ON THE ANALYSIS OF EPIDEMIC MODEL II
(THEORY AND APPLICATION)

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1. Introduction

In the previous paper ([3]), we gave some new epidemic models for predicting the propagation of epidemics. However, we must consider the validity of these deterministic or stochastic models in the light of the real epidemic data, that is, we must consider whether our models are really useful in predicting the number of patients in future. After that, the usefulness of epidemic models is proved. Now the time-continuous models of epidemic which has been developed since Kermack and McKendrick are all theoretical and, still, we have few chance to see its application to epidemic data. Therefore, we doubt whether their models are useful for prediction.

In the present paper, we shall state properties of our deterministic and stochastic epidemic models in the community where the assumption of homogeneous mixing is satisfied and predict the number of infectious cases at the time t, applying the above models to the case of influenza in Isesaki City, Gumma Prefecture, in october, 1957. From so doing, we shall be able to see the validity of our models.

We must explain the following two points before we analyse the epidemic models.

The first is to derive the method of communication of infectious disease. As shown in the previous paper, we treat only the diseases that are infectious in the sense of being communicable at the appropriate stage of the development in an infected individual by adequate contact with susceptible persons. Now, let us assume that the epidemic is started by the introduction of some infected individuals to a population of the susceptible. As soon as the germs unter into the body of susceptible persons by the adequate contact with infected individuals, they undergo certain biological developments within the body during the incubation period, but any kind of infectious material is not exhaled. The difficulty in treating the problems lies in the existence of carriers. There are individuals who are apparently healthy without any manifest

symptom, but discharge the germ micro-organisms and can communicate the disease to others. Little has been done yet on this point, though it is very important. The purpose of the present paper is to treat this problem mathematically under some assumptions. As shown in the previous paper, it is an important fact that all of the susceptible who have had the effective contact with infected person do not always get sick. Even if the micro-organisms would enter into the body of a susceptible person, he would not necessarily show recognizable symptoms. According to the kind of disease, it does not make difference in producing the permanent or temporary immunity in the body of infected persons whether the susceptible who have had the effective contact have recognizable symptoms or not. Considering poliomyelitis, for example, it is said that the rate of the risk of onset when the susceptibles are exposed to the viruses at the same time is less than 1 percent, and the other 99 percent or more of persons do not contract the disease. Yet, most of those infected cases, both with apparent infection and inapparent infection, will acquire temporary or permanent immunity. Now, let us call these cases of inapparent infection followed by the acquisition of immunity "inapparent immunes". Taking into account these inapparent immunes, we feel more or less dissatisfaction for the epidemic models which have been developed since pioneers Hamer, Ross, Soper and McKendrick. As shown in the next section, we shall construct epidemic models taking into consideration the above fact.

The second that we want to point out is the reason why we have taken up the data of influenza epidemic among school-children as an example of epidemic model. The epidemic of influenza commonly affects a high percentage of the population. Once the epidemic takes place, it is not unusual that the incidence rate for all ages amounts to as high as 30% or 40%. The rate tends to be higher at preschool and school ages than at any other ages. Therefore, from the viewpoint of health or school-management, the local public health authorities must take any preventive measure against the epidemic of influenza with emphasis on school-children. For example, the closing of schools may be employed, if it is considered to be effective in checking spread. In case we accept that the closing of school is being of value, we should try to know when it will be desirable to make decision of practising this. If we can know the adequate time for the school closing,

we will be able to expect the most effective way of minimizing the propagation of disease of school community. For this purpose, we must estimate the time when the number of patients of influenza becomes maximum, and the number of patients at that time on the basis of the data for the first several days in the beginning of the epidemic. Thus, if the closure of school is revealed to be effective in controlling the influenza epidemic, we shall be able to give the scientific basis on this counter measure. For such purpose, we surveyed the propagation of influenza among school-children selecting one school district in Isesaki City, Gumma Prefecture.

In sections 3, 4 we shall give prediction of the time of the maximum number of influenza patients using our influenza data.

2. Deterministic treatment (i)

Let us assume that the epidemic is started by the introduction of a infectious individuals into a population of n susceptibles and this community of total size $n+a$ comprises, at time t, x susceptibles, y infectives in circulation, and z removals who are isolated, dead or recovered and healthy immune. Thus $x+y+z=n+a$. As in the previous paper, let β_1, β_2 and γ denote the incidence rate, the inapparent immune rate and the removal rate, respectively.

