δ is a parameter, which is effects of infectious diseases, when the contact rate of the disease is saturated.

The Existence of the Equilibrium Point

Let us study the following system:

$$\begin{cases} X' = c - \dfrac{\omega XY}{1+\delta Y} - dX, \\ Y' = \dfrac{\omega XY}{1+\delta Y} - (d+m)Y \\ S' = b - \dfrac{\beta SY}{1+\delta Y} - \alpha S \\ I' = \dfrac{\beta SY}{1+\delta Y} - (\varepsilon + \alpha + \gamma)I \end{cases} \tag{9.40}$$

Let us get the basic reproductive number of the system (9.40) $E_0 = (X^0, Y^0, S^0, I^0)$ is $\left(\frac{c}{d}, 0, \frac{b}{\alpha}, 0\right)$

$$R_0 = \frac{c\omega}{d(d+m)}.$$

By the positive of the endemic equilibrium point, we can get that if $R_0 > 1$, there is a unique endemic equilibrium $E_+ = (X^*, Y^*, S^*, I^*)$,

which satisfied:

$$X^* = \frac{d+m-c\delta}{d\delta+\omega}, \quad Y^* = \frac{c\omega - d(d+m)}{(d+m)(d\delta+\omega)}, \quad S^* = \frac{b(1+\delta Y^*)}{\beta Y^* + \alpha(1+\delta Y^*)},$$

$$I^* = \frac{b\beta Y^*}{(\varepsilon+\alpha+\gamma)(\beta Y^* + \alpha(1+\delta Y^*))}.$$

So, we can get the following theorem:

Theorem 9.1

The Jacobian matrix of system (9.39) is

$$J=\begin{pmatrix} -d & -\dfrac{\omega X(1+\delta Y)-\delta\omega XY}{(1+\delta Y)^2} & 0 & 0 \\ \dfrac{\omega Y}{1+\delta Y} & \dfrac{\omega X(1+\delta Y)-\delta\omega XY}{(1+\delta Y)^2}-(d+m) & 0 & 0 \\ 0 & -\dfrac{\beta S(1+\delta Y)-\delta\beta SY}{(1+\delta Y)^2} & -\dfrac{\beta Y}{1+\delta Y}-\alpha & 0 \\ 0 & \dfrac{\beta S(1+\delta Y)-\delta\beta SY}{(1+\delta Y)^2} & \dfrac{\beta Y}{1+\delta Y} & -(\varepsilon+\alpha+\gamma) \end{pmatrix},$$

which in the disease-free equilibrium E_0, is

$$J_{E_0}=\begin{pmatrix} -d & -\dfrac{c\omega}{d} & 0 & 0 \\ 0 & \dfrac{c\omega}{d}-(d+m) & 0 & 0 \\ 0 & -\dfrac{b\beta}{\alpha} & -\alpha & 0 \\ 0 & \dfrac{b\beta}{\alpha} & 0 & -(\varepsilon+\alpha+\gamma) \end{pmatrix}.$$

The characteristic equation of the Jacobian matrix J_{E_0} is

$$(\lambda + d)(\lambda - h)(\lambda + \alpha)(\lambda + \varepsilon + \alpha + \gamma) = 0.$$

Here, $h=\frac{c\omega}{d}-(d+m)=(d+m)(R_0-1)$, λ denotes the indeterminate of the polynomial. If and only if $R_0 \leq 1$ all roots of this characteristic equation have negative real parts. It implies that E_0 is locally asymptotically stable.

Theorem 9.2

If $R_0 \leq 1$, the disease – free equilibrium E_0 is locally asymptotically stable; if $R_0 > 1$, the disease – free equilibrium E_0 is unstable.

Let us discuss the global stability of E_0, considering the Liapunov function

$W_1 = X - X^0 - X^0 \ln X + Y$, then

$$W_1' = X' - X^0 \frac{1}{X} X' + Y' = X' \left(1 - \frac{X^0}{X}\right) + Y'$$

$$= \left(1 - \frac{X^0}{X}\right)\left(-d\left(X - X^0\right) - \frac{\omega XY}{1+\delta Y}\right) + \frac{\omega XY}{1+\delta Y} - (d+m)Y$$

$$= -\frac{d\left(X - X^0\right)^2}{X} + \frac{\omega X^0 Y}{1+\delta Y} - (d+m)Y$$

$$= -\frac{d\left(X - X^0\right)^2}{X} + (d+m)Y\left(\frac{\omega X^0}{(1+\delta Y)(d+m)} - 1\right)$$

$$\leq -\frac{d\left(X - X^0\right)^2}{X} + (d+m)Y\left(\frac{\omega X^0}{d+m} - 1\right)$$

$$= -\frac{d\left(X - X^0\right)^2}{X} + (d+m)Y(R_0 - 1)$$

when $R_0 \leq 1$, we can get $W' \leq 1$, and $W' = 0$ has no other closed trajectory in addition to E_0.

The SIS and SIR Stochastic Epidemic Models

Let us analyze the dynamics of infectious disease spread by formulating the maximum entropy (ME) solutions of the susceptible-infected-susceptible (SIS) and the susceptible-infected-removed (SIR) stochastic models. Several

scenarios providing helpful insight into the use of the ME formalism for epidemic modeling are identified. The ME results are illustrated with respect to several descriptors, including the number of recovered individuals and the time to extinction.

Maximum entropy background

In this chapter, let us summarize the ME formalism. Although it is not generally possible to obtain closed-form solutions for the ME distributions, methods for numerical computation are available. Let us consider a random characteristic, , of a stochastic system X.

For example, ξ can denote the time until the end of the epidemic process X. The general theory is common for both the discrete and continuous cases. Let us denote by $f(x)$ the corresponding probability mass function or density function associated with the system characteristic . Let us assume that $f(x)$ takes values in a state space X, so the normalization constraint becomes

$$\int_{\chi} f(\chi)d\chi = 1 \tag{9.41}$$

Of course, the integral in (9.41) reduces to a finite or infinite sum when ξ is a discrete random variable.

Suppose that one is faced with the problem of determining a probability distribution consistent with a given set of mean value constraints which provide

the available information about ξ . It is assumed that the known information about $f(x)$ takes the form of $\overline{m}$ equality constraints

$$\int_{\chi} F_k(\chi) f(\chi) d\chi = F_k \qquad (9.42)$$

for a known set of functions $F_k(x)$ and numbers F_k, for $1 \leq k \leq m$.

The structural form of the mean value constraints ( ) covers important special cases such as:

(i) $F_k(x) = x^k$ (kth moment).

(ii) $F_k(x) = I(-\infty, x_k](x)$ (value of the distribution function at the point x_k).

(iii) $F_k(x) = e^{-s_k x}$ (value of the Laplace–Stieltjes transform or the moment generating function at the point sk).

Now, because the constraints (9.41) and (9.42) do not determine $f(x)$ completely, the inference problem is how to estimate $f(x)$ among all the probability distributions that satisfy the constraints. The PME states that, of all the probability density functions satisfying the mean value constraints (9.41) and (9.42), the minimally prejudiced density (i.e., the density function that introduces the minimum extraneous information) is the one that maximizes the Shannon's entropy functional

$$S(f) = -\int_{\chi} f(\chi) In\, f(\chi)\, d\chi \qquad (9.43)$$

The PME admits a natural generalization that applies to cases when a prior density $g(x)$ that estimates $f(x)$ is known in addition to the constraints (9.41) and (9.42). Then, the principle of minimum cross-entropy generalizes the PME by stating that, of all the densities that satisfy the mean constraints, the minimum cross entropy solution is chosen by minimizing the functional

$$S(f, g) = \int_{\mathcal{X}} f(x) \ln \frac{f(x)}{g(x)} dx.$$

When state space X is a discrete finite set, the PME can be viewed as a special case of cross-entropy minimization when the prior density $g(x)$ in (4) is uniformly distributed on X. The knowledge of a prior density $g(x)$ is not assumed in this paper so in what follows we reduce to the optimization of the Shannon's entropy $S(f)$. For a Bayesian analysis of the SIR epidemic model with prior parameter distributions of Gamma type. The maximization of $S(f)$ can be carried out with the help of Lagrange's method of undetermined multipliers. If there exists a density function that maximizes the entropy (9.43) and satisfies the mean value constraints (9.41) and (9.42), then it has the following form

$$\hat{f}(x) = \exp\left\{-\hat{\alpha}_0 - \sum_{k=1}^{\overline{m}} F_k(x)\hat{\alpha}_k\right\}, \quad x \in \mathcal{X},$$

where $\hat{\alpha}_k$ are the Lagrangian multipliers. Now, the normalization condition (9.41) implies that $\hat{\alpha}_0$ is given by

$$\exp\{\widehat{\alpha}_0\} = \int_{\mathcal{X}} \exp\left\{-\sum_{k=1}^{\overline{m}} F_k(x)\widehat{\alpha}_k\right\} dx.$$

The rest of the Lagrangian multipliers satisfy that

$$-\frac{\partial\widehat{\alpha}_0}{\partial\widehat{\alpha}_k} = F_k, \quad 1 \le k \le \overline{m}. \tag{9.44}$$

Unfortunately, it is usually impossible to solve Eqs. (9.44) for $\hat{\alpha}_k$ explicitly. As an exception we mention the special case where $\overline{m} = 1, X = (0, +\infty)$ and $F_1(x) = x$. Then, the explicit ME – solution is the exponential density

$$f(x) = \frac{1}{F_1} e^{-x/F_1}, \quad x \in \mathcal{X}.$$

Suppose that the second moment is added as a new constraint. Now, it is impossible to get an explicit solution for the pair $(\hat{\alpha}_1, \hat{\alpha}_2)$. Therefore, numerical methods of the solution become important. By combining (9.41) and (9.42) the problem of determining the optimal $\hat{\alpha}_k$, for $1 \le k \le \overline{m}$, is reduced to solve the following system of implicit and nonlinear equations:

$$\int_{\mathcal{X}} (F_i(x) - F_i) \exp\left\{-\sum_{k=1}^{\overline{m}} (F_k(x) - F_k)\,\alpha_k\right\} dx = 0, \tag{9.45}$$
$$1 \le i \le \overline{m}.$$

In fact, the solution of (9.45) amounts to minimizing the following convex potential function

$$F(\alpha_1, \ldots, \alpha_{\overline{m}}) = \log \int_{\mathcal{X}} \exp\left\{-\sum_{k=1}^{\overline{m}} (F_k(x) - F_k)\alpha_k\right\} dx,$$

or, alternatively, the balanced function

$$G(\alpha_1, \ldots, \alpha_{\overline{m}}) = \sum_{i=1}^{\overline{m}} p_i \left(\int_x (F_i(x) - F_i) \times \exp\left\{ - \sum_{k=1}^{\overline{m}} (F_k(x) - F_k)\, \alpha_k \right\} dx \right)^2,$$

where the weights pi are positive and $\sum_{i=1}^{\overline{m}} pi = 1$.

Some basic stochastic epidemic models

The stochastic SIS epidemic model

In the stochastic SIS epidemic model there is a closed population of size N, where each individual is classified as either a susceptible or an infective. Let $S(t)$ and $I(t)$ be the number of susceptible and infectives, respectively, at time t. Since $S(t) + I(t) = N$, the evolution of the epidemic is simply described by the process $\{I(t);\ t \geq 0\}$ with state space $S = \{0, \ldots, N\}$. The infection ends when $I(t) = 0$. The SIS model assumes that a recovered individual does not acquire immunity but immediately becomes susceptible. Thus, the process $\{I(t);\ t \geq 0\}$ is usually modeled as a particular case of a birth-and-death process with an absorbing state 0 and a reflecting state N. The birth and death rates are

$$\lambda_i = \frac{\beta}{N} i(N - i), \quad 0 \leq i \leq N,$$
$$\mu_i = \gamma i, \quad 0 \leq i \leq N,$$

where β is the effective contact rate and γ is the individual recovery rate.

