



***The Scientific Temper***

VOL-X, NO.1&2; JANUARY-JULY, 2019

ISSN 0976 8653, E ISSN 2231 6396

A Web of Science Journal

e-mail: letmepublish@rediffmail.com

Doc ID : <https://connectjournals.com/03960.2019.10.21>

## MATHEMATICAL MODEL FOR INFECTION AND REMOVAL IN POPULATION

UMASHANKAR SHUKLA<sup>1</sup> AND ANIL K. UPADHYAY<sup>2\*</sup>

<sup>1</sup>Department of Mathematics, L.B.S.S. P.G. College, Anand Nagar, Maharajganj (U.P.) INDIA– 273155

<sup>2</sup>Department of Zoology, L.B.S.S. P.G. College, Anand Nagar, Maharajganj (U.P.) INDIA – 273 155

\*Corresponding Author

### ABSTRACT

The present paper deals with epidemic model base on some assumptions for the Population will be affected by diseases and final number of susceptible. Estimated Parameters involved in the model. The proposed model tested some characteristic of a general deterministic epidemic. This includes infectious disease dynamics, where scientific understanding can help capture biological processes in so called mechanistic models and their likelihood functions. However, when the likelihood of such mechanistic models lacks a closed form expression, computational burdens are substantial. In this context, algorithmic advances have facilitated likelihood maximization, promoting the study of novel data motivated mechanistic models over the last decade In particular; we highlight statistical aspects of these models like over dispersion, which has key in the interface between nonlinear infectious disease modeling and data analysis. We also point out potential directions for further model exploration.

**Keywords:** Susceptible, infections in circulation, removal of infections and infection rate, intensity of epidemic, population infection, population ratio.

## INTRODUCTION

Mathematical modeling is a universal method for studying nature. Recently this method has been widely applied to various field of knowledge. Its application to Biology and Medicine appears to be extremely successful. A working conference on mathematical models in "Biology and Medicine" was organized in answer to the continuously increasing interest in mathematical modeling in all countries.

Suppose we have a community of total size  $n$ , comprising at time  $t$ ,

- $x$  – Susceptible, and
- $y$  – Infective in circulation and
- $z$  – Individuals.

Where are isolated, dead, or recovered and immune. Thus  $x + y + z = n$ . It will be realized that, so for as transmission of deceases is concerned and we have  $\beta$  as the infection rate, but now there is also the removal rate  $\gamma$  to be taken into account.

In time  $dt$ , there are  $\beta xydt$  new infection and  $\gamma ydt$  removals. The differential equations are (Anderson, 1988)

$$\left. \begin{aligned} \frac{dx}{dt} &= -\beta xy \\ \frac{dy}{dt} &= \beta xy - \gamma y \\ \frac{dz}{dt} &= \gamma y \end{aligned} \right\} \quad (1.1)$$

It will be convenient in the sequel to make used of, the relative removal rate. We shall consider method of examining these equations, and go on to derive an exact solution.

**Estimation under some conditions:** At the start of the epidemic, when  $t=0$  let  $(x,y,z)$  take the values  $(x_0,y_0,0)$ . In particular if  $y$  is small,  $x_0$  will be approximately equal to  $n$  ( $x_0 = n$ ) now from (1) that unless  $\rho < x_0$  no epidemic can start to build up as

this requires  $\left[ \frac{dy}{dt} \right]_{t=0} > 0$ . The relative removal rate

$\rho = x_0$ , therefore gives threshold density of susceptible.

For the moment let us consider the solution of (1.1) obtained by Kermack and Mekenetrich (1927).

Eliminating  $y$  from the first and third of these equation by division gives,

$$\frac{dx}{dt} = -\beta xy \quad \& \quad \frac{dy}{dt} = \beta xy - \gamma y$$

$$\therefore \frac{dx}{dy} = \frac{(\beta x - \lambda) y}{\beta x y} = 1 - \frac{\gamma}{\beta x}$$

$$\therefore dy = \left( 1 - \frac{\gamma}{\beta x} \right) dx$$

After integrating we get

$$x = x_0 e^{-z/\rho} \quad (1.2)$$

While the third equation can be written

$$\frac{dy}{dt} = \gamma (n - x - z) \quad (1.3)$$

On using  $x+y+z = n$  from (6.2) and (6.3)

$$\frac{dz}{dt} = \gamma \left( n - z - x_0 e^{-z/\rho} \right) \quad (1.4)$$

Direct solution of (6.4) to give  $z$  as a function of  $t$  does not appear possible, although an exact parametric from due to Kendall (1919) is available. Here we consider the approximation the result from expanding the exponential factor in (1.4) as for as the term in  $Z^2$ , giving

$$\frac{dz}{dt} = \gamma \left\{ n - x_0 + \left( \frac{x_0}{\rho} - 1 \right) z - \frac{x_0}{2\rho^2} z^2 \right\} \quad (1.5)$$

Although we are assuming that  $\frac{z}{\rho}$  is small, it is necessary to introduce the second order term as

$\left( \frac{x_0}{\rho} - 1 \right)$  may also be small.