In the infinitesimal time interval $(t, t+dt)$, therefore, there are $\beta_1 xydt$ new infections, $\beta_2 xydt$ new inapparent immune cases, and γydt removals from infectious cases. The basic differential equations are easily seen to be

$$\left.\begin{aligned} \frac{dx}{dt} &= -(\beta_1 xy+\beta_2 xy) \\ \frac{dy}{dt} &= \beta_1 xy-\gamma y \\ \frac{dz}{dt} &= \beta_2 xy+\gamma y \end{aligned}\right\} \qquad (1)$$

Making use of the relative removal rates $\rho_1=(\beta_2/\beta_1)$, $\rho_2=(\gamma/\beta_1)$, we shall be able to give the solution of the above differential equations (1). From the first and second of the above equations, we get, by division, after integration,

$$y=(a+\frac{n}{1+\rho_1}-\frac{\rho_2}{1+\rho_1}\log n)-\frac{x}{1+\rho_1}+\frac{\rho_2}{1+\rho_1}\log x\,. \tag{2}$$

From the second of (1),

$$y=a\exp\left\{\int_0^t(x-\rho_2)dt\right\}\leqq a \qquad \text{if } n\leqq\rho_2\,, \tag{2'}$$

and

$$\frac{dy}{dt}>0 \qquad \text{if } n>x>\rho_2\,, \tag{2''}$$

$$\frac{dy}{dt}<0 \qquad \text{if } n>\rho_2>x\,. \tag{2'''}$$

From (2''), (2'''), the peak of the epidemic curve occures at $x=\rho_2$. Further, from the first of (1) and (2), the parametric solution is given by

$$t=\int_x^n\frac{dw}{w(K-w+\rho_2\log w)} \tag{3}$$

where $K=a(1+\rho_1)+n-\rho_2\log n$. Let η_x be the unique positive root in $0<\eta<\rho_2$ of

$$\eta(K-\eta+\rho_2\,\text{lof}\,\eta)=0\,. \tag{3'}$$

Then η_x represents the number of susceptibles at $t=\infty$, and therefore, $\eta_x\to 0$ as $\rho_2\to 0$. Therefore, $[(n-\eta_x)/(\beta_1+\beta_2)]\,\beta_1$ represents the number of infective and $[(n-\eta_x)/(\beta_1+\beta_2)]\,\beta_2$ inapparent immune cases at $t=\infty$. This is of considerable importance in understanding the mechanism underlying the absence or occurence of outbreaks of epidemic disease.

The numerical solution y_t of differential equations (1) is approximately given by the mean value $\bar{s}_t$ of s_t which will be stated in section 4.

However, in this model, the time when the infectives contracted is not considered. Really, we must remember that the recovering time depends on the time of contracting. Therefore, we need to improve this model. In the next section, we shall give a new deterministic model depending on the contracting time and apply our improved model to the data of influenza.

3. Deterministic treatment (ii)

In this section, we shall construct an epidemic model considering the time of contracting.

Now let $G(\tau, t)$ be the probability that one person infected at the time τ will not recover before the time t. That is, $G(\tau, t)$ shows the

probability of duration of disease from the infected moment τ to the time t. Further, let $h_1(t)$ dt denote the number of persons infected in the infinitesimal time interval $(t, t+dt)$ and $h_2(t)dt$ the number of inapparent immunes, and let $F(t)$ be the number of infectives at the time t and the initial number of infectives equal to $F(0)=a$. Then, according to the principle of Hamer's epidemic propagation, we can get the following equations

$$\left.\begin{aligned} h_1(t)&=\beta_1 F(t)\left\{n-\int_0^t (h_1(\tau)+h_2(\tau))d\tau\right\}, \\ h_2(t)&=\beta_2 F(t)\left\{n-\int_0^t (h_1(\tau)+h_2(\tau))d\tau\right\}, \\ F(t)&=\int_0^t h_1(\tau)G(\tau, t)d\tau+aG(0, t), \end{aligned}\right\} \quad (4)$$

where n is the number of susceptibles at the initial $t=0$, β_1 infection rate and β_2 inapparent immune rate. Now, putting $\bar{h}_1(t)=h_1(t)-h_1(0)$, we are able to give a non-linear integral equation of Volterra's type from the equations (4), that is

$$\bar{h}_1(t)=\int_0^t R(t, \tau, \bar{h}_1(\tau))d\tau+f(t) \quad (5)$$

where

$$R(t, \tau, \bar{h}_1(\tau))=\beta_1\left[\left\{n-\frac{(\beta_1+\beta_2)}{\beta_1}\int_0^t \bar{h}_1(\tau)d\tau-(\beta_1+\beta_2)nat\right\}(\bar{h}_1(\tau)+\beta na)G(\tau, t)\right.$$
$$\left.-\frac{(\beta_1+\beta_2)}{\beta_1}a(\bar{h}_1(\tau)+\beta_1 na)G(0, t)\right], \quad (6)$$

$$f(t)=\beta_1 na\, G(0, t)-\beta_1 na\,. \quad (7)$$

We assume that $f(t)$ satisfies the Lipshitz condition, $h_1(t)$ is bounded in $0\leqq t\leqq\eta$ and $R(t, \tau, \bar{h}_1(\tau))$ is continuous in the domain $D(0\leqq t\leqq\eta, 0\leqq\tau\leqq\eta, 0\leqq\bar{h}_1\leqq\bar{h}_a)$. Then, $R(t, \tau, \bar{h}_1(\tau))$ satisfies the Lipshitz condition in the domain D with respect to $\bar{h}_1(\tau)$[3], $f(0)=0$, and so, there is the unique solution of the non-linear equation (5). Therefore, we can give the number of new infections $h_1(t)$ from $\bar{h}_1(t)$ in the unit interval $(t, t+1)$.