Since the state space is finite, extinction is certain. Roughly speaking, the parameter region where the time to extinction is short can be identified by small values of the reproduction ratio $R_0 = \beta/\gamma$. In contrast, if R_0 is large, then the epidemic tends to persist for a very long time, so a state of quasi – stationary equilibrium may be reached before a random fluctuation leads to the extinction of the epidemic.

Many variants and generalizations of the SIS model have been considered. For example, a more general model is the Verhulst model with infection rates $\lambda_i = \beta i(1 - (\alpha_1 i/N))$, for $0 \leq i \leq N-1, \lambda N = 0$, and recovery rates $\mu_i = \gamma i(1 + (\alpha_2 i/N))$, for $0 \leq i \leq N$. The SIS model corresponds with the particular case where $\alpha_1 = 1$ and $\alpha_2 = 0$.

The stochastic SIR epidemic model

Let us deal with the stochastic SIR epidemic model. In the SIR model, infected individuals remain infectious for a random time, but they recover and become immune. Thus, at time t, the population consists of $I(t)$ infectives, $S(t)$ susceptibles and $R(t) = N - I(t) - S(t)$ immune individuals, where N is the constant population size. Let us assume the initial condition $(I(0), S(0), R(0)) = (m, n, 0)$, so $N = m + n$. When in state (i, j), for $i \geq 1$, the population state moves either to $(i + 1, j - 1)$ due to an infection, or to $(i - 1, j)$ due to the removal of an infective. In the states $(i, 0)$, for $i \geq 1$, only a removal can occur. The state space of the SIR epidemic model is

$S = \{(i,j);\ 0 \leq i \leq m + n, 0 \leq j \leq min\{n, m + n - i\}\}$. Let us notice that states $\{(0,j);\ 0 \leq j \leq n\}$ are absorbing states, so it is reasonable to assume that $m \geq 1$.

Let us assuming the exponential distribution and the independence of the involved random events (i.e., contact periods, recovery times), the process $\{(I(t), S(t));\ t \geq 0\}$ results to be a bidimensional CTMC with infection rates λ_{ij} and removal rates μ_i. A typical choice for the transition rates is

$$\lambda_{ij} = \frac{\beta}{N} ij, \quad (i,j) \in S,$$

$$\mu_i = \gamma i, \quad 0 \leq i \leq m + n,$$

where β and γ denote the contact and the recovery rates. A more general model assumes that infected individuals remain infectious for a random period I. These infectious periods are mutually independent and also independent of the contact process. let N'_{mn} be the number of individuals infected prior to disease extinction (excluding the initial number m). In other words, N'_{mn} amounts to the final size of the epidemics. The distribution of N'_{mn} can be computed from the recursive formula

$$P\{N^I_{mn} = k\} = \binom{n}{k} \phi^{m+k} \left(\frac{(n-k)\beta}{m+n}\right)$$

$$-(1 - \delta_{k0}) \sum_{i=0}^{\cdots} \binom{n-i}{k-i} \phi^{k-i} \left(\frac{(n-k)\beta}{m+n}\right) P\{N^I_{mn} = i\},$$

$$0 \leq k \leq n,$$

where $\varphi(s) = E[e^{-sI}]$ denotes the Laplace transform of the infectious period distribution and δ_{ab} is Kronecker's function defined by 1, when $a = b$, and it equals 0, otherwise.

Global Stability Analysis of a Delayed Susceptible–Infected–Susceptible Epidemic Model

Let $S(t)$ and $I(t)$ be the density of susceptible and infected population at time t, respectively.Let us consider the following delayed SIS model:

$$S'(t) = b - \beta S(t)I(t) - \mu_S S(t) + q\gamma I(t), \tag{9.46}$$

$$I'(t) = \int_0^\infty p(\tau)\, e^{-\mu\tau} \beta S(t-\tau)I(t-\tau)\, d\tau - \mu_I I(t) - \gamma I(t), \tag{9.47}$$

where $b > 0$ denotes a constant birth rate, $\beta > 0$ is the disease transmission rate, $\mu_S > 0$ and $\mu_I > 0$ stand for the death rates of susceptible and infected individuals, respectively. $p(\tau) \geq 0$ with $\tau \in [0, \infty)$ is the probability density function of transmission delay, $\mu \geq 0$ corresponds to the death rate during latent period, $\gamma \geq 0$ is the recovery rate of infected individuals, and $q \in [0, 1]$ denotes the probability of immunity lost.

The SIS model (9.46)–(9.47) always admits a disease-free equilibrium $(S_0, 0)$ with $S_0 := b/\mu_S$. Define the basic reproductive ratio

$$R_0 := \frac{b\beta_1}{\mu_S(\mu_I + \gamma)},$$

Where

$$\beta_1 := \beta \int_0^\infty p(\tau)\, \mathrm{e}^{-\mu\tau}\, \mathrm{d}\tau \leq \beta.$$

If $R_0 > 1$, the model possesses a unique endemic equilibrium (S^*, I^*), where

$$S^* := \frac{\mu_I + \gamma}{\beta_1},$$

$$I^* := \frac{b - \mu_S S^*}{\beta S^* - q\gamma} = \frac{b\beta_1 - \mu_S(\mu_I + \gamma)}{\beta(\mu_I + \gamma) - q\beta_1\gamma} = \frac{\mu_S(\mu_I + \gamma)(R_0 - 1)}{\beta(\mu_I + \gamma) - q\beta_1\gamma}.$$

Since $\beta(\mu_I + \gamma) - q\beta_1\gamma > \beta\gamma - q\beta_1\gamma \geq 0$, it is readily seen that $I^* > 0$ if and only if $R_0 > 1$.

Results 9.3

Let us assume that the probability density function $p(\tau)$ satisfies

$$\int_0^\infty p(\tau)\, \mathrm{e}^{\lambda\tau}\, \mathrm{d}\tau < \infty$$

for some $\lambda > 0$. The suitable state space for our system (9.46)–(9.47) is the Banach space X which consists of all continuous functions $(x^1, x^2) \in C((-\infty, 0], \mathbb{R}^2)$ such that $x^1(\theta)\, e^{\lambda\theta}$ and $x^2(\theta)e^{\lambda\theta}$ are uniformly continuous for $\theta \in (-\infty, 0]$, and that

$$\|(x^1, x^2)\|_X := \sup_{\theta \leq 0}(|x^1(\theta)| + |x^2(\theta)|)\, \mathrm{e}^{\lambda\theta} < \infty.$$

Here, $\|.\|_X$ denotes the weighted norm of X. For a function $\varphi \in C((-\infty, t], \mathbb{R})$,

Let us denote $\varphi_t \in C((-\infty, 0], \mathbb{R})$ such that $\varphi_t(\theta) := \varphi(t + \theta)\, for\, \theta \in (-\infty, 0]$. It follows from the standard theory of well – posedness for functional differential equations [ ] that given any initial conditions

$$x_0 = (x_0^1, x_0^2) \in X,$$

the system (9.46)–(9.47) has a unique solution $x_t = (x_t^1, x_t^2) \in X$ for any $t > 0$.

Proposition 9.4

Given the initial values such that $S(t) \geq 0$ and $I(t) \geq 0$ for all $t \leq 0$, we have $S(t) > 0$ and $I(t) \geq 0$ for all $t > 0$. If, in addition, $S(t)I(t) > 0$ for all $t \leq 0$, then $I(t) > 0$ for all $t \geq 0$.

Proof

First, let us claim that $S(t)$ and $I(t)$ are non – negative for all $t > 0$. If, in contrary, there exists a $t_0 \geq 0$ such that $(S(t), I(t))$ leaves the first quadrant at the first time, we have either (i) $S(t_0) = 0$ and $S'(t_0) < 0$; or (ii) $I(t_0) = 0$ and $I'(t_0) < 0$. Moreover, $S(t) \geq 0$ and $I(t) \geq 0$ for all $t \leq t_0$.

We have to show that $S(t)$ is strictly positive for all $t > 0$. Assume $S(t_1) = 0$ for some $t_1 > 0$. Since $S(t) \geq 0$ for all t, it follows that $t = t_1$ is a critical point of $S(t)$ and thus $S'(t_0) = 0$. On the other hand, obtain from (9.47) that $S'(t_1) = b + q\gamma I(t_1) \geq b > 0$, a contradiction.

Finally, if, in addition, $S(t)I(t) > 0$ for all $t \leq 0$, let us prove by contradiction that $I(t) > 0$ for all $t > 0$. Assume t_2 is the first time when $I(t)$

losses its positiveness, let us have $I(t_2) = I'(t_2) = 0$ and $I(t) > 0$ for all $t < t_2$, which again contradict Equation.

Theorem 9.5

If $R_0 \leq 1$, then the disease-free equilibrium $(S_0, 0)$ of ()–() is globally asymptotically stable; if $R_0 > 1$, then the endemic equilibrium (S^*, I^*) of ()–() is globally asymptotically stable.

Proof

If $R_0 \leq 1$, let us construct the Lyapunov functional $U : X \to \mathbb{R}$ as

$$U(x^1, x^2) := \frac{\beta_1 S_0}{\beta S_0 - q\gamma}[x^1(0) - S_0 \ln x^1(0)] + x^2(0) + \int_0^\infty \int_{-\tau}^0 p(\tau)\, \mathrm{e}^{-\mu\tau} \beta x^1(\theta) x^2(\theta)\, \mathrm{d}\theta\, \mathrm{d}\tau.$$

Restricting U along a solution (S, I) of the system ( )–(), let us have

$$U(t) = \frac{\beta_1 S_0}{\beta S_0 - q\gamma}[S(t) - S_0 \ln S(t)] + I(t) + \int_0^\infty \int_{t-\tau}^t p(\tau)\, \mathrm{e}^{-\mu\tau} \beta S(\theta) I(\theta)\, \mathrm{d}\theta\, \mathrm{d}\tau.$$

Let us use the equalities $x^1(\theta) = S(t + \theta)$ and $x^2(\theta) = S(I + \theta)$ for $\theta \leq 0$, and a linear shift $t + \theta \to \theta$ in the integral representation. Taking derivative with respect to t, Let us have the from Equation ()

$$\frac{\mathrm{d}}{\mathrm{d}t}[S(t) - S_0 \ln S(t)] = [S(t) - S_0]\left[\frac{b}{S(t)} - \beta I(t) - \mu_S + \frac{q\gamma I(t)}{S(t)}\right].$$

Making use of the identity $b = \mu_S S_0$ yields

$$\begin{aligned}\frac{b}{S(t)} - \beta I(t) - \mu_S + \frac{q\gamma I(t)}{S(t)} &= \frac{b}{S(t)} - \beta I(t) - \frac{b}{S_0} + \frac{q\gamma I(t)}{S(t)} - \frac{q\gamma I(t)}{S_0} + \frac{q\gamma I(t)}{S_0} \\ &= [b + q\gamma I(t)]\left[\frac{1}{S(t)} - \frac{1}{S_0}\right] - \left(\beta - \frac{q\gamma}{S_0}\right) I(t).\end{aligned}$$

Thus,

$$\frac{\mathrm{d}}{\mathrm{d}t}[S(t) - S_0 \ln S(t)] \leq -\left(\beta - \frac{q\gamma}{S_0}\right)[S(t) - S_0]I(t).$$

In view of Equation ( ) and the definition of β_1, let us obtain

$$U'(t) \leq -\beta_1[S(t) - S_0]I(t) + \beta_1 S(t)I(t) - (\mu_I + \gamma)I(t) = [\beta_1 S_0 - (\mu_I + \gamma)]I(t).$$

Since $R_0 \leq 1$, let us have $\beta_1 S_0 \leq \mu_I + \gamma$ and consequently, $U'(t) \leq 0$. The largest invariant set of $U'(t) = 0$ is a singleton such that $S(t) \equiv S_0$ and $I(t) \equiv 0$. The trivial equilibrium $(S_0, 0)$ is globally asymptotically stable if $R_0 \leq 1$.

