ON THE SOLUTION OF THE EPIDEMIC EQUATION

SIGEKI SAKINO

(Received Sept. 4, 1966)

1. Introduction

The theory of general stochastic epidemics has not yet been fully explored on the basic epidemic equation. However, some important properties, for example, a probability version of the threshold theorem valid for sufficiently large populations, have been explored. That is, if $\rho > n$, there is likely to be only a minor outbreak of infectives, but if $\rho > n$, we have a U-shaped distribution of total epidemic sizes, where the parameter ρ expresses a relative removal rate and n the initial number of susceptibles. These numerical results were already given by Whittle and Bailey. Some discussions on the stochastic epidemic theory were also given by Bartlett, Kendall and Whittle. They pointed out that the population of infectives was approximately subject to a birth-and-death process with birth-rate βn and death-rate γ when the population size n was large. Whittle gave an ingenious method of investigating limiting behaviour in epidemic propagation. He gave the relation between the probability P_w of the total number of new infectives up to $t=\infty$, not counting the initial a infectives, and the probabilities for every epidemic size state of the restricted process or unrestricted process. The restricted process expresses that no new birth occurs if the total number of individuals who have ever been infected, reaches n+a.

The solution of the basic model is not yet derived. We shall give the solution of the basic model when the size of the initial population is, generally, n. We shall illustrate the numerical results when n=1, 2, 3, 5 in section 4, and compare them with the solution by the Monte Carlo method in section 5.

2. The basic model of epidemic

We suppose here that there are n susceptibles and a infectives at time t=0. Now, we shall denote by $P_{rs}(t)$ the probability that there are r susceptibles still not infected and s infected in circulation at time t. The chance of one new infection in time dt is taken to be $\beta rsdt$, and

the chance of one removal $\gamma s dt$ where the rate β shows the contact rate and γ the removal rate. It will be realized that the stochastic process so defined implies an epidemic model in which (a) new infected individuals are themselves infectious, i.e. the latent period is zero, and (b) the length of time for which an infective remains infectious, i.e., infectious period, has the negative exponential distribution $dF = \gamma e^{-rt} dt$. When we use the time scale given by $\tau = \beta t$ instead of t and denote by $\gamma/\beta = \rho$ the ratio of removal rate to infection rate which we shall call the relative removal rate, we can derive the differential-difference equation as follows:

$$\begin{split} \frac{dP_{rs}}{d\tau} &= (r+1)(s-1)P_{r+1,s-1} - s(r+\rho)P_{rs} + \rho(s+1)P_{r,s+1} \,, \\ (1) & \frac{dP_{na}}{d\tau} = -a(n+\rho)P_{n0} \end{split}$$

where

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

and the initial condition $p_{na}(0)=1$.

The probability generating function given by

(2)
$$\pi(u, v; \tau) = \sum_{r,s} u^r v^s P_{rs}(\tau)$$

satisfies the partial differential equation,

(3)
$$\frac{\partial \pi}{\partial \tau} = (v^2 - uv) \frac{\partial^2 \pi}{\partial u \partial v} + \rho (1 - v) \frac{\partial \pi}{\partial v}$$

where the initial condition is

$$\pi(u,v;0)=u^nv^a.$$

Also, putting the complex variable as λ where the real part is positive, we can derive the following equation by the Laplace transform:

$$(5) (v^2 - uv) \frac{\partial^2 \pi^*}{\partial u \partial v} + \rho (1 - v) \frac{\partial \pi^*}{\partial v} - \lambda \pi^* + u^n v^a = 0$$

where

(6)
$$\pi^* = \pi^*(u, v; \lambda) = \int_0^\infty \pi(u, v; \tau) e^{-\lambda \tau} d\tau.$$

The differential-difference equation (1), the partial differential equation (3) or (5) is said to be the basic model of epidemic. So far these partial differential equations have not been completely solved. But the limiting solution of equation (3) was already given by Whittle as stated

in section 1. If the initial number of susceptibles n is large, it is obvious that the population of infectives is approximately subject to a birth-and-death process with birth rate βn and death-rate γ , respectively. In such a case, the equation (1) was solved by Bartlett, Bailey and Kendall. And, also, investigations of small epidemic with both the latent period and infectious period having negative exponential distribution or general χ^2 -distribution were made by Bailey.