This will be occurring for example, near the Threshold when  $\rho = x_0$  equation (1.5) is solvable by standard method and yields.

$$\left. \begin{aligned} z &= \frac{\rho^2}{x_0} \left\{ \frac{x_0}{\rho} - 1 + \alpha \tan h \left( \frac{1}{2} \alpha \gamma t - \phi \right) \right\} \\ \text{Where } \alpha &= \left\{ \left( \frac{x_0}{\rho} - 1 \right)^2 + \frac{2x_0 y_0}{\rho^2} \right\}^{1/2} \\ \text{and } \phi &= \tanh^{-1} \frac{1}{\alpha} \left( \frac{x_0}{\rho} - 1 \right) \end{aligned} \right\} \quad (1.6)$$

The epidemic curve is therefore

$$\frac{dz}{dt} = \gamma \frac{\alpha^2 \rho^2}{2x_0} \operatorname{sech}^2\left(\frac{1}{2} \alpha \gamma t - \phi\right) \quad (1.7)$$

Which is in general symmetrical bell-shaped curve. It illustrates very well the common observation that in many actual epidemics the number of new cases reported each day climbs to a peak value and then dies away again.

We next consider the total size of the epidemic i.e. the total number of removals after elapse of a very long, ideally infinite period of time. If we let  $t \rightarrow \infty$  in (1.6)

$$z_\infty = \frac{\rho^2}{x_0} \left( \frac{x_0}{\rho} - 1 + \alpha \right) \quad (1.8)$$

we can write this

$$z_\infty \sim 2\rho \left( 1 - \frac{\rho_0}{x_0} \right) \quad (1.9)$$

If  $\frac{2x_0 y_0}{\rho^2}$  can be neglected compared

with  $\left(\frac{x_0}{\rho} - 1\right)^2$ . Since then  $\alpha$  is approximately

equation to  $\left(\frac{x_0}{\rho} - 1\right)$ . The approximate result (1.9)

can also be derived by putting  $\frac{dz}{dt} = 0$  and  $x_0 = n$  is

(1.5). As we have already noted, there will be nature epidemic if  $x_0 < \rho$  suppose now that  $x_0 > \rho$  and

$$x_0 = \rho + v \quad (1.10)$$

Putting (1.10) in (1.9) shows that total size of epidemic is approximately  $2v$ . The initial number of susceptible  $\rho + v$  is thus reduced finally to  $\rho - v$ , i.e. to a value as for below the threshold,  $\rho$  as it was originally above.

#### Exact solution:

Suppose for the moment, we assume that the infection-rate is a function  $\beta(z)$  of  $z$ ,

The equation (1.2) is replaced by

$$x = x_0 e^{\left\{ \frac{1}{\gamma_0} \int \beta(\omega) d\omega \right\}} \quad (2.1)$$

which together with (1.3) gives

$$\frac{dz}{dt} = \gamma \left[ n - z - x_0 e^{\left\{ \frac{1}{\gamma_0} \int \beta(\omega) d\omega \right\}} \right] \quad (2.2)$$

The equation (1.12) is same as the approximation appearing in (1.5) when

$$\beta(z) = \frac{2\beta}{\left(1 - \frac{z}{\rho}\right) + \left(1 - \frac{z}{\rho}\right)^{-1}} \quad (2.3)$$

Thus  $\beta(0) = \beta$  and  $\beta(z) < \beta$  when  $0 < z < \rho$  Kermack and McKendrick's approximation therefore consequently under infection rate and consequently the total size of epidemic as well.

Moreover, if at any time  $z > \rho$ , the model will be quite unrealistic since we should then have a negative infection rate. It the latter is to be kept within 10% of its initial value we must have  $z_\infty \leq 0.373 \rho$ .

Returning now to (1.4) we are led to consider the equation

$$\eta - z - x_0 e^{-z/\rho} = 0 \quad (2.4)$$

Let the unique negative and positive roots to (2.4) be  $-\eta_1$  and  $\eta_2$  respectively.

