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# Fixed Point Analysis of Kermack Mckendrick SIR Model

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#### Abstract

Public health is constantly under risk due to growing microorganisms. Infectious disease spread rapidly among the population in contact and so people take the different steps to reduce the transmission of disease. Compartmental model such as SIR model developed by W. Kermack and G Mckendrick are modeled for the progress of epidemic. Fixed point analysis has been applied to mathematical models of compartmental infectious disease models for understanding the long term outcome of disease. We have applied the analysis to the spread of infectious disease and obtained the threshold value and this threshold value helps us to predict when epidemic peaks.

Keywords: Reproduction number, Fixed point, Threshold value

# 1. Introduction

In 1927 Kermack and McKendrick [1] developed an epidemic model which was considered a generalized model at that time. In SIR model given by Kermack Mckendrick, the total population is assumed to be constant and divided into three classes. Susceptible class contains individuals who have no immunity to the infectious agent; any member of the susceptible class could become infected. Infectious class contains individuals who are currently infected and can transmit the infection to susceptible individuals who they contact. Recovered class contains individuals who have returned to a normal state of health after being infected and those individuals have gained permanent immunity. This model is called the SIR model [2][3]. In this model we assume that:

1. The way a person can leave the susceptible group, S, is to become infected. The way a person can leave the infected group, I, is to recover from the disease.

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- 2. The recovery rate  $\gamma$  and the transmission rate  $\beta$  are the same for all individuals and are supposed positive
- 3. There is homogeneous mixing, which means that individuals of the population make contact at random and do not mix mostly in a smaller subgroup
- 4. The disease is novel, so no vaccination is available
- 5. The population size, N, is constant and large.
- 6. Any recovered person in R has permanent immunity [5]

|           | Table 1                      |               |
|-----------|------------------------------|---------------|
| Variables | Description                  | Units         |
| В         | Transmission rate            | 1/people×Days |
| γ         | Recovery Days                | 1/Days        |
| Т         | Time                         | Days          |
| S         | Number of susceptible people | People        |
| Ι         | Number of Infected people    | People        |
| R         | Number of Recovered people   | People        |
| N         | Total number of people       | People        |

Given these assumptions, Kermack and McKendrick presented the following system:

$$\frac{dS}{dt} = -\beta SI \tag{1}$$

$$\frac{dI}{dt} = I(\beta S - \gamma) \tag{2}$$

$$\frac{dR}{dt} = \gamma I \tag{3}$$

With the initial condition  $S(0) = S_0 > 0$ ,  $I(0) = I_0 > 0$ , R(0) = 0

Using (1), (2) and (3) we have

 $\frac{ds}{s} = -\beta I dt$  $\frac{ds}{s} = -\frac{\beta}{\gamma} \frac{dR}{dt} dt$  $\log S = -\frac{\beta}{\gamma} R + \log C$  $\log \frac{S}{C} = -\frac{\beta}{\gamma} R$  $S = C e^{-\frac{\beta}{\gamma} R}$ 

Using initial condition when t = 0, S = S<sub>0</sub> on integrating equation  $\frac{ds}{s} = -\beta I dt$  on both sides we get

 $\operatorname{Log} S = -\beta It + \log C$ 

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$$\therefore C = S_0$$

$$S = S_0 e^{\frac{-\beta}{\gamma}R}$$
(4)

The epidemic modeling of Kermack and Mckendrick SIR Model is based on Ordinary Differential Equation. An ordinary differential equation is of the form

$$\frac{dx}{dt} = F(x,t) \tag{5}$$

Subject to the condition  $x(0) = x_0$ 

## 2. Fixed Point Analysis

Let  $x^*$  be the equilibrium point of (5)

$$F(x^*) = 0$$
,  $\frac{d}{dt}x^* = F(x^*) = 0$ 

For Such equilibrium points, it is meaningful to talk about stability. For Stability we should know about trajectory that starts near a equilibrium point, stays near the equilibrium point as time increases. There are many types of stability. We consider the most common type of linear stability.