Using the deterministic non-linear integral equation (5), we can predict the number of patients of influenza in school-children at the time t.

Next, the recovering time distribution of influenza is shown in Fig. 1. When we fitted the Γ-type distribution to our data and tested goodness of fit, ω^2-value was given by 4.17×10^{-4} and the variance by $D^2(\omega^2)=$

$(2.1\times10^{-4})^2$. Thus, it can be said that the Γ-type distribution fits fairely well to our data.

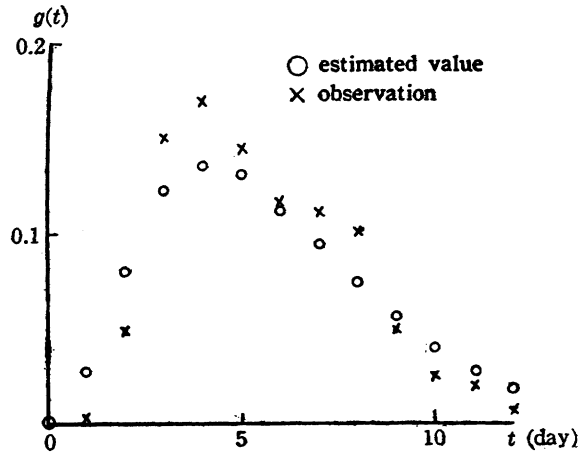

Fig. 1. The recovering time distribution

Next, when we observed the propagation of influenza in school-children for two months from october, 1957, the rates of contraction of lower classes and the upper classes in school-children were as follows.

class \ contraction	the number of infectives at $t=\infty$	the number of non-infections	the rate of apparent immune
lower classes	444	432	0.507
upper classes	409	408	0.501

Table. The rate of apparent immune

In this table it is seen that the rate of contraction of school-children is about 50 percent. Judging from this result, we assumed that the infection rate β_1 equals to the rate of inapparent immune β_2, that is, half of contact members reduces to the infectious members and the other half to the cases of inapparent immunes.

Therefore, $R(t, \tau, h_1(\tau))$ in the non-linear equation (5) is rewritten as

$$R(t,\tau,\bar{h}_1(\tau))=\beta_1\Big[\Big\{n-2\int_0^t\bar{h}_1(\tau)d\tau-2\beta_1nat\Big\}(\bar{h}_1(\tau)+\beta_1na)G(\tau,t)$$
$$-2a(\bar{h}_1(\tau)+\beta_1na)G(0,t)\Big].$$

From Hamer's principle of epidemic propagation, the parameter β_1 is estimated as,

$$\frac{1}{\beta_1}=\frac{1}{n}\sum_{i=1}^{n}\frac{F(t_i)\left(n-2\int_0^{t_i}\bar{h}_1(\tau)d\tau\right)}{\bar{h}_1(t_i)} . \tag{8}$$

Using the data of the first 10 days from the start of influenza, we obtained the estimated value $\hat{\beta}_1=1.94\times10^{-4}$ and the mean recovering time $\overline{t-\tau}=5.2$ days and the variance $v_{(t-\tau)}=10.0$. From the mean time $\overline{t-\tau}$ and the variance $v_{(t-\tau)}$, we determined the Γ-type distribution $1-G(t-\tau)$. From this recovering time distribution $1-G(t-\tau)$ and the parameter $\hat{\beta}_1=1.94\times10^{-4}$, we can derive the numerical solution $h_1(t)$ of the non-linear integral equation (5). As shown in the part of solid line in Fig. 2, the peak of the number of the new patients fits fairly well to the data of influenza. Therefore, we find that we can predict the time of the peak of the number of infectives using the data of the first 10 days.

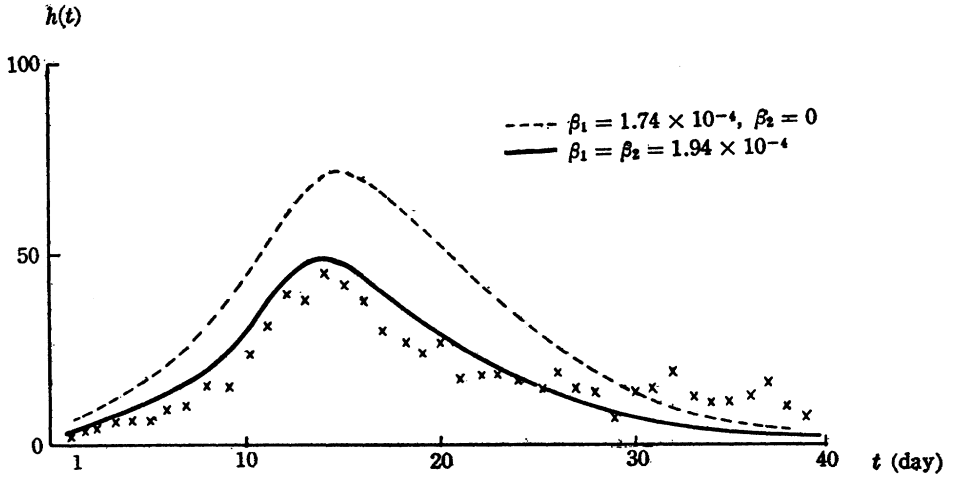

Fig. 2. The number of the new infectines at time t.