For the case $R_0 > 1$, let us construct the Lyapunov functional $V : X \to \mathbb{R}$ as

$$V(x^1, x^2) := \frac{\beta_1 S^*}{\beta S^* - q\gamma} V_S(x^1, x^2) + V_I(x^1, x^2) + V_-(x^1, x^2),$$

where

$$V_S(x^1, x^2) := x^1(0) - S^* \ln x^1(0),$$

$$V_I(x^1, x^2) := x^2(0) - I^* \ln x^2(0),$$

$$V_-(x^1, x^2) := \int_0^\infty \int_{-\tau}^0 p(\tau)\, \mathrm{e}^{-\mu\tau} \beta[x^1(\theta)x^2(\theta) - S^*I^* \ln x^1(\theta)x^2(\theta)]\, \mathrm{d}\theta\, \mathrm{d}\tau.$$

Restricting along a solution (S, I) of the system ()–(), we can rewrite V as

$$V(t) = \frac{\beta_1 S^*}{\beta S^* - q\gamma} V_S(t) + V_I(t) + V_-(t),$$

Where

$$V_S'(t) = [S(t) - S^*]\left[\frac{b}{S(t)} - \beta I(t) - \mu_S + \frac{q\gamma I(t)}{S(t)}\right],$$

$$V_I'(t) = [I(t) - I^*]\left[\int_0^\infty p(\tau)\,\mathrm{e}^{-\mu\tau}\frac{\beta S(t-\tau)I(t-\tau)}{I(t)}\,\mathrm{d}\tau - (\mu_I + \gamma)\right],$$

$$V_-'(t) = \int_0^\infty p(\tau)\,\mathrm{e}^{-\mu\tau}\beta\left[S(t)I(t) - S(t-\tau)I(t-\tau) + S^*I^*\ln\frac{S(t-\tau)I(t-\tau)}{S(t)I(t)}\right]\mathrm{d}\tau.$$

In view of $b - \beta S^* I^* - \mu_S S^* + q\gamma I^* = 0$, let us have

$$\begin{aligned}\frac{b}{S(t)} - \beta I(t) - \mu_S + \frac{q\gamma I(t)}{S(t)} &= \frac{\beta S^* I^*}{S(t)} + \frac{\mu_S S^*}{S(t)} - \frac{q\gamma I^*}{S(t)} - \beta I(t) - \mu_S \\ &\quad + \frac{q\gamma I(t)}{S(t)} - \frac{q\gamma I(t)}{S^*} + \frac{q\gamma I(t)}{S^*} \\ &= [\mu_S S^* + q\gamma I(t)]\left[\frac{1}{S(t)} - \frac{1}{S^*}\right] + (\beta S^* - q\gamma)\left[\frac{I^*}{S(t)} - \frac{I(t)}{S^*}\right].\end{aligned}$$

Therefore,

$$\frac{\beta_1 S^*}{\beta S^* - q\gamma}V_S'(t) \le \beta_1 S^*[S(t) - S^*]\left[\frac{I^*}{S(t)} - \frac{I(t)}{S^*}\right].$$

On the other hand, since $\mu_I + \gamma = \beta_1 S^*$, let us obtain from the definition of β_1 that

$$V_I'(t) = \int_0^\infty p(\tau)\,\mathrm{e}^{-\mu\tau}\beta[I(t) - I^*]\left[\frac{S(t-\tau)I(t-\tau)}{I(t)} - S^*\right]\mathrm{d}\tau.$$

Combining the above formulas and using the definition of β_1, let us have

$$V'(t) \le \int_0^\infty p(\tau)\,\mathrm{e}^{-\mu\tau}\beta W(t,\tau)\,\mathrm{d}\tau,$$

where

$$W(t,\tau) := S^*[S(t) - S^*]\left[\frac{I^*}{S(t)} - \frac{I(t)}{S^*}\right] + [I(t) - I^*]\left[\frac{S(t-\tau)I(t-\tau)}{I(t)} - S^*\right] + \left[S(t)I(t) - S(t-\tau)I(t-\tau) + S^*I^* \ln\frac{S(t-\tau)I(t-\tau)}{S(t)I(t)}\right].$$

Simplifying the above equation gives

$$W(t,\tau) = S^*I^*\left[2 - \frac{S^*}{S(t)} - \frac{S(t-\tau)I(t-\tau)}{S^*I(t)} + \ln\frac{S(t-\tau)I(t-\tau)}{S(t)I(t)}\right].$$

Note that $2 - a - b + ln(ab) \leq 0$ for any $a > 0$ and $b > 0$; and the equality is satisfied if and only if $a = b = 1$. Let us obtain $W(t,\tau) \leq 0$ and consequently, $V'(t) \leq 0$. Moreover, the largest invariant set of $V'(t) = 0$ is a singleton where $S(t) \equiv S^* and\, I(t) \equiv I^*$. By the Lyapunov–LaSalle invariance principle let us obtain global asymptotic stability of the endemic equilibrium (S^*, I^*) under the condition $R_0 > 1$.

CHAPTER X

APPLICATION OF MARTINGALE THEORY TO SOME EPIDEMIC MODELS I

Picard [29] gives some very simple applications of martingales to epidemics. The results are all connected with stopping times T and include the expression of the joint generating function Laplace transform of $X_T, \int_0^T X_u, Y_u du$ and $\int_0^T Y_u\, du$ and simple relations between moments of these three variables. Several relations between different types of epidemics are derived at the end.

Stopping Time

Let $(\Omega, \mathcal{F}, P)$ be a prsobability space and $[\mathcal{F}_n, n \geq 1]$ an increasing sequence of sub σ – algebras of $\mathcal{F}$ (ie) $\mathcal{F}_1 \subset \mathcal{F}_2 \subset \cdots \ldots \subset \mathcal{F}$. A measurable function $T = T(w)$ taking values 1,2,…….. is called a stopping time relative to $\{\mathcal{F}_n\}$ if $\{T = j\} \in \mathcal{F}_j$, j = 1,2,……..

Downstons Classical Model

Let us consider Downton's classical model (ie) a time homogeneous two type birth and death process $(X_t, Y_t), t > 0$ such that

$$P\left[X_{t+\triangle t} = r, Y_{t+\triangle t} = {}^{S}/_{X_t} = i, Y_t = j\right]$$

$$= \begin{cases} \alpha\pi ij\Delta t + o(\Delta t) & if\ r = i-1, s = j+1 \\ \alpha(1-\pi)ij\Delta t + o(\Delta t) & if\ r = i-1, s = j \\ \beta j\Delta t + o(\Delta t) & if\ r = i, s = j-1 \\ 1-(\alpha i+\beta)\Delta t + o(\Delta t) & if\ r = i, s = j \\ o(\Delta t) & in\ all\ \ other\ cases \end{cases}$$

Where $\alpha > 0, \beta > 0, 0 \leq \pi \leq 1$ are parameters and x_0, y_0 the initial data.

$(X_t, Y_t), t \geq 0$ will have its values in

$$D = \{(i,j) \in N^2 / 0 \leq 1 + j \leq x_0 + y_0\}$$

Where

$X_t -$ the number of susceptibles at time t and

$Y_t -$ the number of carriers at the same time.

Any susceptible may be removed or changed into carrier while a carrier may be removed only.

Theorem 10.1

$\mathcal{F}_t$ is the σ field generated by X_u, Y_u for $0 \leq u \leq t$.

Put $V_t = a(X_t, Y_t)e^{-Z_t}$.

$Z_t = \int_o^t h(X_u, Y_u)du$ where a and h are functions of D into R then prove that $(V_n, \mathcal{F}_t), t \geq 0$ is a martingale.

Proof

To prove that

(i) $E\{|a(X_t, Y_t)e^{-Z_t}|\} < +\infty$

(ii) $E\{a(X_t, Y_t)e^{-Z_t}/\mathcal{F}_{t_0}\} = a(X_{t_0}, Y_{t_0})e^{-Z_{t_0}}, \quad 0 \le t_0 \le t$

Since $0 \le a(X_t, Y_t) < \max\ a(i, j)$

Therefore (X_t, Y_t) will have its values in D.

Therefore (i) is true.

To prove (ii)

Let us take $m(t) = E_{t_0}(a(X_t, Y_t)e^{-Z_t}), \quad 0 \le t_0 \le t$

Where $E_{t_0} = E(\ldots\ldots/\mathcal{F}_n)$.

For $\Delta t > 0$,

$$m(t + \Delta t) = E_{t_0}[a(X_{t+\Delta t}, Y_{t+\Delta t})e^{-Z_{t+\Delta t}}]$$

Since D is finite and $E_{t_0} = E_{t_0}E_t$

$$m(t + \Delta t) = E_{t_0}\{[a(X_t - 1, Y_t + 1)\pi\alpha X_t Y_t \Delta t$$

$$+a(X_t - 1, Y_t)(1 - \pi)\alpha X_t Y_t \Delta t$$

$$+a(X_t, Y_t - 1)\beta Y_t \Delta t]e^{-Z_t}$$

$$+a(X_t, Y_t)[1 - \alpha X_t Y_t + +\beta Y_t \Delta t]e^{-Z_t}$$

$$(1 - h(X_t, Y_t)\Delta t - 1) + o(\Delta t)\}$$

Therefore

$$\frac{m(t+\Delta t) - m(t)}{\Delta t} = E_{t_0}\{[a(X_t - 1, Y_t + 1)\pi\alpha X_t Y_t$$

$$+a(X_t - 1, Y_t)(1 - \pi)\alpha X_t Y_t$$

$$+a(X_t, Y_t - 1)\beta Y_t$$

$$-a(X_t, Y_t)[\alpha X_t Y_t + \beta Y_t]e^{-Z_t}$$

$$-a(X_t Y_t)h(X_t, Y_t)]e^{-Z_t} + o\frac{(\Delta t)}{\Delta t}\Big\}$$

Using Lebesgue's theorem

$$m_r'(t) = E_{t_0}\{[a(X_t - 1, Y_t + 1) - a(X_t, Y_t))\pi\alpha X_t Y_t +$$

$$+(a(X_t - 1, Y_t) - a(X_t, Y_t))(1 - \pi)\alpha X_t Y_t$$

$$+(a(X_t, Y_t - 1) - a(X_t, Y_t)\beta Y_t$$

$$-a(X_t, Y_t)h(X_t, Y_t)]e^{-Z_t}\}$$

$m_r'(t)$ being the derivative on the right of m.

When $\Delta t < 0$, put $\Delta t' = -\Delta t, t' = t + \Delta t$ and proceed in the same way using

$$\frac{m(t+\Delta t) - m(t)}{\Delta t} = \frac{m(t' + \Delta t') - m(t')}{\Delta t'} \quad for\ \Delta t' \geq 0$$

As a sample path of the process is a.s a step function which is continuous in t.let us obtain for the derivative on the left $m_r'(t)$ just the expression we have got for the one on the right.

So $m'(t)$ exists and if we choose a and h such that

$$[a(i-1,j-1)-a(i,j)]\pi\alpha ij+[a(i-1,j)-a(i,j)](1-\pi)\alpha ij$$

$$+[a(i,j-1)-a(i,j)]\beta j=a(i,j)h(i,j)\quad i,j\in D$$

$a(-1,j)$ and $a(i,-1)$ having any real value.

Therefore we have $m'(t)=0$.

Therefore $m(t)=\ m(t_0), t\geq t_0$.

Therefore

$$E_{t_0}(a(X_t,Y_t)e^{-Z_t})=E_{t_0}\left(a\left(X_{t_0},Y_{t_0}\right)e^{-Z_{t_0}}\right)\ =a\left(X_{t_0},Y_{t_0}\right)e^{-Z_{t_0}}$$

Thus we proved result (ii).

Therefore $\{Vn,\mathcal{F}_t\}$ is a martingale.

To find the solution of (). Put $h(i,j)=(Ai+B)j\qquad a(i,j)=C_i\lambda^j$.

