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# A Mathematical Modeling on the Study for the Growth of Epidemic Disease with the Help of Basic Reproduction Number and Runge Kutta Method

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***Abstract:*** *Epidemic disease has a long history. Chikungunya is one of them. It is highly contagious disease. A mathematical model presented all possible situation with the help of differential equations and a systematic study of the growth on Chikungunya. The improved model provides the best result of epidemic model and discussed Runge Kutta Method numerically.*

***Key Words:*** *Basic Reproduction Number, Runge Kutta Method, Epidemic Model.*

## 1. INTRODUCTION:

A disease is an anomalous state which influences negatively the construction and function of a living being. Diseases are known as medicinal states that are related with particular indications. There are many reasons for causing the diseases such as external factors like pathogens or by internal dysfunctions. In human being's lives, disease is referred to any state which brings soreness, dysfunction, agony, social troubles, or death of a person who is affected with diseases and other persons who are in touch with the affected person. The people can affect mentally not only physically by diseases and their lives are changed altogether due to these diseases. Chikungunya is a viral disease transmitted by the Aedes mosquitoes, primarily the Aedes aegypti and Aedes albopictus species. The name "Chikungunya" is derived from the Makonde language, meaning "to become contorted" or "to walk bent over" describing the characteristic posture of individuals suffering from joint pain associated with the disease. Historically, Chikungunya was mainly found Africa, Asia and the Indian subcontinent. However, in recent years, the disease has spread to other places of the world. It is characterized by symptoms like fever, severe joint pain, muscle pain, headache, rash, and fatigue. While the illness is rarely fatal, the joint pain can be debilitating and persist for weeks or even months, affecting the quality of life for those infected.

Chikungunya is a viral disease and transmitted with the rate of transmission $\beta$ over the population which is given by differential equation model:

$$\frac{dS}{dt} = \Delta - \beta SI - \mu S \quad (1)$$

$$\frac{dE}{dt} = \beta SI - \gamma_1 E - \mu E \quad (2)$$

$$\frac{dI}{dt} = \gamma_1 E - \gamma_2 I + \gamma_3 R - \mu I \quad (3)$$

$$\frac{dR}{dt} = \gamma_2 I - \gamma_3 R - \mu R \quad (4)$$

**Variables and Parameter Description:**

S=Susceptible class= 14346,I=Infected class=1185,E=Exposed Class=1102,R=1 or 1022

| Parameter | Meaning | Values |
|---|---|---|
| $\beta$ | Transmission rate | 0.1234 |
| $\gamma_1$ | Expose rate | 0.2404 |
| $\gamma_2$ | Infection rate | 0.0755 |
| $\gamma_3$ | Recovery rate | 1.0021 |
| $\Delta$ | Birth rate | 17.377 |

| | | |
|---|---|---|
| $\mu$ | Death rate | 7.380 |
| T | Time | 1 – 7 days |

## 2. NUMERICAL ANALYSIS:

### Basic Reproduction Number

The basic reproduction number ($R_0$) is a key parameter in epidemiology that quantifies the average number of secondary infections caused by a single infected individual in a susceptible population. It is a fundamental concept used to understand the transmission dynamics of infectious diseases. The basic reproduction number ($R_0$) is typically estimated using mathematical models, and several methods exist for its calculation.

The basic reproduction number ($R_0$) is defined for an epidemic disease by using SIR model. If $R_0 < 1$, then the disease-free equilibrium point will be stable otherwise, it will be unstable for $R_0 > 1$. We have, the basic reproduction number for Chikungunya: $R_0 = (\text{birth rate})/(\text{death rate})$. As per Annexture I, we have the value of the basic reproduction number that is$R_0 = 2.355 > 1$. So there is risk for complex situation for the society to face another bad effect of epidemic disease.

### Runge Kutta method:

The Runge – Kutta method is a numerical technique used for solving ordinary differential equations. It is widely employed in various fields, like physics, engineering, mathematical modelling and epidemiology. The method provides an approximate solution to the ordinary differential equations by discretizing the continuous problem into of iterative calculations.

The Runge-Kutta method can be adapted for various types of ODEs. Its versatility and efficiency make it valuable in solving complex mathematical models, such as those used in epidemiology to study disease dynamics and growth.It's important to note that while the Runge-Kutta method provides a numerical approximation to the solution, it may introduce some error compared to the exact analytical solution. The accuracy of the method depends on the step size chosen and the smoothness of the ODE. Therefore, it is crucial to select an appropriate step size and assess the convergence and stability of the method for each specific problem.

Let $f_1(SEIR^*) = = \Delta - \beta SI - \mu S$

$f_2(SEIR^*) = \beta SI - \gamma_1 E - \mu E$

$f_3(SEIR^*) = \gamma_1 E - \gamma_2 I + \gamma_3 R - \mu I$

$f_4(SEIR^*) = \gamma_2 I - \gamma_3 R - \mu R$

The general equations for $r \geq 0$ is given by

$$S_{r+1} = S_r + K = S_r + \frac{1}{6}[K_1 + 2(K_2 + K_3) + K_4]$$

$$E_{r+1} = E_r + L = E_r + \frac{1}{6}[L_1 + 2(L_2 + L_3) + L_4]$$

$$I_{r+1} = I_r + M = I_r + \frac{1}{6}[M_1 + 2(M_2 + M_3) + M_4]$$

$$R_{r+1} = R_r + N = R_r + \frac{1}{6}[N_1 + 2(N_2 + N_3) + N_4]$$

Where K, L, M and N are defined as

$$K_1 = hf_1(S_0, E_0, I_0, R_0) = h[\Delta - h\beta S_0 I_0 - \mu S_0]$$

$$K_2 = hf_1\left(S_0 + \frac{1}{2}hK_1, E_0 + \frac{1}{2}hL_1, I_0 + \frac{1}{2}hM_1, R_0 + \frac{1}{2}hN_1\right) =$$