As stated in the above, we cannot solve the partial differential equation (3) or (5) directly, but from the epidemic equation (1), we can easily derive the solution of the equation (3) or (5). Now, using the Laplace transform, we can replace the differential-difference equation (1) by the recurrence relation

(7)
$$q_{rs} = \frac{(r+1)(s-1)}{\lambda + s(r+\rho)} q_{r+1,s-1} + \frac{\rho(s+1)}{\lambda + s(r+\rho)} q_{r,s+1},$$

$$q_{na} = \frac{1}{\lambda + a(n+\rho)}$$

where

(8)
$$q_{rs} = P_{rs}^*(\lambda) = \int_0^\infty P_{rs}(\tau) e^{-\lambda \tau} d\tau$$

and the real part $R(\lambda)$ of the complex variable λ is positive. Any q_{rs} where suffices fall outside the permitted ranges is taken to be identically zero. An exact calculation of the probability for the number of susceptibles r and infectives s is extremely laborious, but very simple.

Now, from the recurrence relation (7), we shall give the general solution of the differential-difference equation (1). For this purpose, a convenient simplication of the recurrence relation (7) is given by putting

$$q_{rs} = \frac{n! \rho^{n+a-r-s}}{r! s} f_{rs}.$$

Then, the transformation (9) gives the new recurrence formulae

(10)
$$f_{rs} = \frac{s}{\lambda + s(r+\rho)} (f_{r+1,s-1} + f_{r,s+1}),$$

$$f_{na} = \frac{a}{\lambda + a(n+\rho)}.$$

From the new recurrence formulae (10), we can express f_{rs} as a linear function of $f_{r+1,i}$, $i=s-1, s, \dots, n+a-r-1$:

(11)
$$f_{rs} = \sum_{i=s-1}^{n+a-r-1} \prod_{j=s-1}^{i} \frac{(j+1)}{\{\lambda + (j+1)(r+\rho)\}} f_{r+1,i} \quad \text{for } s \ge 2,$$

$$f_{r1} = \frac{f_{r2}}{\lambda + r + \rho}.$$

Thus, starting with f_{na} , we can calculate all the f_{rs} successively.

Now, we shall assume the number of the initial infectives to be a=1, without losing generality. Then, if $\delta_l(i_l)$ expresses the function

(12)
$$\delta_{l}(i_{l}) = \begin{cases} 1, & \text{if } i_{l} = 1, \\ 0, & \text{if } i_{l} \neq 1, \end{cases}$$

 f_{rs} is expressed as follows:

Thus, we can obtain $q_{rs}(\lambda)$ by using the transformation (9). Then, from this complex function $q_{rs}(\lambda)$, we find that the generating function $\pi^*(u, v; \lambda) = \sum_{r,s} u^r v^s q_{rs}(\lambda)$ is evidently the solution of the partial differential equation (5). Also, as its inverse Laplace transform with respect to time τ is

(14)
$$\pi(u, v; \tau) = \frac{1}{2\pi i} \int_{y-i\infty}^{y+i\infty} \pi^*(u, v; \lambda) e^{\lambda \tau} d\lambda,$$

where the real part $R(\lambda)=y$ is positive, we can derive the solution of the partial differential equation (3) by using the above inverse Laplace transform. If we show the probability of an epidemic of total size w by P_w , we have the relation

(15)
$$P_{w} = \lim_{\tau \to \infty} P_{n-w,0}(\tau) = \lim_{\lambda \to 0} \rho q_{n-w,1}, \qquad 0 \leq w \leq n.$$

The probability P_w was given by Whittle. But it can also easily be calculated from (9) and (13).

We shall show the alternative method using the set of generating functions in the next section.