If $\beta_2=0$, the estimated value of β_1 during the first 10 days is 1.74×10^{-4}. Then, the epidemic curve of influenza shows much larger values than observations. Thus it does not seem that the model with $\beta_2=0$ is useful to predict the number of the new infectives at the time t.

Furthermore, we can calculate the number of infectives at the time t from the third of equation (4). The numerical values of $F(t)$ are shown in Fig. 3. We find that our result coincides, fairly well with observations. Judging from this result, the authorities of public health will be able to decide an adequate time of taking preventive

measures against the epidemic of influenza and to bring the maximum effect of the prevention against the epidemic of influenza among school-children.

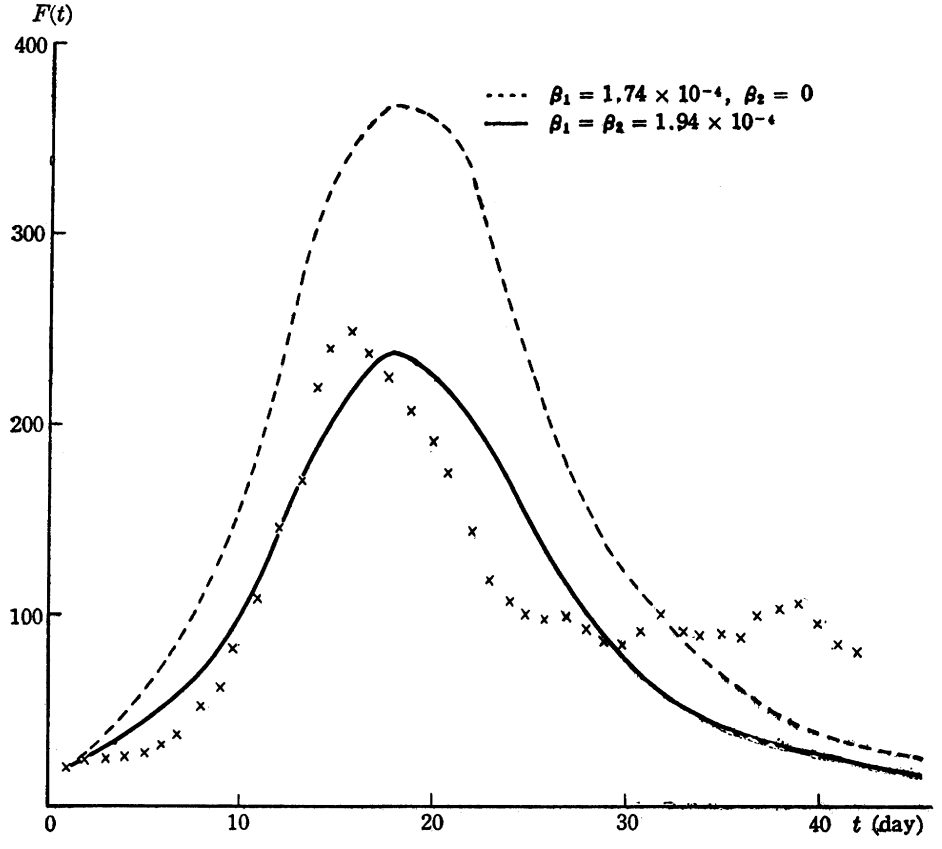

Fig. 3.

Now, we cannot estimate the breadth of fluctuation at every time when we use such a deterministic model. In the next section, we shall construct the stochastic epidemic model by taking into account such a fact.

4. Stochastic treatment

Whether or not an infective person actually communicates his disease to susceptible persons is plainly a matter of chance. The magnitude of this chance may depends on the virulence of the organisms, the extent to which they are discharged, the natural resistance of the susceptibles, the degree of the latter's proximity to the infectives, and

soon. As will be seen in this chapter, suitable assumptions are such that the chance of one new infective or one inapparent immune case in a very short time interval is jointly proportional to the length of the time interval, and the numbers of susceptibles and infectives.

Models based on the above assumptions usually imply that in the community considered all susceptibles and infectives mix together homogeneously. As a first approximation, this idea is almost nearly realized in small groups as households, but is generally at variance with the observed facts in a large group as a town or city. When we try to deal with stochastic processes in large communities, this should always be borne in mind.

Now, we shall state, simply, the real stochastic epidemic model which is shown in the previous paper and apply our model to the data of influenza.