A,B,λ being arbitrary positive constants.

Therefore we have

$$\left(C_{i-1}\lambda^{j+1}-C_i\lambda^j\right)\pi\alpha ij+\left[\left(C_{i-1}\lambda^j-C_i\lambda^j\right)\right](1-\pi)\alpha ij$$

$$+\left(C_i\lambda^{j-1} - C_i\lambda^j\right)\beta j = C_i\lambda^j(Ai+B)j$$

$$\left(\lambda C_{i-1}\lambda^{j+1} - C_i\right)\lambda^j\pi\alpha ij + (C_{i-1} - C_i)\lambda^j(1-\pi)\alpha ij$$

$$+C_i\lambda^j\left(\frac{1}{\lambda} - 1\right)\beta j = C_i\lambda^j(Ai+B)j$$

Put j = 0 we get an identity. For j > 0.

$$(\lambda C_{i-1} - C_i)\pi\alpha i + (C_{i-1} - C_i)(1-\pi)\alpha i$$

$$+C_i\left(\frac{1}{\lambda} - 1\right)\beta = C_i(Ai+B)$$

$$C_i\left(A_i - \frac{\beta}{\lambda} + \alpha_i + B - \beta\right) = C_{i-1}[\alpha i(1-\pi+\lambda_n\pi)]$$

Put $\lambda = \lambda_n = \frac{\beta}{(A+\alpha)n+B+\beta}$ in ()

$$(A+\alpha)(i-n)C_i = C_{i-1}\alpha i(1-\pi+\lambda_n\pi)$$

Take $C_0 = C_1 = \cdots \ldots \ldots \ldots = C_{n-1} = 0$

$$C_n = \lfloor n\left(\frac{\alpha}{A+\alpha}\left(1-\pi+\lambda_n\pi\right)\right)^n$$

Therefore () becomes

$$C_n = \frac{i}{i-n}\frac{\alpha}{A+\alpha}\left(1-\pi+\lambda_n\pi\right)C_{i-1} \quad \text{for i > n}$$

Put $(i)_n = i\ (i-1) \ldots \ldots \ldots \ldots \ldots i-(n-1)$

The general form of C_i is

$$C_i = \frac{\lfloor i}{i-1}\left(\frac{\alpha}{A+\alpha}\left(1-\pi+\lambda_n\pi\right)\right)^i$$

$$= i(i-1).....i-(n-1)\left(\frac{\alpha}{A+\alpha}\left(1-\pi+\lambda_n\pi\right)\right)^i$$

$$= \left(i\right)_n\left(\frac{\alpha}{A+\alpha}\left(1-\pi+\lambda_n\pi\right)\right)^i$$

Theorem 10.2

For A and B positive constants $\in N$, $\lambda_n = \beta\left((A+\alpha)n+B+\beta\right)^{-1}$ and

$$V_{t,n} = \left(X_i\right)_n\left(\frac{\alpha}{A+\alpha}\left(1-\pi+\pi\lambda_n\right)\right)^{X_i}\left(\lambda_n\right)^{Y_i} e^{-\int_0^t (AX_u+B)Y_u du}$$

Then $\left(V_{t,n};\mathcal{F}_t\right)_{t\geq 0}$ is a martingale. Also $\underset{t\geq 0}{Sup}\left|V_{t,n}\right| < \infty$.

Proof

We have proved that

$$C_i = \left(i\right)_n\left(\frac{\alpha}{A+\alpha}\left(1-\pi+\lambda_n\pi\right)\right)^i, i \in N$$

and $V_{t,n} = a_n\left(X_t, Y_t\right)e^{Z_t}$, $Z_t = \int_0^t h\left(X_u, Y_u\right)du$

Take $a_n\left(X_i, Y_i\right) = CX_i\left(\lambda_n\right)^{Y_i}$

$$h(X_u, Y_u) = \left(AX_u + B\right)Y_u$$

Therefore

$$V_{t,n} = \left(X_i\right)_n\left(\frac{\alpha}{A+\alpha}\left(1-\pi+\pi\lambda_n\right)\right)^{X_i}\left(\lambda_n\right)^{Y_i}e^{-\int_0^t\left(AX_u+B\right)Y_u du}$$

is a martingale.

Also $\underset{t\geq 0}{Sup}\left|V_{t,n}\right| < +\infty$

The stopping times and the main relation

Let $T_0 = Inf\{t: Y_t = r\}$ for r integer such that $0 \leq r < y_0$

$T_1 = Inf\{t: X_t + Y_t = r\}$ for r integer such that $x_0 \leq r < x_0 + y_0$

$T_2 = Inf\{t: 2X_t + Y_t = r\}$ for r integer such that $2x_0 \leq r < 2x_0 + y_0$

(ie) $T_\in = Inf\{t: \in X_t + Y_t = r\}$ for r integer such that $\in x_0 \leq r < \in x_0 + y_0$

with $\in = 0,1,2$.

Now the classical theorem on stopping times for martingales $E\left[V_{T_\in}, n\right] = V_{0,n}$.

$$\in X_{T_\in} + Y_{T_\in} = r$$

Theorem 10.3

For $T_\in = Inf\{t: \in X_t + Y_t = r\}$, $\in x_0 \leq r <\in x_0 + y_0$, $\in = 0,1,2.$

$$E\left(X_{T_\in}\right)_n \left(\frac{\alpha}{A+\alpha}\left(1-\pi+\pi\lambda_n^{-\in}\right)\right)^{X_{T_\in}} e^{-\int_0^{T_\in}(AX_u+B)Y_u du}$$

$$= \left(x_0\right)_n \left(\frac{\alpha}{A+\alpha}\left(1-\pi+\pi\lambda_n\right)\right)^{x_0} \lambda_n^{y_0-\in}$$

Where

$$\lambda_n = \frac{\beta}{\left(\left(A+\alpha\right)n+B+\beta\right)}\left(1-\pi+\pi\lambda_n^{-\in}\right)$$

Proof

$$E\left[V_{T_\in}, n\right] = V_{0,n}$$

Let us have

$$E\left(X_{T_\in}\right)_n\left(\frac{\alpha}{A+\alpha}\left(1-\pi+\pi\lambda_n\right)\right)^{X_{T_\in}} e^{-\int_0^{T_\in}(AX_u+B)Y_u du}$$

$$=\left(x_0\right)_n\left(\frac{\alpha}{A+\alpha}\left(1-\pi+\pi\lambda_n\right)\right)^{x_0} \lambda_n^{y_0-\in}$$

Multiply by λ_n^{-r}

$$E\left(X_{T_\in}\right)_n\left(\frac{\alpha}{A+\alpha}\left(1-\pi+\pi\lambda_n\right)\lambda_n^{-\in}\right)^{X_{T_\in}} e^{-\int_0^{T_\in}(AX_u+B)Y_u du}$$

$$=\left(x_0\right)_n\left(\frac{\alpha}{A+\alpha}\left(1-\pi+\pi\lambda_n\right)\right)^{x_0} \lambda_n^{y_0-r}$$

Using $\epsilon x_0 + y_0 = r.$

The joint distribution of $X_{T_\in}, \int_0^{T_\in} X_u du \text{ and } \int_0^{T_\in} X_u Y_u du$.

Let $U = (u_n)_{n\geq 0}$ be a sequence of real numbers. For any $n \in N, Q_n(x;U)$ be the unique polynomial in x of degree n satisfying for every $i \in N, Q_n^i(u_i;U) = \delta_{ni}$ where δ_{ni} is Kronecker's function

$Q_n(x,U)$ can be expressed in the following way.

1. $Q_0(x,U) = \delta_{00} = 1$

2. $Q_n(x,U) = \int_{u_0}^{x} d\xi_0 \int_{u_1}^{\xi_0} d\xi_1 ..... \int_{u_{n-1}}^{\xi_{n-2}} d\xi_{n-1}, n > 0$

$Q_n(x,U)$ only depends on $u_0, u_1, \ldots . u_{n-1}$ and not on the whole sequence U.

$$Q_n(x,U) = \int_{u_0}^{x} d\xi_0 \left(\xi_0 - \xi_1\right) = \frac{\xi_0^2}{2} - u_1\xi_0 \Big]_{u_0}^{x}$$

$$Q_2(x) = \frac{x^2}{2} + \frac{u_0^2}{2} - u_0 x = \frac{\left(x - u_0\right)^2}{\lfloor 2}$$

Similarly

$$Q_n(x) = \frac{\left(x - u_0\right)^n}{\lfloor n}$$

Property 10.4

If R is a polynomial of degree n then we have Abel's expansion

$$R(x) = \sum_{j=0}^{n} R^j(u_j) Q_j(x)$$

Proof

Put

$$R(x) = \sum_{k=0}^{n} b_k Q_k(x)$$

$$R^j(u_j) = \sum_{k=0}^{n} b_k Q_k^j(u_j) = \sum_{k=0}^{n} b_k \delta_k^j = b_j$$

Therefore

$$R(x) = \sum_{j=0}^{n} R^j(u_j) Q_j(x)$$

If for every $u_n = u_0$ then

Note

$$(i) \qquad R(x) = \sum_{j=0}^{n} R^j(u_j) Q_j(x)$$

$$= R^0(u_0)Q_0 + R^1(u_1)Q_1(x) + R^2(u_2)Q_2(x) + ... + R^n(u_n)Q_n(x)$$

$$= b_0 + R^1(u_1)\frac{(x-u_0)}{\lfloor 1} + R^2(u_2)\frac{(x-u_0)^2}{\lfloor 2} + ... + R^n(u_n)\frac{(x-u_0)^n}{\lfloor n}$$

Therefore R(x) is a Taylor's classical expansion

(ii) $$f(v) = E\left[v^{x_{T\in}} e^{-\int_0^{T\in}(AX_u+B)Y_u du}\right]$$

$$u_n = \frac{\alpha}{A+\alpha}.\frac{1-\pi+\pi\lambda_n}{\in}$$

$$f'(u_n) = E\left[u_n^{x_{T\in}} e^{-\int_0^{T\in}(AX_u+B)Y_u du}\right]\left[x.\frac{1}{u_n}\right]$$

$$f"(u_n) = E\left[\frac{1}{u_n^2}\left[u_n^{x_{T\in}} e^{-\int_0^{T\in}(AX_u+B)Y_u du}\left(x_{T_\in}\right)\left(x_{T_\in}-1\right)\right.\right.$$

$$f^n(u_n) = E\left[\frac{1}{u_n^n}\left[u_n^{x_{T\in}} e^{-\int_0^{T\in}(AX_u+B)Y_u du}\left(x_{T_\in}\right)\left(x_{T_\in}-1\right).\left(x_{T_\in}-(n-1)\right)\right.\right.$$

CHAPTER XI

APPLICATIONS OF MARTINGALE THEORY TO SOME EPIDEMIC MODELS – II

Let us consider Wiess and Downton's models with parameters π, α and β depending on i number of susceptibels and j number of carriers. A martingale argument is performed when π and α/β only depend on i or, in Weiss case when α/β is the product of a function of i by a function of j. In these cases the martingale approach proves very valuable and gives explicit results quite easily. In particular it shows that well – known relations between moments and integrals along a trajectory are still true for any stopping time and for more general models than the classic ones given by [30].

Introduction

Picard simple and explicit results for classical epidemics by a martingale argument. The purpose of the present Chapter is to show that such arguments are more powerful than one could have expected and also work for some generalizations of classical models. A Similar approach to the robustness of martingale theory has recently been developed by Heyde.

In classical epidemic models the parameters are considered as constants or exceptionally as function of time. Of course this is a rather crude approximation of reality and some writers have tried to build more realistic

models. In a real epidemic the increase of the number j of infectives usually generates sanitary measures in order to isolate infectives and prevent contacts with susceptibles.

