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Qualitative study of Kermack and Mckendrick's epidemic model

Simeon Chioma Inyama
Department of Mathematics and Computer Science,
Federal University of Technology, Owerri
Nigeria
e-mail: scinyama2003@yahoo.com

Abstract

In this paper, we carry out a qualitative study of Kermack and Mckendrick's epidemic model. We derive a special case of this model for recurrent diseases (relapse – recovery model). Using the new model, we investigate the severity of the epidemic and then test the stability of the original model. It is then shown that the number of invectives after a very long time from the inception of the epidemic is a constant. It is also shown that the steady state is unstable. Trajectories that help to know the extent of the severity are also presented. Through these trajectories it is shown that the severity of this epidemic can be estimated when the rate of infectiousness (r) and the removal rate (δ.) are estimated.

Keywords: Qualitative study, Kermack and Mckendrick's epidemic model recurrent diseases, relapse – recovery model. Severity.

1.0 Introduction

A lot of epidemic models have been presented in the literature. Some of them include [4,5,8]. Barley, [2] considered recurrent epidemic and endemicity. He looked at a basic deterministic model on measles. He modified the model by making an additional assumption that the stock of susceptibles is continually replenished by those who recovered from the disease. He introduced a birth parameter μ and modified the model. He obtained the steady state. He later showed that solution outside the steady state involve damped harmonic train of waves with period $2\pi/\xi$.

Webb [9] analyzed an epidemic model of an infectious Phenomenon. The model allows for an age–dependency to describe the phase of incubation, recovery and relapse, and for a spatial dependency to describe diffusion of the population in geographical space.

For more work on recurrent epidemics see [1, 4, and 10].

The discrete version of Kermack and Mckendrick's model as presented in [4, 5, 6, 7] is

$$x_{n+1} = e^{-ayn}\, x_n \qquad (1.1)$$
$$y_{n+1} = (1 - e^{-ayn})\, x_n + by_n$$
$$z_{n+1} = z_n + (1 - b)y_n$$

where x_n = number of susceptibles in period n
y_n = number of infectives
z_n = number of removals
a = rate of infection
b = removal rate.

The continuous time version of this model as in [5] is

$$\frac{dS}{dt} = -rIS\ ,\ \frac{dI}{dt} = rIS - \delta I\ ,\ \frac{dR}{dt} = \delta I \qquad (1.2)$$

where

S = number of susceptibles
I = number of infectives
R = number of removals
r = infection rate
δ = removal rate
N = population size.

In this investigation we derive a special case of (1. 2) for recurrent diseases (relapse – recovery model). We derive the model, investigate the severity of the epidemic and then test the stability of the original model.

2.0 Relapse–recovery model

Relapse–recovery diseases are those diseases in which a susceptible is infected, recovers and becomes a susceptible again. This is denoted by the graph $S \rightarrow I \rightarrow S$.
Examples of this type of disease include Gonorrhea and Malaria

Suppose that after a fixed length of time, say,τ, and an infective return to being fully susceptible again. Then instead of the model in (1.2), we have

$$\frac{dS}{dt} = -rI(t)S(t) + rI(t-\tau)S(t-\tau) \qquad (2.1)$$

$$\frac{dI}{dt} = -rI(t-\tau)S(t-\tau) + rI(t)S(t)$$

Since $I + S = N \Rightarrow S = N - I$, hence (2.1) reduces to the single equation

$$\frac{dI}{dt} = r\{I(t)[N - I(t)] - I(t-\tau)[N - I(t-\tau)]\} \qquad (2.2)$$

We now discuss the severity of the epidemic

2.1 Severity of the Epidemic

Here we determine the number of infectives after a long time ($t \rightarrow \infty$). We then put this in a Theorem

***Theorem* 2.1**

As $t \rightarrow \infty$, $I \rightarrow I^*$ and I^* is a constant

Proof

We now determine the value of I^*. Before we can do this, we first solve (2.2).