Let us assume that the epidemic is started by the introduction of a infectious individuals into a population of n susceptibles. Therefore, we have the community, the size of which is $n+a$ individuals at time $t=0$. Suppose that, at the time t, there are r susceptibles, s infectives in circulation and q individuals who are isolated, dead, or recovered. Thus we have $r+s+q=n+a$. Now, suppose that, on the assumption of the homogeneous mixing of the susceptibles and infectives in circulation, the conditional probability of one new infection taking place in the very short time interval $(t, t+dt)$ is given by $\beta_1 rs\,dt$ where β_1 shows the constant infection rate. Similarly, suppose that the conditional probability of one new inapparent immune case in $(t, t+dt)$ is given by $\beta_2 rs\,dt$ where β_2 in the inapparent immune rate. Further, suppose that the conditional probability of one infectious patient being removed from circulation in the same interval is given by $rs\,dt$. Then, we can give the differential-difference equation on the probability $P_{rs}(t)$ that at the time t there are r susceptibles still uninfected and s infectious cases in circulation.

$$\left.\begin{aligned}\frac{dP_{rs}(t)}{dt}&=(r+1)(s-1)P_{r+1,\,s-1}(t)+\rho_1(r+1)sP_{r+1,\,s}(t)\\&\quad-(rs+\rho_1 rs+\rho_2 s)P_{rs}(t)+\rho_2(s+1)P_{r,\,s+1}(t)\,,\\\frac{dP_{na}(t)}{dt}&=-(na+\rho_1 na+\rho_2 a)P_{na}(t)\,,\end{aligned}\right\}\qquad(9)$$

where

$$0 \leqq r+s \leqq n+a\ , \quad 0 \leqq r \leqq n\ , \quad 0 \leqq s \leqq n+a\ .$$

The inital condition is $P_{na}(0)=1$, and $\rho_1=(\beta_2/\beta_1)$, $\rho_2=(\gamma/\beta_1)$ show the relative rates to the infection rate. In the previous paper ([3]), we gave the differential-difference equation (9) and illustrated numerically this model by the Monte Carlo Method. Now, we shall predict the number of patients of influenza in school-children at the time t, using this stochastic model. Before doing so, we must state the method of estimation of parameters. Based on the first some day's observations from the start of epidemic, we can estimate the parameters and predict the subsequence number of infectious cases.

For simplicity, we shall consider the case of inapparent immune rate β_2 to be 0. Suppose that we obtained the following sequence as the result of observations,

$$\begin{array}{l} I_0, R_1, \cdots, R_{k_1}, \quad I_1, \quad R_{k_1+1}, \cdots R_{k_2}, \quad I_2, \cdots, R_{k_m}, \qquad I_m \\ (r_0, s_0), \cdots\cdots, (r_0-1, s_1), \cdots\cdots, (r_0-2, s_2), \cdots\cdots, (r_0-m, s_m) \end{array}$$

where I_i shows the i^{th} occurrence of new infection and R_j the j^{th} occurrence of now removal, (r_0-i, s_i) the numbers of susceptibles and infectives when i^{th} new infection occurred. Although bailey gave the variance $V_{(1/m)\Sigma r_i s_i t_i}=(1/m\beta_1^2)$, assuming that $(r_i s_i t_i)$ is independent of $(r_j s_j t_j)$. But $(r_i s_i t_i)$ is dependent of $(r_j s_j t_j)$ so the variance $V_{(1/m)\Sigma r_i s_i t_i}$ is not equal to $(1/m\beta^2)$. We considered the ratio estimate of (γ/β) by the next method. That is, we gave the distribution of the time interval t_{1i} to I_{i+1} from I_i

$$\lambda_1^{(i)} \exp\left(-\lambda_1^{(i)} t_{1i} dt_{1i}\right) \tag{10}$$

where

$$\lambda_1^{(i)}=\frac{\beta r_i}{\beta r_i+\gamma}=\frac{\beta(r_0-i)}{\beta(r_0-i)+\gamma}\ .$$

Therefore, the distribution is independent of the number of infectives s_i. Put

$$t_i=\frac{t_{1i}}{\beta r_i s_i+\gamma s_i} \tag{11}$$

and the distribution of the time interval t_i corresponds to the distribution of the time interval between the i^{th} and $(i+1)^{\text{st}}$ new infection.

r_i is constant when we consider the sequence of occurrences of new infections. From (10), it is seen that the means $E\{r_i(t_{1i}-1)\}=(\gamma/\beta)$, $E\left\{\frac{1}{m}\sum_{i=0}^{m-1} r_i(t_{1i}-1)\right\}=\frac{\gamma}{\beta}$ and the variance $V_{(1/m)\sum(t_{1i}-1)}=(\gamma^2/m\beta^2)$ tend to 0 when $m\to\infty$. The statistic $(1/m)\sum r_i(t_{1i}-1)$ is a sufficient and unbiased estimate with the mean (γ/β) and the variance $(\gamma^2/m\beta^2)$. Therefore, we can test the difference between the ratio estimates (γ/β) obtained from two different groups by means of the variance ratio test. When m is large, the precision of the ratio estimate (γ/β) from a single epidemic would be rather high as the coefficient of variation is $m^{-(1/2)}$. Now, when we estimated the parameters using the first 10 day's observations from the start of the epidemic of influenza, the parameters β_1, β_2, γ were given by

$$\beta_1=1.94\times10^{-4}$$
$$\beta_2=1.94\times10^{-4}$$
$$\gamma\ =1.0\times10^{-1}\ .$$

Using these parameters, we shall illustrate numerically the subsequence number of patients of influenza at the time t by the Monte Carlo Method. As stated in the deterministic model, there were 1673 susceptibles and 20 infectives at the start of the epidemic of influenza. Starting from the initial number $n=1673$, $a=20$, we gave numerically