In this chapter let us introduce Downton's model but with the following generalizations: the parameters α and β are supposed to be functions of i and j. π being a function of i only. Such a model may seem intractable but when α_{ij}/β_{ij} does not depend on j, or when $\pi = 0, \alpha_n/\beta_n$ being the product of a function of i by a function of j,martingale arguments work quite well as in classical models.

Definitions and Notations

For convenience let us sometimes write a instead of α_{ij} or $\alpha(t,j)$. β instead of β_{ij} or $\beta(i,j)$, $\int_0^t h\, du$ instead of $\int_0^t h(X_u, Y_u)\, du$, $\int_0^t a\, X_u, Y_u\, du$ instead of $\int_0^t a(\, X_u, Y_u)\ X_u Y_u\, du$ and so on. $f: \mathbb{N} \to \mathbb{R}$ is any function. Let us denote $jf(j)$ by $\hat{f}(j)$ and martingale V_t instead of $(V_t, \mathcal{F}_t), t \geq 0$.

Hypotheses and the key theorem

Let us take $h_{ij} = L_i \beta_{ij}, L_i \geq 0$ and suppose that the following hypotheses H_1 and $H_2(n),\ n = 0,1,2, \ldots \ldots \ldots, x_0$ are fulfilled.

H_1: For any i and j, $\alpha_{ij} = \beta_{ij}\eta_i$ with $\eta > 0$ for $i > 0$.

$H_2(n)$: For $i = n, n+1, \ldots\ldots, x_0$,

$(\hat{\eta}_t - \hat{\eta}_n + L_t - L_n)(i-n)^{-1}$ is defined and $\neq 0$.

Let us change $\pi, \alpha, \beta, Ai + B$ into $\pi_i, \alpha_{ij}, \beta_{ij}, \ldots\ldots L_i\beta_{ij}$.

Theorem 11.1

For $\lambda_n = (1 + L_n + \hat{\eta}_n)$

$$\hat{\gamma}_{n(s)} = \gamma n(s+n)$$

$$h_{ij} = L_i\, \beta_{ij}$$

and $V_t, n = (X_t)_n \pi \hat{\gamma}_{n(s)} \lambda_n^y exp\left(-\int_0^t h(x_u, y_u)\, du\right)$

Then $(V_t, n, \mathcal{F}_t), t < 0$ is a martingale.

Proof

Put $\pi = \pi_i$.

$$\alpha = \alpha_{ij}\ , \beta = \beta_{ij}.$$

$$A_i + B = L_i\, \beta_{ij}$$

$$\lambda_n = \frac{\beta}{(A+\alpha)n + B + \beta} = \frac{\beta_{ij}}{L_n \beta_n} + \alpha_{ij} n + \beta_{ij}$$

$$= \frac{\beta_{ij}}{Ln\beta_{nj} + \beta_{ij} n_i^n + \beta_{ij}} = \frac{\beta nj}{\beta nj(Ln + \eta_n n + 1)}$$

$$\lambda_n = \frac{1}{Ln + \hat{\eta}_n + 1}$$

$$\hat{\gamma}_{n(s)} = \gamma n(s+n)$$

$$\gamma_{n(i)} = (1 - \pi_i + \lambda_n \pi_i)(\hat{\eta}_i - \hat{\eta}_n + L_i - L_n)^{-1}(i-n)\eta_i$$

$$V_{t,n} = (X_i)n(\alpha/A)_\alpha (1 - \pi + \pi\lambda_n)^{X_i}(\lambda_n)^{Y_i} exp\left[-\int_0^t (Ax_u + B)y_u du\right]$$

$$V_t, n = (X_i)_n \pi \prod_{s=1}^{X_i - n} \gamma_{n(s)}\, \lambda_n^{Y_i} exp\left(-\int_0^t h(x_u, y_u)\, du\right)$$

is a martingale.

Corollary 11.2

For any stopping time T and $n = 0,1, \ldots \ldots \ldots, x_0$

$$E\left(V_{T,n}\right) = V_{0,n}$$

Relations between moments and integrals along a trajectory

When $n = 0$ the martingale $V_{t,n}$ is very simple. Putting

$$L_i = Af_i\hat{\eta}_i + B \qquad (11.1)$$

Where A and B are non – negative constants and $f\hat{\eta}$ is a function $\mathbb{N} \to \mathbb{R}$, let us have

$$\lambda_n = \frac{1}{1+B} \qquad \hat{\gamma}_0(s) = \gamma_0(s) = \frac{1 + (1-\pi_s)B}{(1+B)(1+Af_s)} \qquad (11.2)$$

Denoting $V_{t,0}(A,B)$ instead of $V_{t,0}$ in order to point to the dependence upon A and B

$$V_{t,0}(A,B) = \prod_{s=1}^{X_i} \frac{1+(1-\pi_s)B}{(1+B)(1+Af_s)} \, (1+B)^{-Y_j} \, exp\left(-\int_0^t h \, du \right)$$

$$= \prod_{s=1}^{X_i} (1+Af_s)^{-t} \;\; exp\left(-A \int_0^t f(X_u) \, \alpha(X_u, Y_u) \, X_u Y_u du \right)$$

$$\times \prod_{s=1}^{X_i} (1+(1-\pi_s)B) \, (1+B)^{-X_i - Y_j} \, exp\left(-B \int_0^t \beta(X_u, Y_u) Y_u \, du \right)$$

(11.3)

Let us have the following result.

Theorem 11.3

For any stopping time T and any non negative A, B and

$f_{\hat{\eta}}, V_{T,0}(0,B) = V_{T,0}(A,0), V_{T,0}(0,B)$ (11.4)

and $V_{T,0}(A,0)$ and $V_{T,0}(0,B)$ being uncorrelated.

Proof

$V_{T,0}(A,0)$ and $V_{T,0}(0,B)$ are martingale.

$$E\left[V_{T,0}(A,0), V_{T,0}(0,B)\right] = E\left[V_{T,0}(A,B)\right] = V_{0,0}(A,B)$$

$$= V_{0,0}(A,0), V_{0,0}(0,B)$$

$$= E\left(V_{T,0}(A,0)\right) E\left(V_{T,0}(0,B)\right)$$

Theorem 11.4

For any $f_{\widehat{\eta}}: \mathbb{N} \to \mathbb{R}$.

$$\sum_{i=1}^{X_i} f_i + \int_0^t f(X_u)\ \alpha(X_u, Y_u)\ \ X_u Y_u\ \ du$$

$$\sum_{i=1}^{X_i} (f_i)^2 + \left(\sum_{i=1}^{X_i} f_i + \int_0^t (X_u)\ \alpha(X_u, Y_u)\ \ X_u Y_u\ \ du \right)^2$$

are martingales. The first two are uncorrelated with the last two.

Proof

Let us develop $V_{T,0}(A,0)$ and $V_{T,0}(0,B)$ according to A and B and pick up terms in A, A^2, B and B^2.

Theorem 11.5

For any $f_{\widehat{\eta}}: \mathbb{N} \to \mathbb{R}_+$, any $g: \mathbb{N} \to \mathbb{R}_+$ and any stopping time T:

$$E\left(\int_0^t f(X_u)\ \alpha(X_u, Y_u)\ \ X_u Y_u\ \ du \right) = E\left(\sum_{i=x_T}^{X_s} f_i \right) \qquad (11.5)$$

$$E\left(\int_0^t g(X_u)\,\beta(X_u,Y_u)Y_u\ du\right)$$

$$= E\left\{\sum_{i=x_T}^{X_s}(g_0\pi_i + (g_i - g_0)/\hat{\eta}_i) + g_0(y_0 - Y_t)\right\} \quad (11.6)$$

Proof

The martingale property applied to the first martingale in Theorem (11.5) gives immediately. As for (11.6) let us put

$$g_i = g_0 + (g_i - g_0)\hat{\eta}_i/\hat{\eta}_i$$

and then

$$E\left(\int_0^t g(X_u)\,\beta(X_u,Y_u)Y_u\ du\right)$$

$$= g_0 E\left(\int_0^t \beta(X_u,Y_u)Y_u\ du\right) + E\left(\int_0^t \frac{g(X_u) - g(0)}{\hat{\eta}\ \ (X_u)}\,\alpha(X_u,Y_u)Y_u\ du\right)$$

Using (11.5) and the martingale property applied to the third martingale Theorem 11.2 let us obtain (11.6).

Theorem 11.4

For any Stopping time $T, E\left\{\int_0^t \alpha(X_u, Y_u) X_u Y_u \, du\right\}$ is the expected number of susceptibles involved in the epidemic between tome 0 and T and $E\left\{\int_0^t \beta(X_u, Y_u) Y_u \, du\right\}$ is the expected number of detected and eliminated carriers during the same period.

Applications

Relation such as (11.5) are interesting when let us have to solve statistical Problems. For instance if α is a constant (11.5) suggests introducing $(x_0 - X_T)^{-1} \int_0^t X_u, Y_u du$ as an estimator for $1/\alpha$ whichever β and π may be constants or not. If $\alpha_n = \alpha_0 + \alpha_1 i$. α_0 and α_1 being unknown constants $U_k = \int_0^t X_u^k, Y_u du$ and $f_i = i^k, k \in N$ into (11.5), let us get

$$a_0 E(U_{k+1}) + a_1 E(U_{k+2}) = E\left(\sum_{i=X_T}^{g_u} i^k\right) \qquad (11.7)$$

This relation used for $k = 0$ and $k = 1$ gives a_0 and a_1 as soon as $E(J_1), E(U_2), E(U_3), E(X_T), E(X_T^2)$ are known. Therefore if we find these five expectations it is possible to get estimates for a_0 and a_1.

The joint distribution of X_{T_0} and $\int_0^{T_0} h \, du$

Let us make use of the stopping times T_0 defined already.

1. A particular Case:

Take $\pi_i = \pi_0, \eta_i = (c_0 + c_1 i)^{-1}, h_{ij} = L_i \beta_{ij} j = (A' \hat{\eta}_i + B') \beta_{ij} j$ with π, c_0, c_1, A', B' constants. First check that $H_2(n)$ is fulfilled for any n, then let us find

$$\lambda_n = \frac{c_0 + c_1 n}{(1 + B')c_0 + \big(1 + A'(1 + B')\big)n} \tag{11.8}$$

and

$$\gamma_n(i) = (1 - \pi + \pi\lambda_n)(1 + c_1 n / c_0)(1 + A')^{-1} \tag{11.9}$$

which does not depend on i and will be denoted γ_n. As a consequence $\prod_{s=1}^{X_t - n} \hat{\gamma}_n(s)$ is now $\gamma_n^{X_t - n}$ and theorem 11.2 takes the form of theorem.

Applications

1. $\beta_{ij} = c_0 + c_1 i, \alpha_{ij}$ being a constant. This case has been studied in Routlet.
2. Two cases in which $\alpha_{ij} \beta_{ij}^{-1} = (c_0 + c_1 i)^{-1}$ and α, β^{-1} are increasing functions of i.
   i. $a_{ij} = (b_0 + b_1 i)(c_0 + c_1 i), \beta = b_0 + b_1 i$ with $b_0, c_0, -b_1, -c_1$ positive constants and $x_0 < -c_0/c_1 < -b_0/b_1$.
   ii. $a_{ij} = a_0 + a_1 i, \beta_{ij} = (a_0 + a_1 i)(c_0 + c_1 i)$ with $a_0, a_1, c_0, -c_1$ positive constants and $x_0 < -c_0/c_1 < -a_0/a_1$.
3. η_i not a special form: After introducing a generalization Gontcharoff's polynomials it is possible to study the general case. The argument is

always of the same kind but the results are of course less easy to handle and will not be given here.

A Basic Martingale

Let us suppose that $\pi = 0$ and α/β is the product of a function of i by a function of j, hence H_1 is replaced by

$H_1 \coloneqq \alpha_{ij} = \eta_i \mu_i \chi_{ij}, \beta_{ij} = \rho_i \chi_{ij}$ with $\eta_i > 0$ for $i > 0, \mu_i > 0, \rho_i > 0$ for $j > 0$, $\chi_{ij} > 0$ for $i \geqq 0, j \geqq 0$.