As we have an initial value  $x_0 = x^* + \delta x_0$  where  $\delta x_0$  is small in an approximate norm

Let  $x_0 \to x(t)$ ,  $x^* + \delta x_0 \to x^* + \delta x(t)$   $\therefore \frac{d}{dt} \delta x(t) = F(x^* + \delta x) = \left(\frac{\partial F}{\partial x}\right)_{x=x^*} \delta x$ . The factor  $\delta x(t)$  is very small, so the stability depends on Eigen values of a matrix  $J^* = \left(\frac{dF}{dx}\right)_{x^*}$  consider the Ordinary differential equation  $\frac{dx}{dt} = F(x)$ Where  $x = (S, I, R)^T$ ,  $F(x) = (-\beta SI, I(\beta S - \gamma), \gamma I)^T$ 

Since the population is constant  $\frac{d(S+I+R)}{dt} = 0$ 

 $S + I + R = N = cons \tan t$ Therefore I = N - S - R (6) Using (4) in (6) we have  $\beta_{R}$ 

$$I = N - S_0 e^{\frac{-r}{\gamma}} - R \tag{7}$$

Substitute the value of (7) in (3) we get

$$\frac{dR}{dt} = \gamma (N - S_0 e^{-\frac{\beta}{\gamma}R} - R)$$
(8)

In order to reduce the number of parameter and to make it more amenable to analysis, let us introduce a new variable

$$u = \frac{\beta}{\gamma}R$$

Since  $\beta$  being an infection rate (constant) and  $\gamma$  being an recovery rate(constant) and R has the dimension of population so u has the dimension of a pure number. Multiply (8) on both sides by  $\frac{\beta}{\alpha}$ 

$$\therefore \frac{d}{dt} (\frac{\beta}{\gamma} R) = \frac{\beta}{\gamma} \gamma [N - S_0 e^{-u} - R]$$

$$\frac{du}{dt} = \beta N - \beta S_0 e^{-u} - \beta R$$

$$\frac{1}{\gamma} \frac{du}{dt} = \frac{\beta N}{\gamma} - \frac{\beta S_0}{\gamma} e^{-u} - u$$
(9)
$$\beta S_0 = 1 du = N - u = \gamma$$

Let us divide the (9) on both sides by  $\frac{\beta S_0}{\gamma}$  we get  $\frac{1}{\beta S_0} \frac{du}{dt} = \frac{N}{S_0} - e^{-u} - \frac{\gamma}{\beta S_0} u$ 

Let us introduce new time variable

$$d\tau = \beta S_0 dt$$
(Hence (9) reduces to (10)
$$\frac{du}{d\tau} = p - qu - e^{-u} \qquad \text{say} \quad f(u)$$
(10)
Where  $p = \frac{N}{c}$  and  $q = \frac{\gamma}{cr}$ , using initial condition we have

Where  $p = \frac{1}{S_0}$  and  $q = \frac{1}{\beta S_0}$ , using initial condition we have As  $p = \frac{N}{S_0} = \frac{S_0 + I_0}{S_0} \ge 1$  while  $q = \frac{\gamma}{\beta S_0} > 0$ 

As 
$$f(u) = p - qu - e^{-u}$$
  $p \ge 1, q > 0, u \ge 0$ 

To Sketch the curve it is sufficient to know the Behavior of f(u) as  $u \to 0$  and  $u \to \infty$  and to determine whether the curve has maxima and minima

### 2.1 Behavior at 0

We have f(0) = p - 1 since  $p \ge 1$ 

 $\therefore f(0) \ge 0$  Let us consider the case p > 1 then  $\frac{S_0 + I_0}{S_0} > 1 \Longrightarrow I_0 > 0$ 

This shows that there are some sick people present initially. Then f(0) > 0

#### 2.2 Behavior for large u values

As  $u \to \infty$  then exponential term dies away as  $u \to \infty$  :  $f(u) \approx -qu$ f(u) becomes very large and negative and behaves like a straight line as  $u \to \infty$ 