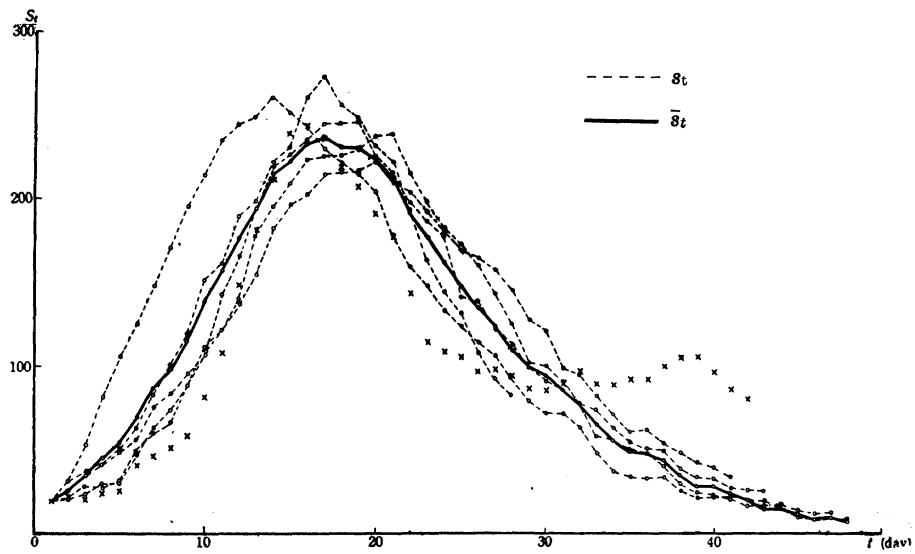

Fig. 4. The number of patients s_t at time t.

the five epidemic curves by the Monte Carlo Method and their mean. The result is shown in Fig. 4. The time at the peak of the number of infectives in the mean epidemic curve fits fairly well to the data of influenza. Consequently, we shall be able to predict successfully the time of the peak of the number of infectives using the first 10 day's data of the epidemic of influenza. Then, the authorities of public health will be able to decide the adequate time of taking the preventive measure against the epidemic of school-children's influenza. If they do so, they will be able to expect the most effective way of minimizing the propagation of disease in school community.

In sections 3, 4, we stated that these epidemic models were useful for predicting the peak of the number of infectives of influenza and deciding the effect of preventive measures. But one difficult problem in our model is that we shall not be able to observe the inapparent immune cases successfully. If this problem is solved, our model will be very useful.

5. The limiting solution of the differential-difference equation (9)

From the differential-difference equation (9), we shall derive the limiting solution $\lim_{t\to\infty} P_{n-w,0}(t)$ where w shows the sum of the total numbers of new infections and new inapparent immune cases up to the time t. This solution at $t=\infty$ is most easily obtained by using the Laplace transform and its inverse with respect to time.

$$\left.\begin{aligned} q_{rs}(\lambda)&=\int_0^\infty e^{-\lambda t}P_{rs}(t)dt, \quad R(\lambda)>0\ , \\ P_{rs}(t)&=\frac{1}{2\pi i}\int_{\sigma-i\infty}^{\sigma+i\infty} e^{\lambda t}\ q_{rs}(\lambda)d\lambda\ . \end{aligned}\right\} \tag{12}$$

Use of the Laplace transformation (12) replaces (9) by

$$\begin{aligned}(r+1)(s+1)q_{r+1,s-1}+\rho_1(r+1)s\ q_{r+1,s}-\{(r+\rho_1 r+\rho_2)s+\lambda\}q_{rs}\\ +\rho_2(s+1)q_{r,s+1}=0\ , \quad \text{if } r\neq n \text{ or } s\neq a\ ,\end{aligned} \tag{13}$$

and

$$-\{(n+\rho_1 n+\rho_2)a+\lambda\}p_{na}+1=0\ , \qquad \text{if } r=n \text{ and } s=a\ .$$

Any q_{rs} whose suffices fall outside the permitted ranges is taken to be identically zero. From the equation (12), we can calculate all the q_{rs} in succession. Expansion in terms of partial fractions for λ and applic-

ation of the inverse Laplace transformation will exhibit each $P_{rs}(t)$. However, no satisfactory way of handling such expressions has yet been found.