We can therefore integrate (1.4) to give.

$$t = \frac{1}{\gamma_0} \int \frac{d\omega}{\eta - \omega - x_0 e^{-\omega/\rho}}, \quad 0 \leq z < \eta_2 \quad (2.5)$$

Which, when taken in conjunction with (1.4) gives

formal solution for the epidemic curve  $\frac{dz}{dt}$ , in term of a pair of a pair of parametric equation.

The whole of the curve for  $0 \leq t \leq \infty$  is involved since the integral in (2.5) diverges when  $z_\infty \rightarrow \eta_2$  and therefore  $z_\infty = \eta_2$ .

Unfortunately the integral also diverges at the lower limit as  $x_0 \rightarrow \eta_1$  so that in this case an

infinite time elapse before the epidemic starts. The latter difficulty is overcome by changing to origin to the point where  $x = \rho$ , which may be called centre of epidemic.

Since

$$\frac{d}{dt} \left( \frac{dz}{dt} \right) = \gamma^2 y \left( \frac{x}{\rho} - 1 \right) \quad (2.6)$$

As we find by differentiating (1.4) and putting in (1.1) and (1.2), the peak of the epidemic curve occurs as the centre. From third equation of (1.1) we see that maximum number of infective also occurs at the same time.

We now write  $x_0 = \rho$ , and can still choose to take  $z_0 = 0$ .

The consequence of this is that the numerical value of  $z(t)$  is the number of removals in  $(0, t)$  for  $t > 0$  and in  $(t, 0)$  if  $t < 0$ .

$$\therefore \left[ \begin{aligned} t &= \frac{1}{\gamma} \int_0^z \frac{d\omega}{y_0 - \omega + \rho(1 - e^{\omega/\rho})} \\ \text{and } \frac{dt}{dz} &= \gamma \{ y_0 - z - \rho(1 - e^{z/\rho}) \} \end{aligned} \right] \quad (2.7)$$

where

$$\& -\xi_1 < z < \xi_2$$

the quantities  $-\xi_1$  and  $\xi_2$  now being the unique negative and positive roots, respectively at

$$y_0 - \xi + \rho(1 - e^{-\xi/\rho}) = 0 \quad (2.8)$$

It will be seen that this way of looking at an epidemic has involved a certain change of attitude. Instead of regarding it as a continuous process starting at a specific point of time with  $x_0$  susceptible dies and  $y_0$  infectives. We are considering the whole epidemic as an existing in the interval  $-\infty$  to  $\infty$  with origin located for convenience at the point corresponding to the peak of the epidemic curve.

#### Application:

Total number of susceptible that finally contracts the disease namely

$$i = \frac{\xi_1 + \xi_2}{N} \quad (3.1)$$

Thus we see that the number  $n$  at  $t = -\infty$ , the quantities  $(x, y, z)$  specifying the constitution of the

population take the values  $(N, 0, -\xi_1)$  while at the other end of the time scale when  $t = \infty$  we have  $(N - N_i, 0, N_i - \xi_2)$ . From the modified form (1.2) applicable here namely

$$x = N e^{-(z+\xi_1)/\rho} \quad (3.2)$$

It follows that

$$N - N_i = N e^{-N_i/\rho} \quad (3.3)$$

$$\frac{N}{\rho} = \frac{\log(1-i)}{i} \quad (3.4)$$

Table (A) gives the value of  $N/\rho$  for various values of  $i$ , we can obtain further explicit information by considering the constitution of the population where  $t = 0$ ,

i.e.  $(\rho, y_0, 0)$ . This time (3.2) give

$$\rho = N e^{-\xi/\rho} \quad (3.5)$$

from which we obtain in conjunction with

$$\left[ \begin{aligned} \frac{\xi_1}{\xi_1 + \xi_2} &= \frac{\rho}{N_i} \log \frac{N}{\rho} \end{aligned} \right] \quad (3.6)$$

This expression also tabulated in table (A) we can also calculate the number of

infectives at  $t = 0$  from

$$Y_0 = N - \rho - \xi_1$$

$$\text{i.e. } y_0 = N - \rho - \rho \log \frac{N}{\rho} \quad (3.7)$$

#### TABLE – A: Some characteristic of a general deterministic epidemic

Thus 9% of population will be affected by disease and final number of susceptible will be about 96.  $N=105, \rho=100, N/\rho=1.05, i=0.09$