Besides, let us take

$$h_{ij} = \left(L_t \hat{\mu}_t + \widehat{M}_t\right)\chi_{ij} \text{ with } L \geqq 0, M \geqq 0 \qquad (11.10)$$

and keep the auxiliary hypothesis $H_2(n)$ unmodified. Now

$$a(i,j) = C_1 D_1$$

and α, β taken according to H_3, led to

$$(C_{i-1} - C_i) D_j \hat{\eta}_i \hat{\mu}_i \chi_{ij} + C_t \left(D_{j-1} - D_j\right) \rho_j \chi_{ij} = \left(L_i \hat{\mu}_j + \widehat{M}_j\right) C_i D_j \chi_{ij} \quad (11.11)$$

and after a routine argument,

$$C_i = (i)_n \prod_{s=1}^{i-n} \gamma_n(s+n), \qquad D_j = \prod_{s=1}^{j} \delta_n(s), \qquad (11.12)$$

with

$$\delta_n(s) = \frac{\rho_s}{\rho_s + M_s + (\hat{\eta}_n + L_n)\mu_s}, \qquad \gamma_n(i) = \frac{\eta_i (i-n)}{\hat{\eta}_i - \hat{\eta}_0 + L_i - L_n} \quad (11.13)$$

Finally have the following result.

Theorem 11.5

h, δ_n and γ_n being defined by (11.10) and (11.13) put

$$W_{t,n} = (X_T)_n \prod_{s=1}^{X_t - n} \gamma_n(s+n) \prod_{s=1}^{Y_t} \delta_n(s)\ exp\left(- \int_0^t h\ du \right)$$

then $\left(W_{t,n}; \mathcal{F}_t\right)_{t \geqq 0}$ is a martingale.

Now put

$$L_i = A f_i \hat{\eta}_i, \qquad \widehat{M}_i = B g_j \rho_j \tag{11.14}$$

A, B non – negative constants. $f\hat{\eta}$ and $g\hat{\rho}$ functions $\mathbb{N} \to \mathbb{R}_+$, have a quite simple $W_{t,0}$

$$W_{t,0} = \prod_{s=1}^{X_t - n} (1 + A f_i)^{-1}\ exp\left(-A \int_0^t f(X_u)\ \alpha(X_u, Y_u) X_u Y_u\ du \right)$$

$$+ \prod_{s=1}^{X_t - n} (1 + B g_s)^{-1}\ exp\left(-B \int_0^t g(Y_u)\ \beta(X_u, Y_u) Y_u\ du \right)$$

These Theorems are valid with W substituted for V, and

$$\sum_i^{Y_t} g_s + \int_0^t g\beta Y_u\ du \ and\ \sum_i^{Y_t} g_s^2 + \left(\sum_i^{Y_t} g_s + \int_0^t g\beta Y_u\ du \right)^2$$

Substituted for the third and the fourth martingales.

CHAPTER XII

A MODIFICATION OF THE GENERAL STOCHASTIC EPIDEMIC MOTIVATED BY AIDS MODELLING

In this Chapter let us consider a model for the spread of an epidemic in a closed, homogeneously mixing population in which new infections occur at rate $\beta xy/(x+y)$, where x and y are the numbers of susceptible and infectious individuals, respectively, and β is an infection parameter. This contrasts with the standard general epidemic in which new infections occur at βxy. Both the deterministic and stochastic versions of the modified epidemic are analysed. The deterministic model is completely soluble. The time – dependent solution of the stochastic model is derived. Threshold theorems, analogous to those of Whittle and Williams for the general stochastic epidemic, are proved for the stochastic model, given by [16].

Introduction

The considerable literature now existing on stochastic epidemic models is mainly concerned with closed population epidemics, such as the general stochastic epidemic, and thus is of limited direct use in modelling most AIDS epidemics where immigrations into and deaths from the class of susceptibles can be an important feature. Nevertheless there have been many studies of closed population models of AIDS. As such models can provide a good

description of the short term behaviour of an epidemic. They can provide a useful indication of the likely effects of some parameters in more complicated models incorporating immigration and deaths. However standard stochastic epidemic theory is often still not applicable because the infection process is modelled slightly differently. βxy term where x and y are the numbers of susceptible and infectives for the rate of new infections is replaced by $\beta xy/(x+y)$.

So if removed individuals are no longer available as sexual partners and new patterns are chosen at random from the population of possible partners, then the probability that a new partner of a given susceptible is infected is $y/(x+y)$. The Purpose of the present paper is to analyze deterministic and stochastic closed population epidemics with the above modified infection.

First let us define the stochastic version of our model more precisely. Consider a closed population consisting initially of a infectives and n susceptibles. For $t \geqq 0$, let $X(t), Y(t)$ and $Z(t)$ be respectively the numbers of susceptible, infective and removed individuals at time t. suppose further that $X(t)+Y(t)+Z(t) = n+a$ $(t \geqq 0)$ so the process is completely determined by $\{(X(t), Y(t)), t \geqq 0\}$ which we assume is a continuous – time Markov chain on the state space $\{(x,y) \in \mathbb{Z}^2 : x+y \leqq n+a, 0 \leqq x \leqq n, y \geqq 0\}$ with transition probabilities

$$Pr\{(X(t+\Delta t), Y(t+\Delta t)) = (x-1, y+1) | (X(t), Y(t)) = (x, y)\}$$

$$= \beta xy(x+y)^{-1}\Delta t + o(\Delta t)$$

$$Pr\{(X(t+\Delta t), Y(t+\Delta t)) = (x, y-1) | (X(t), Y(t)) = (x, y)\}$$

$$= \gamma y \Delta t + o(\Delta t)$$

and all other transitions having probability $o(\Delta t)$. Let us refer to this epidemic model as the modified stochastic epidemic.

The Chapter is structured as follows. The deterministic version of our modified stochastic epidemic is considered. N contrast to the general deterministic epidemic, this surprisingly admits a complete closed – form solution. The stochastic version is explained. Its temporal solution is derived using the Method of Kryscio [25]. The total size distribution is also examined and threshold theorems, analogous to those of Whitttle and Williams are proved. The effect of introducing varying susceptibilities to the disease into the model is considered. Using the methods similar to those of Ball [16].

Deterministic Model

Exact Solution and Final Outcome:

For $t \geqq 0$, let $x(t), y(t)$ and $z(t)$ be respectively the numbers of susceptible, infective and removed individuals at time t. The deterministic model of the modified epidemic is given by

$$\frac{dx}{dt} = -\beta xy \tag{12.1}$$

$$\frac{dy}{dt} = \frac{\beta xy}{x+y} - \gamma y, \tag{12.2}$$

$$\frac{dz}{dt} = \gamma y \tag{12.3}$$

With initial conditions $x(0) = n\,, \quad y(0) = a, \quad z(0) = 0.$ (12.4)

Equations (12.1) and (12.2) imply that

$$\frac{dx}{dz} = \frac{-x}{\rho(n+a-z)} \tag{12.5}$$

Where $\rho = \gamma/\beta$, which together with (12.4) yields

$$x(t) = n(1 - z(t)/(n+a))^{1/p} \qquad (t \geqq 0) \tag{12.6}$$

Substituting (12.5) into (12.3)

$$x(t) + y(t) + z(t) = n + a \qquad (t \geqq 0) \tag{12.7}$$

After integration and $\rho = 1$ then

$$\left.\begin{aligned} x(t) &= n\exp(-a\gamma t/N) \\ y(t) &= a\exp(-a\gamma t/N) \\ z(t) &= N(1-\exp(-a\gamma t/N)) \end{aligned}\right\} \tag{12.8}$$

Where $N = n + a$. If $\rho \neq 1$

$$\left.\begin{aligned} x(t) &= n\{\mathrm{N}^{-1}(\,n + a\exp(\beta-\gamma)t))\}^{1/(\rho-1)} \\ y(t) &= a\{\mathrm{N}^{-1}(\,n + a\exp(\beta-\gamma)t))\}^{1/(\rho-1)}\exp(\beta-\gamma)t) \\ z(t) &= N\left[1 - \{\mathrm{N}^{-1}(\,n + a\exp(\beta-\gamma)t))\}^{1/(\rho-1)}\right] \end{aligned}\right\} \qquad (12.9)$$

Let $T = \lim_{n\to\infty} z(t) - a$ be the total size of the epidemic, i.e the number of initial susceptibles that are ultimately infected by the epidemic. Thus we get

$$T = \begin{cases} n & if\ \rho \leqq 1, \\ n\left(1 - (n/N)^{1/(\rho-1)}\right) & if\ \ \rho > 1. \end{cases} \qquad (12.10)$$

Thus if $\rho \leqq 1$ the epidemic ultimately sweeps through the whole population. This contrasts sharply with what one might except to occur in real – life epidemics, and also with the final outcome of the general deterministic epidemic.

Threshold Behaviour

It is well known that the threshold behaviour of the general deterministic epidemic is governed by the value of the relative removal rate $\rho = \gamma/\beta$, where $\gamma\ and\ \beta$ are respectively the infection and removal rates.If $\rho < n$, no true epidemic occurs, since $dy/dt\,|_{t=0} < 0$.

However, the situation is not so straightforward for the modified epidemic. By noting that

$$\frac{dy}{dt} \lesseqgtr 0\ \ when\ \rho \lesseqgtr \frac{x}{x+y}$$

and

$$\frac{d}{dt}\left(\frac{x}{x+y}\right) = \frac{xy(\gamma-\beta)}{(x+y)^2} \lesseqgtr 0 \ \ when\ \rho \lesseqgtr 1$$

Let us use the previous results to summarise the threshold behaviour of the modified epidemic as follows:

1. $\rho > 1$, $\frac{dy}{dt} < 0$ for all t, $x(\infty) > 0$;
2. $\frac{n}{n+a} \leqq \rho \leqq 1$, $\frac{dy}{dt} < 0$ for all t $\left(except\ t = 0\ if\ \rho = \frac{n}{n+a}\right) x(\infty) > 0$;
3. $\rho < \frac{n}{n+a}$, $dy/dt\,|_{t=0} > 0$, $x(\infty) > 0$;

In particular note that it is possible for all of the initial susceptibles to ultimately contract the disease even if the number of infectives is always decreasing.

Comparison with General Deterministic Epidemic

For $t \geqq 0$, let $\bar{x}(t), \bar{y}(t)$ and $\bar{z}(t)$ denote, respectively, the number of susceptible, infectious ad removed individuals in a general deterministic epidemic with infection rate $\beta/(n+a)$, removal rate γ and initial condition $\left(\bar{x}(0), \bar{y}(0), \bar{x}(0)\right) = (n, a, 0)$. Thus

$$\left.\begin{aligned} \frac{d\bar{x}}{dt} &= \frac{-\beta}{(n+a)}\bar{x}\bar{y} \\ \frac{d\bar{y}}{dt} &= \frac{\beta}{(n+a)}\bar{x}\bar{y} - \gamma\bar{y} \\ \frac{d\bar{z}}{dt} &= \gamma\bar{y} \end{aligned}\right\} \qquad (12.11)$$

The above epidemic and our modified epidemic have identical initial rate of spread. In the modified epidemic the infection rate increases as the epidemic progresses, while it remains constant in the general epidemic. Thus the spread of infection is faster and more severe in the modified epidemic than in the general epidemic. This can be shown as follows:

By letting $t \to \infty$ (12.6) and (12.7) we find that $z(\infty) = \lim_{t\to\infty} z(t)$ is given by the smallest root in $[0, n+a]$ of $f(z) = 0$, where

$$f(z) = n + a - z - n\left(1 - \frac{z}{n+a}\right)^{1/\rho} \qquad (12.12)$$

A similar argument for the general epidemic shows that $\bar{z}(\infty)$ is given by the unique root in $[0, n+a]$ of $g(z) = 0$, where

$$g(z) = n + a - z - n\exp\{-z/((n+a)\rho)\} \qquad (12.13)$$

Now $\exp(-x) > 1 - x\ (x > 0)$. So $f(z) > g(z)(z > 0)$ and hence $z(\infty) = \bar{z}(\infty)$. Thus the total size of the modified epidemic is strictly larger than that of the general epidemic.

$$\frac{dz}{dt} = \gamma f(z) \qquad and \qquad \frac{d\tilde{z}}{dt} = gf(\tilde{z})$$

So it also follows that $z(t) \geqq \tilde{z}(t)$ for all $t \geqq 0$,with strict inequality for $t > 0$. Finally, using (12.6) and a corresponding equation for the general epidemic yields that $x(t) \leqq \tilde{x}(t)$ for all $t \geqq 0$, and again the inequality is strict for $t > 0$.