In spite of these difficulties, useful results can be obtained if we attempt to investigate the distribution of the value of w for $t=\infty$, not counting the initial infectives a. Since the epidemic ceases to involve fresh susceptibles as soon as $s=0$, it is easily seen that P_w of an epidemic of total size w, which does not contain the initial infectives a, is given by

$$\begin{aligned} P_w &= \lim_{t\to\infty} P_{n-w,0}(t) , \quad 0 \leqq w \leqq n \\ &= \lim_{\lambda\to 0} \lambda\, q_{n-w,0} , \\ &= \lim_{\lambda\to 0} \rho_2\, q_{n-w,1} . \end{aligned} \tag{14}$$

These are, in effect, the equations used by Baily for computation of the P_w when $\beta_2=0$. Putting

$$f_{rs}=\lim_{x\to 0} q_{rs} , \tag{15}$$

we can get the following equations from (13),

$$\begin{aligned} (r+1)(s-1)f_{r+1,s-1}+\rho_1(r+1)s\,f_{r+1,s}-(r+\rho_1 r+\rho_2)s\,f_{rs} \\ +\rho_2(s+1)f_{r,s+1}=0 , \end{aligned} \tag{16}$$

and

$$-(n+\rho_1 n+\rho_2)a\,f_{na}+1=0 .$$

The equations (16) are simplified by putting

$$f_{rs}=\frac{n!}{s(r!)}\frac{\left(r+\frac{\rho_2}{1+\rho_1}-1\right)!}{\left(n+\frac{\rho_1}{1+\rho_2}\right)!}\frac{{\rho_2}^{n+a-r-s}}{1+\rho_1}\,g_{rs} . \tag{17}$$

Then, we have the recurrence formula

$$\left.\begin{aligned} &\frac{g_{r+1,s-1}}{1+\rho_1}-g_{rs}+\frac{\rho_1}{\rho_2(1+\rho_1)}\,g_{r+1,s}+\frac{g_{r,s+1}}{(1+\rho_1)\left(r+\frac{\rho_2}{1+\rho_1}\right)}=0 , \\ &\text{and} \\ &g_{na}=1 . \end{aligned}\right\} \tag{18}$$

This formula is most easily solved by adapting a method used by Whittle (1955). When we put

$$\alpha_r = \frac{1}{(1+\rho_1)\left(r+\frac{\rho_2}{1+\rho_1}\right)} \tag{19}$$

and use the set of generating functions

$$H_r(x) = \sum_{s=1}^{n+a-r} g_{rs} x^{s+1}, \quad 0 \leqq r \leqq n, \tag{20}$$

we obtain the following system of equations from (18)

$$H_r(x) = \frac{x}{(1+\rho_1)(x-\alpha_r)} \left\{ \left(x+\frac{\rho_1}{\rho_2}\right) H_{r+1}(x) - (1+\rho_1)\alpha_r x g_{r1} \right\} \tag{21}$$

where

$$r = n-1,\ n-2, \cdots\cdots.$$

A direct solution of (21) shows that

$$g_{r1} = \frac{\alpha_r^{-2}}{(1+\rho_1)} \left(\alpha_r + \frac{\rho_1}{\rho_2}\right) H_{r+1}(\alpha_r), \tag{22}$$

as the expression (21) of H_r is a finite series in x. From the equations (21), (22), we obtain a relation

$$H_r(x) = \frac{x}{(1+\rho_1)(x-\alpha_r)} \left\{ \left(x+\frac{\rho_1}{\rho_2}\right) H_{r+1}(x) - \alpha_r^{-1}\left(\alpha_r+\frac{\rho_1}{\rho_2}\right) x H_{r+1}(\alpha_r) \right\}, \tag{23}$$

which holds for $r = n-1,\ n-2, \cdots\cdots$, and also for $r=n$ if we introduce a function

$$H_{n+1}(x) = x^a. \tag{24}$$

Therefore,

$$\begin{aligned} H_{r+1}(\alpha_r) &+ \frac{\alpha_r^{-2}\alpha_{r+1}^{-1}\left(\frac{\rho_1}{\rho_2}+\alpha_{r+1}\right)}{(1+\rho_1)(\alpha_r-\alpha_{r+1})} H_{r+2}(\alpha_{r+1}) \\ &+ \frac{\alpha_r\left(\frac{\rho_1}{\rho_2}+\alpha_r\right)}{(1+\rho_1)(\alpha_r-\alpha_{r+1})} \cdot \frac{\alpha_r^{-2}\alpha_{r+1}^{-1}\left(\frac{\rho_1}{\rho_2}+\alpha_{r+2}\right)}{(1+\rho_1)(\alpha_r-\alpha_{r+2})} H_{r+3}(\alpha_{r+2}) + \cdots \\ &+ \frac{\alpha_r\left(\alpha_r+\frac{\rho_1}{\rho_2}\right)}{(1+\rho_1)(\alpha_r-\alpha_{r+1})} \frac{\alpha_r\left(\alpha_r+\frac{\rho_1}{\rho_2}\right)}{(1+\rho_1)(\alpha_r-\alpha_{r+2})} \cdots\cdots \end{aligned} \tag{25}$$

$$\cdots\frac{\alpha_r\left(\alpha_r+\frac{\rho_1}{\rho_2}\right)}{(1+\rho_1)(\alpha_r-\alpha_{n+1})}\frac{\alpha_r^{-2}\alpha_n^{-1}\left(\alpha_n+\frac{\rho_1}{\rho_2}\right)}{(1+\rho_1)(\alpha_r-\alpha_n)}H_{n+1}(\alpha_n)$$

$$=\frac{\alpha_r\left(\alpha_r+\frac{\rho_1}{\rho_2}\right)}{(1+\rho_1)(\alpha_r-\alpha_{r+1})}\cdots\cdots\frac{\alpha_r\left(\alpha_r+\frac{\rho_1}{\rho_2}\right)}{(1+\rho_1)(\alpha_r-\alpha_n)}.$$

From the equations (15), (17), (22), (25), we introduce the following relations

$$\sum_{w=0}^{j}\binom{n-w}{n-j}\left(\frac{1+\rho_1}{\rho_2}\right)^{w+1}\left(\alpha_{n-j}+\frac{\rho_1}{\rho_2}\right)^{-(w+1)}P_w =\binom{n}{j}(\rho_2\alpha_{n-j})^{a-1} \qquad (j=0,1,\cdots n) \tag{26}$$

where $\sum_{w=0}^{n}P_w=1$.