Let $I(t-\tau) = \frac{1}{2}I(t)$

$$\Rightarrow \frac{dI}{dt} = r\left\{I(t)[N - I(t)] - \frac{1}{2}I(t)[N - \tfrac{1}{2}I(t)]\right\} = r\left\{\frac{1}{2}I(t)N - I(t) + \frac{1}{4}I^2(t)\right\}$$

$$= r[\frac{1}{2}I(t)N - \frac{3}{4}I^2(t) = r\left\{I(t)\left[N - \frac{3}{2}I(t)\right]\right\}$$

$$\therefore \quad \frac{dI}{\frac{1}{2}I(t)\left[N - \frac{3}{2}I(t)\right]} = rdt$$

Using partial fractions in the L. H. S. and Simplifying gives $\left(\frac{\frac{1}{2}N}{I} + \frac{\frac{3}{2}N}{2N - 3I}\right)dI = \frac{r}{4}dt$. Integrating gives

$\frac{I}{2N - 3I} = ae^{\frac{1}{2}\text{Nrt}}$. Applying the initial boundary conditions $I(o) = I_0$ we have $\frac{Io}{2N - 3Io} = a$

Therefore, $\frac{I}{2N - 3I} = \left(\frac{Io}{2N - 3Io}\right)e^{\frac{1}{2}Nrt}$. Solving for I gives $I = \frac{2NIo}{3Io + (2N - 3Io)e^{-\frac{1}{2}Nrt}}$.

As $t \to \infty$, $I \to I^*$, where $I^* = \frac{2NIo}{3Io} = \frac{2}{3}N$ which is a constant.

Note that we assumed $I(t-\tau) = \frac{1}{2}I(t)$. In general, if $I(t-\tau) = \frac{1}{n}I(t)$. Then

$$I^* = \left(\frac{n}{n+1}\right)N \qquad (2.3)$$

which is a constant. Hence, the number of infectives after a very long time from the day of the inception of the epidemic is a constant.

Alternatively, we can investigate the severity of the epidemic by the differential equations in (1.2). Taking the ratio of the first two equations in (1.2) we get

$$\frac{dS}{dI} = -\frac{rIS}{rIS - \delta I} = \frac{-rS}{rS - \delta}$$

Therefore, $dI = \left(\frac{\delta}{rS} - 1\right)dS$. Integrating this equation gives $I = \left(\frac{\delta}{r}\right)\log S - S + C$, where C is the constant of integration. Using the initial conditions $I(t) = I_o$ and $S(t) = S_o$ at $t = 0$, we have

$$C = I_o - \left(\frac{\delta}{r}\right)\log S_o + S_o$$

$$\Rightarrow \qquad I = \left(\frac{\delta}{r}\right)\log(S/S_o) + (S_o - S) + I_o \qquad (2.4)$$

Fig. 1 below shows the typical trajectories describing this solution in the infinitesimal sampling process, the threshold level of S^* becomes

$$S^* = (1 - b)/(1 - e^{-a}) \sim \delta/r .$$

S^* is the value of S for which $dI/dS = 0$.

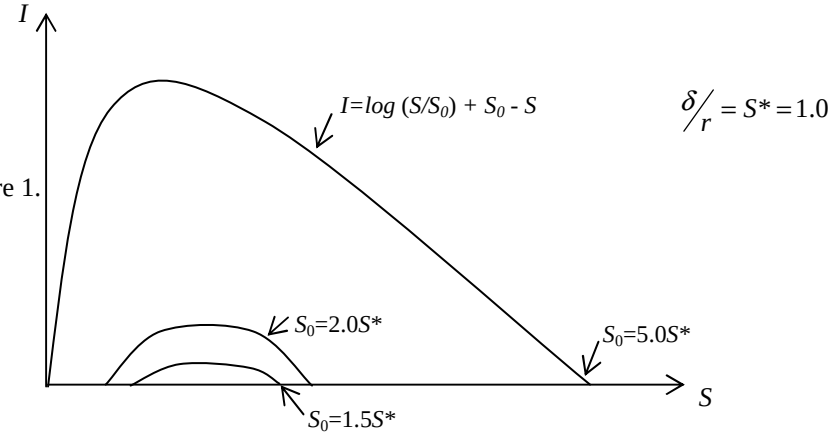

Figure 1.