3. An alternative expression of f_{rs}

From the recurrence relation (7), we can give the alternative expression that shows the solution f ($s \ge 1$) using the set of generating functions

(16)
$$G_r(x) = \sum_{s=1}^{n-r+1} x^{s+1} f_{rs}, \qquad 0 \le r \le n$$

Multiplying the first equation in (10) by x^{s+1} and summing over s, we get

(17)
$$\frac{\lambda x - (r+\rho)x + 2}{x\{1 - (r+\rho)x\}} G_r(x) - G_r'(x) = \frac{x^2}{1 - (r+\rho)x} G_{r+1}'(x)$$

where

$$(18) G_{n+1}(x) = x$$

and $G'_{r}(x)$ expresses the derivative dGr(x)/dx. Therefore, from the relation (17), we can derive the equation

(19)
$$G_r(x) = \frac{x^2}{\{(r+\rho)x-1\}^{1/(r+\rho)+1}} \int_{-\infty}^{x} \{(r+\rho)u-1\}^{1/(r+\rho)} du,$$

$$r = 0, 1, 2, \dots, n.$$

Furthermore, from the relation (19), we can give every $G_r(x)$ $(r=0, 1, 2, \dots, n)$ as follows:

$$\begin{split} G_{n}(x) &= \frac{x^{2}}{\lambda + n + \rho} , \\ G_{n-1}(x) &= \frac{2x^{2}}{(\lambda + n + \rho)(\lambda + n - 1 + \rho)\{\lambda + 2(n - 1 + \rho)\}} \\ &\quad + \frac{2x^{3}}{(\lambda + n + \rho)\{\lambda + 2(n - 1 + \rho)\}} , \\ G_{n-2}(x) &= \prod_{i=1}^{3} \prod_{k=1}^{i} \frac{1}{\{\lambda + k(n - i + 1 + \rho)\}} \\ &\quad \times [\{4(\lambda + 3(n - 1 + \rho)) + 12(\lambda + n - 1 + \rho)\}x^{2} \\ &\quad + (\lambda + n - 2 + \rho)\{4(\lambda + 3(n - 2 + \rho)) + 12(\lambda + n - 1 + \rho)\}x^{3} \\ &\quad + 6(\lambda + n - 1 + \rho)(\lambda + n - 2 + \rho)(\lambda + 2(n - 2 + \rho))x^{4}] , \end{split}$$

Generally, $G_r(x)$ is expressed as

(20)
$$G_{r}(x) = \frac{x^{2}}{\{(r+\rho)x-1\}^{1/(r+\rho)+1}} \left[\int^{x} \int^{x_{r+1}} \cdots \int^{x_{n}} \{(r+\rho)x_{r+1}-1\}^{1/(r+\rho)} \times \prod_{k=r+1}^{n} \frac{x_{k}\{(k+\rho-\lambda)x_{k}-2\}\{(k+\rho)x_{k+1}-1\}^{1/(r+\rho)}}{\{(r+\rho)x_{k}-1\}^{1/(r+\rho)+2}} \times dx_{n+1} dx_{n} \cdots dx_{r+1} \right]$$

From the above set of generating functions $G_r(x)$ $(r=0, 1, \dots, n)$, we can calculate all f_{rs} :

(21)
$$f_{rs} = \frac{1}{(s+1)!} \frac{\partial^{s+1} G_r(x)}{\partial x^{s+1}} \Big|_{x=0} s=1, 2, \dots, n+1-r.$$

From the transformation (9) and the inverse Laplace transform, we can give every P_{rs} . Then, the probability $P_{rs}(t)$ is evidently the solution of the epidemic basic equation (1) or (3).

4. Examples

We obtained the solution $q_{rs}(\lambda)$ of the epidemic equation (5) from the equation (13) when the initial number of susceptibles is n and that of infectives a=1. Now, as examples, we shall show the solution when the initial number of susceptibles n is 1, 2, 3, or 5. Here, for the sake of simplicity, we used the relative removal rate $\rho=0.501$ because the equation (13) has only the first order poles when $\rho=0.501$.

5. Monte Carlo method

In the preceding sections, we did not consider the infected time of the infective. But it is important in the analysis of epidemic that we consider the time when the infective is infected. From such a point of view, 200 epidemics were observed in order to obtain the present results. Thus the standard error in a probability whose value is p is $[p(1-p)/200]^{1/2}$, or about 0.0212 for values near 0.1 in the following Monte Carlo experiments. We calculated the mean number of infectives \bar{S}'_t , the variance V'_s , the correlation coefficient C'_{rs} between the numbers of susceptibles and infectives, and the distribution $A(\tau, t)$ of the progress time τ of the infective at time t by the Monte Carlo method when the initial size of

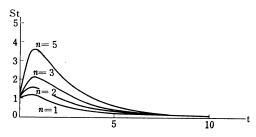


Fig. 1. S_t expresses the mean number of infectives at time t and n the initial number of susceptibles when $\rho = \gamma/\beta = 0.501$.