Intensity of epidemic $i$	Ratio of population to threshold $n/\rho$	Percentage of Population infections at central approach $Y_0/N$	Percentage of removals occurring before central approach $\xi_1/\xi_1 + \xi_2$
0.00	1.000	0.00	50.0
0.10	1.054	0.13	49.5
0.20	1.116	0.56	49.1
0.30	1.189	1.33	48.5
0.40	1.277	2.55	47.9
0.50	1.386	4.30	47.1
0.60	1.527	6.79	46.2

0.70	1.720	10.33	45.0
0.80	2.012	15.55	43.4
0.90	2.558	24.20	40.8
0.95	3.153	31.87	38.3
0.98	3.992	40.27	35.4

### RESULT AND DISCUSSION:

For value of we took  $N = 201$ . From the last column of table (A) we can see the degree of skewness

exhibited by the epidemic curve when  $\frac{N}{\rho}$  is as high as 4, nearly two third of the removals occur after the peak, and this is in fact the type of asymmetry often found in actual notifications of infectious diseases.

While the general pattern of events portrayed in (A) Table applies to epidemics that exists over the whole interval  $-\infty$  to  $+\infty$  are started up by a mere trace of infections. It is not difficult to deduce the consequence of introducing a non-zero number of infectious in to a population of susceptible at some time.

Over dispersion has been studied from multiple perspectives, including applications involving count data, applied probability involving stochastic processes of counts, and statistical modeling involving both. The study of over dispersion in the context of infectious disease dynamics has been and can be further facilitated by the synergy between mechanistic models and it generated filtering algorithms. The interaction between plug and play algorithms and mechanistic modeling is similar to a mutualistic symbiosis Mechanistic modeling often involves describing mechanisms as sequences of Actions or events that result in change. Such descriptions naturally translate into Simulation algorithms that in turn are the basis of plug and play methods. In return, plug and play methods extract evidence from data that might suggest changes to the initially hypothesized mechanisms and, accordingly to the simulation algorithms. For the transmission models simulation is often possible using appropriate Numerical algorithms, like Runge Kutt a methods for ordinary differential equations, Euler type algorithms for diffusions and Lévy driven

differential equations, and exact Gillespie,1977) or approximate algorithms (Gillespie,2001) for continuous time Markov chains. The synergy exists between mechanistic modeling and it related filtering but it does not address issues that in general affect likelihood maximization or sequential Monte Carlo, including rough surfaces (Fasiolo, Pyaand Wood,2016), Small measurement variances, system dimensionality and parameter identifiably. This synergy can bee exploited to further explore over dispersion in measurement models.

### REFERENCES:

- Anderson DH (1988): Lecture notes in Biomathematics; Springer Verlag Berlin, NY.
- Brumpt E (1949): The human parasites of the genus plasmodium, In Malariology, M.F. Boyd (ed.) 65121.3.
- Fasiolo M, PyaNand Wood SN (2016): A Comparison of Inferential Methods for Highly Nonlinear State Space Models in Ecology and Epidemiology. Statistical Science. 31: 96118.
- Gillespie DT (1977): Exact stochastic simulation of coupled chemical reactions. Journal of Physical Chemistry, 81:23402361.
- Gillespie DT (2001): Approximate accelerated stochastic simulation of chemically reacting systems. The Journal of Chemical Physics, 115:17161733.
- Huppert A and Katriel G (2013): Mathematical modeling and prediction in infectious disease epidemiology. Clin Microbial Infect. 19(11):9991005.
- Kendall DG (1919): Stochastic model and population growth, Proc. Royal Statistical society, 11,pp 210264.
- Kermack W and McKendrick A (1927): "A Contribution to Mathematical Theory of Epidemics", Proc. R Society London A, 115 pp.7007219.
- MacDonald G (1950): The Epidemiology and Control of malaria London: Oxford University Press.
- Molineaux L and Gramiccia G (1980): The Garki Project, World Health Organization.
- Needleman J (1985): Some new thoughts about some old malaria model. Math. Biosci,73, 159182.
- Needleman J 1985): Estimation for a model of multiple malaria infections. Biometric, 447453.
- Stiletto IC and Russo L (2013): Mathematical modeling of infectious disease dynamics. Virulence. 4(4): 295306.Landes Bioscience.
- Singer Band JE Cohen (1980): Estimating malaria in incidence and recovery rates from panels surveys.Math.Bio.Sci.49, 273-305.

<http://www.scientifictemper.com/>