Stochastic Model

Let us now consider the simplest probability version of the deterministic model. As before, assume a homogeneously mixing group of n + 1 individuals and suppose for simplicity that the epidemic starts at time t = 0 with one infective and n susceptibles. This time let us take the random variables X(t) and Y(t) to represent the number of susceptibles and infetives respectively at time t, where $x(t) + y(t) = n + 1$ .Then the chance of a contact between any two specified individuals in an interval Δt is $\beta \Delta t + o(\Delta t)$, where β is the contact rate, and $\beta = constant$. It follows that the chance of one new infection in the whole group in Δt is βXY Δt to order Δt. When this transition occurs X decreases by one unit and Y increases by one unit. Suppose if take the possibility of removal, then the chance of one removal in Δt can be taken as $\gamma y \Delta t$ where γ is the removal rate. The variable Y decreases by one unit after the transition, but X remains unchanged.

Let us suppose that at time t = 0, there are n susceptibles and a infectives. Let $Pn(t)$ be denoted as the probability that at time t, there are r susceptibles

still uninfected and s infectives in circulation. The chance of one new infection in time Δt is taken to be $\beta rs\,\Delta t$ and the change of one removal $\gamma s\Delta t$. Also the time interval from the infection of any given susceptible to his eventual removal has a negative exponential distribution. Also the time scale is given by $\tau = \beta t$, instead of t and $\gamma / \beta = \rho$, the ration of removal rate to infection rate which we shall call the relative removal rate.

If $\beta = 1$ then $\gamma = \rho$. For $t \geqq 0$, let $p_{r,s}(t) = Pr\{(X(t), Y(t)) = (r, s)\}$ $\Big((r, s) \in E_{n,a}\Big)$,

where $E_{n,a} = \{(r, s) \in \mathbb{Z}^2 : 0 \leqq r + s \leqq n + a, 0 \leqq r \leqq n, 0 \leqq s \leqq n + a\}$ is the set of possible states that the epidemic can visit.

Let us have,

$$\frac{dp_{r,s}}{dt} = \frac{(r+1)(s-1)}{(r+s)} p_{r+1,s-1} + \rho(s+1)p_{r,s+1} - s\left(\frac{r}{r+s} + \rho\right)p_{r,s}$$

$$\Big((r, s) \in E_{n,a}\Big), \quad (12.14)$$

and $p_{r,s} \equiv 0$ if $(r, s) \notin E_{n,a}$, together with the initial condition $p_{n,a}(0) = 1$.

For $(r, s) \in E_{n,a}$ let

$$q_{r,s}(\lambda) = \int_0^\infty \exp(-\lambda u) p_{r,s}(u) du \qquad (\lambda \geqq 0)$$

Taking the Laplace transform of (12.14) yields

$$(r+1)(s-1)q_{r+a,s-1} + \rho(r+s)(s+1)q_{r,s-1}$$

$$-\big(sr + (r+s)(\rho s + \lambda)\big)q_{r,s} = 0$$

$$\Big((r,s) \in E_{n,a} | \{n,a\}\Big) \quad (12.15)$$

$$\left[\lambda + a\left(\frac{n}{n+a} + \rho\right)\right] q_{n,a} - 1 = 0 \quad (12.16)$$

By solving (2.15) and (2.16) can be solved to get $q_{r,s}\Big((r,s) \in E_{n,a}\Big)$, which can then be inverted to obtain the time – dependent solution of the epidemic.

The epidemic may be viewed as a random walk on $E_{n,a}$, defined as follows. For $k = 1,2, \ldots\ldots$, let (X_k, Y_k) denote the kth state of $E_{n,a}$ visited by the epidemic, and $(X_0, Y_0) = (n, a)$. The Markov property implies that the epidemic will remain in a state $(X_k, Y_k) = (x, y) \in E_{n,a}$ for a time A_k having a negative exponential distribution with mean $(xy/(x+y) + \rho y)^{-1}$ and on leaving the state (X_k, Y_k) the epidemic will proceed according to the transition probabilities

$$Pr\{(X_{k+1}, Y_{k+1}) = (x-1, y+1) | (X_k, Y_k) = (x,y)\} = \frac{x}{x + \rho(x+y)},$$

$$Pr\{(X_{k+1}, Y_{k+1}) = (x, y-1) | (X_k, Y_k) = (x,y)\} = \frac{\rho(x+y)}{x + \rho(x+y)},$$

corresponding to the occurrence of an infection and a removal, respectively. The epidemic terminates as soon as $Y_k = 0$ for some $k > 0$. supposing that $k = m$, say, the sets $\{(X_k, Y_k): 0 \leqq k \leqq m\}$ and $\{A_k: 0 \leqq k \leqq m\}$ describe the progress of a random walk on $E_{n,a}$ where the (X_k, Y_k)'s correspond to the states visited and the A_k's are the holding times in these states.

Let us derive an expression for $p_{r,s}(t)$ by conditioning on $R(n,a)$ following a particular path from $(N-a, a)$ to (r,s) and taking a weighted sum over all such paths, with weights given by the probabilities that the process traverses the different paths.

Let us adopt the following notation. A path d from (m,w) to (r,s) is a set of ordered points $\left\{\left(s_{1d}^{(0)}, s_{2d}^{(0)}\right), \left(s_{1d}^{(1)}, s_{2d}^{(1)}\right), \ldots\ldots\ldots\ldots\ldots\ldots\ldots\left(s_{1d}^{(E)}, s_{2d}^{(E)}\right)\right\}$, where

(i). $E = 2(m-r) + (w-s)$ is the path length

(ii). $\left(s_{1d}^{(0)}, s_{2d}^{(0)}\right) = (m,w)$;

(iii). $\left(s_{1d}^{(E)}, s_{2d}^{(E)}\right) = (r,s)$;

(iv). $\left(s_{1d}^{(j)}, s_{2d}^{(j)}\right) - \left(s_{1d}^{(j+1)}, s_{2d}^{(j+1)}\right) = (1, -1 \text{ or } (0,1)\ (j = 0,1, \ldots\ldots, E)$

(v). $s_{2d}^{(j)} > 0 \quad (j = 0,1, \ldots\ldots, E)$

Let D denote the set of all paths from $(N-a,a)$ to (r,s). writing π_d for the probability that the process takes path d and $p^*_{r,s}(t,d)$ for $p_{r,s}(t)$ conditional on taking path d, then

$$p_{r,s}(t) = \sum_{d\in D} \pi_d p^*_{r,s}(t,d) \tag{12.17}$$

From (12.17)

$$\pi_d = \prod_{j=1}^{E} q_j \left[s_{1d}^{(j-1)} + \rho(s_{1d}^{(j-1)} + s_{2d}^{(j-1)})\right]^{-1}$$

Where $q_j = s_{1d}^{(j-1)}$ or $\rho(s_{1d}^{(j-1)} + s_{2d}^{(j-1)})$ depending upon whether the jth step in $R(n,a)$ is an infection or a removal, respectively. However, since a path from $(N-a,a)$ to (r,s) must always contain $N-a-r$ infections and $N-r-s$ removals, the product of the $q_j's$ is completely determined, so that

$$\pi_d = \frac{(N-a)!}{r!}\,\rho^{N-r-s}\,\frac{N!}{(r+s)!}\prod_{j=1}^{E}\left(b_d^{(j)}\right)^{-1} s_{2d}^{(j-1)} \tag{12.18}$$

Where

$$b_d^{(j)} = s_{2d}^{(j-1)}\left[s_{1d}^{(j-1)} + \rho(s_{1d}^{(j-1)} + s_{2d}^{(j-1)})\right] \tag{12.19}$$

To evaluate $p^*_{r,s}(t,d)$ let us prove that the following result.

Theorem 12.1

Let $T_1, T_2, \ldots\ldots\ldots, T_n$ be independent random variables having negative exponential distributions with distinct means $\mu_1^{-1}, \mu_2^{-1}, \ldots\ldots\ldots, \mu_n^{-1}$, respectively, and -$S_n = \sum_{k=1}^{n} T_k$. Then

$$Pr\{S_n < t\} = 1 - \sum_{j=1}^{n} C_{n,j} \exp(-\mu_j t)$$

Where

$$C_{n,j} = \prod_{\substack{i=1 \\ i \neq j}}^{n} \mu_i (\mu_i - \mu_j)^{-1} \qquad (j = 1,2, \ldots\ldots, n)$$

The time spent by $R'(n,a)$ in state $(s_{1d}^{(j-1)} + s_{2d}^{(j-1)})$ has negative exponential distribution with mean $\tilde{b}_d^{(j)}$, where

$$\tilde{b}_d^{(j)} = b_d^{(j)} (s_{1d}^{(j-1)} + s_{2d}^{(j-1)})^{-1} \tag{12.20}$$

Now since $R'(n,a)$ enters state (r,s) after E steps and leaves at the $(E+1)$ th step, $p_{r,s}^*(t,d)$ is simply the probability that the process enters (r,s) before t and leaves after t. Thus, writing $W_{i,j}$ is the time elapsing between the ith and jth steps,

$$p_{r,s}^*(t,d) = Pr\{W_{1,E} < t, W_{1,E+1} > t\}$$

$$= Pr\{W_{1,E+1} > t\} - Pr\{W_{1,E} > t\} \tag{12.21}$$

Since $W_{1,E+1}$ and $W_{1,E}$ are both sums of negative exponential random variables we may apply theorem 2.1, provided that $\tilde{b}_d^{(j)}(j = 1,2, \ldots \ldots, E+1)$ are distinct. Let us assume that ρ is such that

$$Y(x/(x+y)+\rho)\left((x,y) \in E_{n,a}\ and\ y = 0\right) \text{ are distinct}$$

Let us get

$$p_{r,s}^{*}(t,d) = \sum_{k}^{E+1} \prod_{j=1}^{E} \tilde{b}_d^{(j)} \prod_{\substack{i=1 \\ i \neq j}}^{n} \left(\tilde{b}_d^{(j)}{}_i - \tilde{b}_d^{(k)}\right)^{-1} exp\left(-\tilde{b}_d^{(k)} t\right) \quad (12.22)$$

Combining (12.18) and (12.22) and collecting together coefficients of the same exponential term yields

$$p_{r,s} = \frac{(N-a)!}{r!}\, \rho^{N-r-s} \frac{N!}{(r+s)!} \sum_{m=r}^{N-a} \sum_{w=M}^{N-m} \sum_{d \in D_{mw}} \left(\prod_{j=1}^{E} \left(\frac{s_{2d}^{(j-1)}}{(s_{1d}^{(j-1)} + s_{2d}^{(j-1)})} \right) \right)$$

$$\times \prod_{\substack{k=1 \\ k \neq L+1}}^{n} \left(\tilde{b}_d^{(k)} - \tilde{b}_d^{(L+1)}\right)^{-1} exp\left(-w\left(\frac{m}{m+w} + \rho\right) t\right)$$

(12.23)

Where D_{mw} is the set of all paths from $(N-a, a)$ to (r, s) that pass through $(m, w), L = 2(N-m) - (w+a)$ is thelength of the path from $(N-a, a)$ to (m, w) and $M = max(1, r+s-m)$ is the smallest value w may take given that the path must end at (r, s). Let D_1 denote the set of all paths from