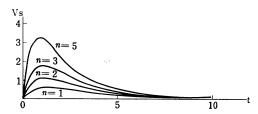


Fig. 2. V_s expresses the variance of the number of infectives at time t, when ρ =0.501.

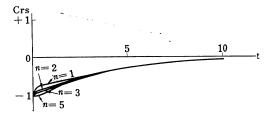


Fig. 3. C_{rs} expresses the correlation coefficient between the numbers of infectives and susceptibles at time t, when $\rho=0.501$.

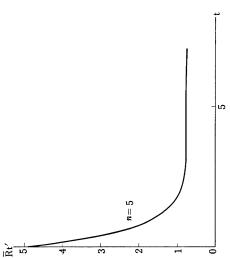


Fig. 6. R_t' expresses the mean number of susceptibles at time t by the Monte Carlo method.

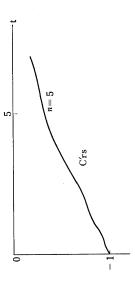
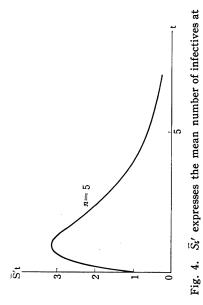
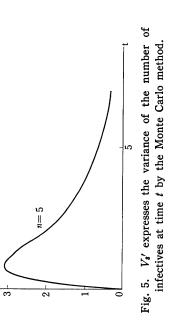


Fig. 7. C_{rs} expresses the correlation coefficient between r and s at time t by the Monte Carlo method.



time t by the Monte Carlo method.



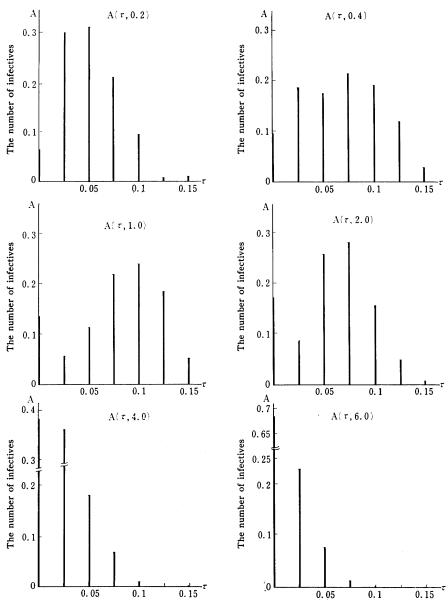


Fig. 8. Each $A(\tau,t)$ expresses the distribution of the duration time τ of the epidemic at time t.

susceptibles is n=5. As stated in section 2, we assumed, of course, that (a) new infected individuals were themselves infectious i.e. the latent period was zero, and (b) the length of time to the recovering time from the infected time had the negative exponential distribution $dF = \gamma e^{-r\epsilon}$ where γ expressed the recovering-rate. These results are shown in figs. 4-8. The point which is different from the method of sections 2 and 3 is

that we considered each epidemic path. As shown in these graphs, these results do not differ so largely from those of section 4. But, really, we must consider the duration time of the epidemic so as to analyze the epidemic data and predict the number of infectives at time t from such a point of view.

6. Conclusion

We obtained the general solution of epidemic equation (1) using the recurrence relation and gave the numerical examples of the means and variances of the number of infectives at time t for the initial number of susceptibles n=1,2,3,5 (in sections 2, 3 and 4). Then (in section 5), considering the infected time, we constructed the epidemic model by the Monte Carlo method and calculated the distribution of the duration time τ from the infected time at time t.

Acknowledgement

Thanks are due to Mr. Koki Takahasi for his help in programming of computation.

THE INSTITUTE OF STATISTICAL MATHEMATICS

REFERENCES

- [1] Norman T. J. Bailey, "The total size of general stochastic epidemic," *Biometrika*, 40 (1953), 177-185.
- [2] Norman T. J. Bailey, "Some stochastic models for small epidemics in large populations," *Appl. Statist.*, 13 (1964), 9-19.
- [3] P. Whittle, "The outcome of a stochastic epidemic —a note on Bailey's paper—," Biometrika, 42 (1955), 116-122.