#### 2.3 Maxima and Minima

Let us evaluate  $f'(u_0) = 0$   $\Rightarrow -q + e^{-u_0} = 0$  $\Rightarrow u_0 = -\log q$ 

For q < 1 this point exist in the range u > 0 and the second derivative is  $f''(u_0) = -e^{-u_0}$ 

This is always negative. Hence the point  $u_0 = -\log q$  if it exists is maximum

Across the x –axis we have

 $u \xrightarrow{\lim} 0 f(u) > 0, u \xrightarrow{\lim} \infty f(u) < 0$ 

f (u) has at most one local maximum on u > 0 thus it shows that this is a stable equilibrium point. Epidemic will be at peak if the number of infectious is maximum.

 $\frac{dI}{dt} = 0 \implies$  The number of infectious is at maximum

That is therefore  $\frac{d^2 R}{dt^2} = \gamma \frac{dI}{dt} = 0$  at peak the infection stops accelerating. Since  $\mathbf{R} \propto u$ 

$$\frac{d^2u}{dt^2} = 0 \text{ at peak therefore}$$
$$\frac{d^2u}{dt^2} = \frac{d}{dt}\left(\frac{du}{dt}\right) = \frac{d}{dt}(f(u)) = f'(u)$$
$$\frac{du}{dt} = f'(u)f(u)$$

Thus at peak f'(u) = 0 (since  $f'(u) \neq 0$ ) Therefore we realized that only if q < 1 then the epidemic peaks

- 1) The number of infectious people increases if  $\frac{d^2u}{dt^2} > 0$
- 2) If f'(u) = 0 then at peak acceleration stops
- 3)  $\frac{d^2u}{dt^2} = f'(u)f(u) < 0$  is always, this means the number of infectious decreases from the start.

Parameter  $q = \frac{\gamma}{\beta S_0}$  is called the threshold value. if q < 1 then the epidemic accelerates if

q > 1 then epidemic decreases from start.



Fig. 1 Graph when q < 1

Figure 1 is the graph between the function  $f(u) = p - qu - e^{-u}$  and the variable u. From the graph it is clear that if We take  $q = \frac{\gamma}{\beta S_0} = \frac{1}{3*(.12)*(90)} = .03086 < 1$  and  $p = \frac{N}{S_0} = \frac{100}{90} = 1.1111$  then f(u) = 1.111 - 0.03086u - e<sup>-u</sup>, it shows that the number of infectious people increases at first and reaches at peak and then the number of infectious people start decreasing which is plotted using SCILAB. Similarly taking p = 1.111 and q = 1.23 > 1 and using the equation  $f(u) = 1.111 - 1.23 u - e^{-u}$ . Using the SCILAB, we have figure 2 which is graph between f(u) and u if q > 1.



Fig:2 Graph when q > 1

Graph shows that if q > 1 then the number of infectious people decreases from the he starting epidemic does not reach at the peak. This is only possible if the infectious rate  $\beta$  decreases and the recovery rate increases.

# **3.** Conclusion

Evolution of mathematical epidemiology into separate area of population dynamics is parallel to mathematical ecology. we have focused on the role of the threshold value (basic reproduction number)  $R_0$ , which is defined as the average number of people infected when a typical infective enters

an entirely susceptible population. We have illustrated the significance of the threshold value  $R_0 = \frac{\beta S_0}{\gamma}$ . The disease can invade the completely susceptible people if and only if  $R_0 > 1$  and epidemic . dies out if  $R_0 < 1$ .

# 4. Appendix

SCILAB Code

```
1) u = (0:1:10)

y = 1.111 - .03086*(u) - \%e^{-}(u);

plot(y) (for Fig-1.)

2) u = (0:1:10);

y = 1.1111-1.2*(u)-\%e^{-}(u);

plot(y) (for Fig-2.)
```

## 6. Referenes

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