$(N-a,a)$ to (m,w) and D_2 denote the set of all paths from (m,w) to (r,s). consider the function $\eta: D_{mw} \to D_1 \times D_2$ defined by

$$\eta\left(\left(s_{1d}^{(0)}, s_{2d}^{(0)}\right), \left(s_{1d}^{(1)}, s_{2d}^{(1)}\right), \dots\dots\dots\dots\dots\dots \left(s_{1d}^{(E)}, s_{2d}^{(E)}\right)\right)$$

$$= \left(\left\{\left(s_{1d}^{(0)}, s_{2d}^{(0)}\right), \left(s_{1d}^{(1)}, s_{2d}^{(1)}\right), \dots\dots\dots\dots\dots\dots \left(s_{1d}^{(L)}, s_{2d}^{(L)}\right),\right.\right.$$

$$\left.\left.\left(s_{1d}^{(L)}, s_{2d}^{(L)}\right), \left(s_{1d}^{(L+1)}, s_{2d}^{(L+1)}\right), \dots\dots\dots\dots\dots\dots \left(s_{1d}^{(E)}, s_{2d}^{(E)}\right)\right\}\right)$$

It is easily verified that η is a bijection from D_{mw} on $D_1 \times D_2$, so every $d \in D_{mw}$ has a unique image $\eta(d) = (d_1(d), d_2(d))$, say, where $d_j(d) \in D_j (j = 1,2)$. Using this and fact that $|D_{mw}| = |D_1||D_2|$ we may rewrite (12.23) in the form

$$p_{r,s} = \frac{(N-a)!}{r!}\, \rho^{N-r-s}\, \frac{N!}{(r+s)!}$$

$$\times \sum_{m=r}^{N-a} \sum_{w=M}^{N-m} C_1(m,w|N-a,a)\, C_2(m,w|r,s)\, exp\left(-w\left(\frac{m}{m+w}+\rho\right)t\right)$$

Where using (12.19) and (12.20)

$$C_1(m,w|N-a,a) = \sum_{d_1 \in D_1} \prod_{j=1}^{L} s_{2d_1}^{(j-1)} \left\{s_{2d_1}^{(j-1)} + s_{1d_1}^{(j-1)} \left[s_{1d_1}^{(j-1)} + s_{2d_1}^{(j-1)}\right]\right.$$

$$\left.\rho s_{2d_1}^{(j-1)} - exp\left(\left(\frac{m}{m+w}+\rho\right)t\right)\right\}^{-1}$$

and

$$C_2(m,w|r,s)=\frac{w}{s}.\frac{(r+s)}{(m+w)}\sum_{d_2\in D_{12}}\prod_{j=1}^{E-L}s_{22}^{(j)}\left\{s_{2d_{12}}^{(j)}s_{1d_{12}}^{(j)}\left[s_{1d_2}^{(j)}+s_{2d_2}^{(j)}\right]\right.$$

$$\left.\rho s_{2d_2}^{(j)}-w\left(\frac{m}{m+w}+\rho\right)\right\}^{-1}$$

Total size

For $w=0,1,2,\ldots\ldots\ldots,n$,let $P_w=Pr\{Z(\infty)=a+w\}$ be the probability of an epidemic with total size w.

For $w=0,1,2,\ldots.n$

$$P_w=\lim_{t\to\infty}p_{n-w,0}(t),$$

$$=\lim_{\lambda\to 0}\lambda q_{n-w,0}(\lambda),$$

$$=\lim_{\lambda\to 0}\rho q_{n-w,1}(\lambda),$$

Putting $r=m-w$ and $s=0$ in (2.2). Thus

$$P_w=\rho f_{n-w,1}\qquad\qquad(w=0,1,2,\ldots\ldots,n)$$

where

$$f_{r,s}==\lim_{\lambda\to 0}q_{r,s}(\lambda),\qquad\qquad\left((r,s)\in E_{n,a}\right)$$

Setting λ = 0 in (12.15) and (12.16) we obtain

$$\begin{cases} (r+1)(s-1)f_{r+1,s-1} + \rho(r+s)(s+1)f_{r,s+1} \\ \quad -s\{r+\rho(r+s)\}f_{r,s} = 0 \ \ (r,s) \in E_{n,a}\{n,a\}) \\ a\left(\frac{n}{n+a}+\rho\right)f_{n,a} = 1 \end{cases} \tag{12.24}$$

Threshold Theorems

In this section let us consider the threshold behaviour of the modified stochastic epidemic. In the Literature, there are two different types of threshold theorems for stochastic epidemics, originating in the papers of Whittle and Williams. Let us prove corresponding theorems for the modified stochastic epidemic.

Whittle's Threshold Theorem

Let $i = (Z(\infty) - a)/n$ be the intensity of the epidemic, i.e. the proportion of initial susceptibles that are ultimately infected.

For $i \in [0,1]$ let

$$\pi_i = \sum_{w=0}^{[ni]} P_w,$$

Where $[ni]$ denotes the integer part of ni, be the probability that the intensity of the epidemic doesnot exceed i. Now for such epidemics

$$n(1-i) \leqq X(t) \leqq n \qquad (t \geqq 0)$$

and

$$Z(t) \leqq a + ni \qquad (t \geqq 0)$$

So

$$\frac{\beta n(1-i)Y(t)}{n+a} \leqq \frac{\beta X(t)Y(t)}{X(t)+Y(t)} \leqq \frac{\beta nY(t)}{n(1-i)} \qquad (t \geqq 0)$$

It follows that, for epidemics whose intensity does not exceed i, the modified stochastic epidemic can be sandwiched between two birth – and – death processes, each having death rate γ, but with birth rate $\beta n(1-i)/(n+a)$ and $\beta/(1-i)$ respectively. Let T_1 and T_2 be the respective total sizes of the two birth – and – death processes.

Then

$$Pr\{T_U \leqq [ni]\} \leqq \pi_i \leqq Pr\{T_L \leqq [ni]\} \qquad (12.25)$$

Now

$$Pr\{T_L \leqq [ni]\} \leqq Pr\{T_L < \infty\}$$

and $Pr\{T_U \leqq [ni]\} = Pr\{T_U < \infty\} - Pr\{T_U \in (ni, \infty)\}$.

Further $Pr\{T_U \in (ni, \infty)\}$ tends to 0 as n tends to infinity. It follows that for sufficiently large n, let us have

$$[min\{\rho(1-i), 1\}]^a \leqq \pi_i \leqq \left[min\left\{\frac{\rho(n+a)}{n(1-i)}, 1\right\}\right]^a \qquad (12.26)$$

Thus, for large n, if $\rho \geqq 1$ there is zero probability of an epidemic exceeding any fixed intensity $i > 0$; while if $\rho > 1$ the probability of an epidemic is approximately $1 - \rho^a$, for small i.

William's threshold Theorem

Let us consider the modified stochastic epidemic with n initial susceptibles and a initial infectives, and for $w = 0,1, \ldots \ldots, n$ and let $P_w^{(n)}$ be the probability of an epidemic with final size w. in order to derive a Williams – type threshold theorem we need to determine

$P_w = \lim_{n\to\infty} P_w^{(n)}$ $(w = (0,1, \ldots \ldots)$ and finding conditions under which $\sum_{w=0}^{\infty} P_w < 1$, so the limiting total size distribution has a non – zero mass at infinity. Let us consider the embedded random walk R(n,a) defined in section (3.1). Using (3.4) yields that

$$P_w^{(n)} = \frac{n!}{(n-w)!}\frac{(n+a)!}{(n-w)!}\rho^{w+a}\sum_{d\in D}\left\{\prod_{j=1}^{E}\left(s_{1d}^{(j-1)} + \rho(s_{1d}^{(j-1)} + s_{2d}^{(j-1)})\right)\right\}^{-1} \tag{12.27}$$

Where D is the set of all paths from (n, a) to $(n - w, 0)$, $E = 2w + a$ is the length of any path in D, and $\left(s_{1d}^{(k)} + s_{2d}^{(k)}\right)$ $(k = 0,1, \ldots \ldots, E)$ are the coordinates of the path d. The factorial expressions in (3.3) may be expressed as $n(n-1) \ldots \ldots (n-w+1)(n+a)(n+a-1) \ldots \ldots \ldots (n-w+1)$, so $P_w^{(n)}$ is ρ^{w+a} times the sum of product of terms of the form

$$(n-m)\left\{s_{1d}^{(j-1)}+\rho\left(s_{1d}^{(j-1)}+s_{2d}^{(j-1)}\right)\right\}^{-1}$$

$$(m=-a,-a+1,.,w-1;j=0,1,\ldots,E-1)$$

Now, for $j = 0,1,\ldots\ldots\ldots,E-1, n-w \leqq s_{1d}^{j} \leqq n$ and $n-w+1 \leqq s_{2d}^{j} + s_{1d}^{j} \leqq n+a$, so by the sandwhich theorem

$$\lim_{n\to\infty}(n-m)\left\{s_{1d}^{(j-1)}+\rho\left(s_{1d}^{(j-1)}+s_{2d}^{(j-1)}\right)\right\}^{-1} = (1+\rho)^{-1}$$

$$(m=-a,-a+1,.,w-1;j=0,1,\ldots,E-1) \quad (12.28)$$

Using the Ballot theorem

$$|D| = \frac{(2w+a-1)!\,a}{w!\,(w+a)!} \quad (12.29)$$

It now follows from (12.26) – (12.29) that

$$P_w = \frac{(2w+a-1)!\,a}{w!\,(w+a)!}\,\frac{\rho^{w+a}}{(1+\rho)^{2w+a}} \quad (12.30)$$

The limiting distribution given by (12.30) is the same as that found by Williams for the general stochastic epidemic, and corresponds to the total size of a birth – and – death process, with birth rate 1, death rate ρ and initial population size a. Thus in the limit as n tends to infinity, the probability of a finite epidemic is given by $\{min(\rho,1)\}^a$, so a major epidemic can occur if and only if $\rho < 1$.

Conclusion

The purpose of the topic is to give some simple application of martingales to epidemics. The results are connected with stopping times. The expression of the joint generating functions Laplace transforms of $X_T, \int_0^T X_u Y_u \, du$ and $\int_0^T Y_u \, du$ is obtained. X_u and Y_u denote the numbers of susceptibles and Carriers, Several relations between different types of epidemics are given. Here, Downston's is discussed. We have proved simple relation between moments here.

Daniels has shown that when the Threshold is large but the population size is much larger the distribution of the number remaining uninfected in a large epidemic has approximately a Poisson form with deterministic manner. This chapter gives the rather intuitive proof of Daniels result. The proof is based on a construction of this epidemic process which is more explicit than the usual description.

Results on SIS SIR SIRS models are summarized. For the SIR and SIRS models three subscripts are required for the probabilities. The basic reproduction number R_0 plays a fundamental role for through the Threshold results differ some what. The comparison of Thresholds results for the determinants and stochastic version of the homogeneous Si model with recruitment death due to the disease the background death rate are discussed.

Wiess's and Downston's model with parameter π, α and β depending on i number of susceptibles and j number of carriers. A martingale argument is performed where π and α/β depend on i or Weiss case. Martingale approach proved very valuable and given explicit results. At the end of this chapter well known results between moments and integrals along a trajectory are still true for any stopping time.

A model for the spread of an epidemic in a closed, homogeneously mixing population in which new infections occur at rate $\beta xy/(x+y)$, where x and y are the numbers of susceptible and infectious individuals, respectively, and β is an infection parameter is discussed. This contrasts with the standard general epidemic in which new infections occur at βxy. Both the deterministic and stochastic versions of the modified epidemic are analysed. The deterministic model is completely soluble. The time – dependent solution of the stochastic model is derived. Threshold theorems, analogous to those of Whittle and Williams for the general stochastic epidemic, are proved for the stochastic model.

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