From Figure1, we see that trajectories starting near but above S^* describe epidemics that end at comparable distance below this value. Trajectories that start well above S^* and end up near $S = 0$. However, in each case, the final size of the susceptible population, S_∞, is where the trajectory meets the $I = 0$ axis. Therefore, solving the equation,

$$S - \left(\frac{\delta}{r}\right)\log S = C$$

for its smaller of two roots gives the final size. Hence, where the rate of infectiousness (r) and the removal rate (δ) are estimated, the epidemic severity can be estimated. From (2.4), this analysis shows that

(i) if $S^* = \frac{\delta}{r} < I_o + S_o$, then $S \to S^*$

(ii) if $S \rightarrow I_o + S_o$, the infection dies out of the population, and
(iii) when $S \rightarrow S^*$, the disease is endemic.

3.0 The steady state and its stability

The steady state occurs at the point where $\frac{dS}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = 0$. From (1.1),

$$- rI^o S^o = 0 \qquad (i)$$
$$rI^o S^o - \delta I^o = 0 \qquad (ii)$$
$$\delta I^o = 0 \qquad (iii)$$

where S^o, I^o and R^o are the steady state values of S, I and R respectively.
(ii) $\Rightarrow I^o (rS^o - \delta) = 0 \Rightarrow I^o = 0$ or $S^o = \delta/r$. Hence the steady state is $(S^o, I^o, R^o) = \left(\delta/r, 0, 0\right)$. To discuss the stability of the steady state, we first linearize (1.1) to get

$$D = \begin{pmatrix} -rI^o & -rS & 0 \\ rI^o & -rS^o - \delta & 0 \\ 0 & \delta & 0 \end{pmatrix}$$

We now obtain the eigenvalues of D.

$$|D - I\lambda| = \begin{vmatrix} -rI^o - \lambda & -rS^o & 0 \\ rI^o & rS^o - \delta - \lambda & 0 \\ 0 & \delta & 0 - \lambda \end{vmatrix} = 0$$

$\Rightarrow \lambda(- rI^o - \lambda)(rS - \delta - \lambda) = 0, \Rightarrow \lambda = 0, - rI^o, r S^o - \delta$. Hence the eigenvalues of D are $\lambda_1 = 0$, $\lambda_2 = - rI^o$, $\lambda_3 = rS^o - \delta$. The steady state above is stable if $\lambda_1 > 0$, $\lambda_2 > 0$ and $\lambda_3 > 0$. But $\lambda_1 = 0$, $\lambda_2 = 0$ since $r > 0$ and $I^o = 0$ and $\lambda_3 = 0$ since $S^o = \delta/r$. Hence the steady state $(S^o, I^o, R^o) = \left(\delta/r, 0, 0\right)$ is not stable, rather it is a saddle point.

4.0 Summary and conclusion

We have considered the Kermack and Mckendrick's model. We considered the relapse – recovery case and hence modified the model. We investigated the severity of the epidemic and found that the number of infectives after a long time from the inception of the epidemic is a constant. Considering the severity in terms of the number of susceptibles, it was shown that (i) if $S^* = \delta/r < I_o + S_o$, then $S \rightarrow S^*$ (ii) if $S \rightarrow I_o + S_o$, the infection dies out of the population and (iii) when $S \rightarrow S^*$ which is when $S^* < I_o + S_o$, the disease will be endemic. We observed that the original model has a non-trivial steady state. This steady state is not stable but is a saddle point

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