If $\rho_1=0$, the relations (26) coincide with results of Foster, Whittle and Kendall, respectively. Now, we can calculate P_w from (26) as

$$P_0=(\rho_2\alpha_n)^{a-1}\frac{\rho_1}{1+\rho_2}\left(\alpha_n+\frac{\rho_1}{\rho_2}\right),$$

$$P_1=\binom{n}{1}(\rho_2\alpha_{n-1})^{a-1}\left(\frac{\rho_2}{1+\rho_1}\right)^2\left(\alpha_{n-1}+\frac{\rho_1}{\rho_2}\right)^2-\binom{n}{1}\left(\frac{\rho_2}{1+\rho_1}\right)\left(\alpha_{n-1}+\frac{\rho_1}{\rho_2}\right)P_0,$$

$$\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots. \tag{27}$$

$$\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots.$$

$$P_k=\binom{n}{k}(\rho_2\alpha_{n-k})^{a-1}\left(\frac{\rho_2}{1+\rho_1}\right)^{k+1}\left(\alpha_{n-k}+\frac{\rho_1}{\rho_2}\right)^{k+1}-\binom{n}{n-k}\left(\frac{\rho_2}{1+\rho_1}\right)^k\left(\alpha_{n-k}+\frac{\rho_1}{\rho_2}\right)^kP_0$$

$$\cdots\cdots\cdots\cdots+(-1)^k\binom{n-k+1}{n-k}\frac{\rho_2}{1+\rho_1}\left(\alpha_{n-k}+\frac{\rho_1}{\rho_2}\right)P_{k-1},$$

$$\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots$$

$$P_n=1-\sum_{i=0}^{n-1}P_i.$$

Assuming that the initial $a=1$ infective is introduced into a population of $n=10$ uninfected and susceptible individuals and $\rho_1=0.05$, we can calculate all the P_w from the equations (27). These results are shown in Fig. 5, and all show the U-shaped distributions. It is immediately clear from the figure that when the inapparent immune rate ρ_1 is fixing, and the relative removal rate ρ_2 is large, the epidemic tends to be small and conversely.

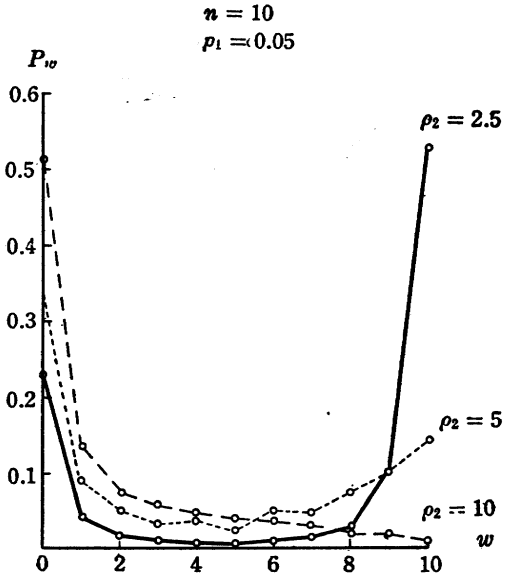

Fig. 5. Final total size of removals w at $t=\infty$

6. Summing-up of the results

As stated in the introduction, we must construct an epidemic mode from a real point of view. A constructed model must be useful, at least, for predicting the number of infectious patients. If the authorities of public health can obtain the information on the peak of the number of infectives in epidemic times, they will be able to take a preventive measure against the epidemic at the appropriate time. We think that the problem "When to take any preventive measure against the epidemic" will be very important for the public health authorities.

From such real point of view, we constructed the epidemic models in section 3, 4 and investigated the validity of our models through the data of the propagation of influenza in school-children. The point to pay attention is that the recovering distribution $1-G(t-\tau)$ in section 3 is essentially different from the probability of recovering in section 4. That is, $1-G(t-\tau)$ means the probability that one person infected at the time τ will recover before the time t and $\beta\gamma s\,dt$ means the probability that some one infective of many infectives will recover at the time interval $(t, t+dt)$. Surely, when we consider whether one infective will recover or not at the time t, it must depend on his infective moment τ.

The next problem through sections 2, 3, 4 is that we considered the inapparent immune rate β_2 from a group of susceptibles. Considering from the epidemiological phenomenon, β_2 is, generally, not zero. In section 5, we gave the limiting solution of the stochastic differential-difference equation (9) from mathematical interest, but this is not useful for application.

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