$$= h\left[\Delta - h\beta\left(S_0 + \frac{1}{2}hK_1\right)\left(I_0 + \frac{1}{2}hM_1\right) - \mu\left(S_0 + \frac{1}{2}hK_1\right)\right]$$

$$K_3 = hf_1\left(S_0 + \frac{1}{2}hK_2, E_0 + \frac{1}{2}hL_2, I_0 + \frac{1}{2}hM_2, R_0 + \frac{1}{2}hN_2\right) =$$

$$= h\left[\Delta - h\beta\left(S_0 + \frac{1}{2}hK_2\right)\left(I_0 + \frac{1}{2}hM_2\right) - \mu\left(S_0 + \frac{1}{2}hK_2\right)\right]$$

$$K_4 = hf_1(S_0 + hK_3, E_0 + hL_3, I_0 + hM_3, R_0 + hN_3)$$

$$= h[\Delta - h\beta(S_0 + hK_3)(I_0 + hM_3) - \mu(S_0 + hK_3)]$$

Then $K = \frac{1}{6}[K_1 + 2(K_2 + K_3) + K_4]$

Similarly, $L_1 = hf_2(S_0, E_0, I_0, R_0) = h[\beta S_0 I_0 - (\gamma_1 + \mu)E_0]$

$$L_2 = hf_2(S_0 + \frac{1}{2}hK_1, E_0 + \frac{1}{2}hL_1, I_0 + \frac{1}{2}hM_1, R_0 + \frac{1}{2}hN_1)$$
$$= h[\beta(S_0 + \frac{1}{2}hK_1)(I_0 + \frac{1}{2}hM_1) - (\gamma_1 + \mu)(E_0 + \frac{1}{2}hL_1)]$$
$$L_3 = hf_2(S_0 + \frac{1}{2}hK_2, E_0 + \frac{1}{2}hL_2, I_0 + \frac{1}{2}hM_2, R_0 + \frac{1}{2}hN_2)$$
$$= h[\beta(S_0 + \frac{1}{2}hK_2)(I_0 + \frac{1}{2}hM_2) - (\gamma_1 + \mu)(E_0 + \frac{1}{2}hL_2)]$$
$$L_4 = hf_2(S_0 + hK_3, E_0 + hL_3, I_0 + hM_3, R_0 + hN_3)$$
$$= h[\beta(S_0 + hK_3)(I_0 + hM_3) - (\gamma_1 + \mu)(E_0 + hL_3)]$$

Then $L = \frac{1}{6}[L_1 + 2(L_2 + L_3) + L_4]$

$$M_1 = hf_3(S_0, E_0, I_0, R_0) = h[\gamma_1 E_0 - (\gamma_2 + \mu)I_0 + \gamma_3 R_0]$$
$$M_2 = hf_3(S_0 + \frac{1}{2}hK_1, E_0 + \frac{1}{2}hL_1, I_0 + \frac{1}{2}hM_1, R_0 + \frac{1}{2}hN_1$$
$$= h[\gamma_1(E_0 + \frac{1}{2}hL_1) - (\gamma_2 + \mu)(I_0 + \frac{1}{2}hM_1) + \gamma_3(R_0 + \frac{1}{2}hN_1)]$$
$$M_3 = hf_3\left(S_0 + \frac{1}{2}hK_2, E_0 + \frac{1}{2}hL_2, I_0 + \frac{1}{2}hM_2, R_0 + \frac{1}{2}hN_2\right)$$
$$= h[\gamma_1(E_0 + \frac{1}{2}hL_2) - (\gamma_2 + \mu)I_0 + \gamma_3 R_0]$$
$$M_4 = hf_3(S_0 + hK_3, E_0 + hL_3, I_0 + hM_3, R_0 + hN_3)$$
$$= h[\gamma_1(E_0 + hL_3) - (\gamma_2 + \mu)(I_0 + hM_3) + \gamma_3(R_0 + hN_3)]$$

Then $M = \frac{1}{6}[M_1 + 2(M_2 + M_3) + M_4]$

$$N_1 = hf_4(S_0, E_0, I_0, R_0) = h[\gamma_2 I_0 - (\gamma_3 + \mu)R_0]$$
$$N_2 = hf_4\left(S_0 + \frac{1}{2}hK_1, E_0 + \frac{1}{2}hL_1, I_0 + \frac{1}{2}hM_1, R_0 + \frac{1}{2}hN_1\right)$$
$$= h[\gamma_2(I_0 + \frac{1}{2}hM_1) - (\gamma_3 + \mu)(R_0 + \frac{1}{2}hN_1)]$$
$$N_3 = hf_4\left(S_0 + \frac{1}{2}hK_2, E_0 + \frac{1}{2}hL_2, I_0 + \frac{1}{2}hM_2, R_0 + \frac{1}{2}hN_2\right)$$
$$= h[\gamma_2(I_0 + \frac{1}{2}hM_2) - (\gamma_3 + \mu)(R_0 + \frac{1}{2}hN_2)]$$
$$N_4 = hf_4(S_0 + hK_3, E_0 + hL_3, I_0 + hM_3, R_0 + hN_3)$$
$$= h[\gamma_2(I_0 + hM_3) - (\gamma_3 + \mu)(R_0 + hN_3)]$$

Then $N = \frac{1}{6}[N_1 + 2(N_2 + N_3) + N_4]$

Therefore, on the bases of above measurements, we constructed the following graphs with the help of MATLAB.

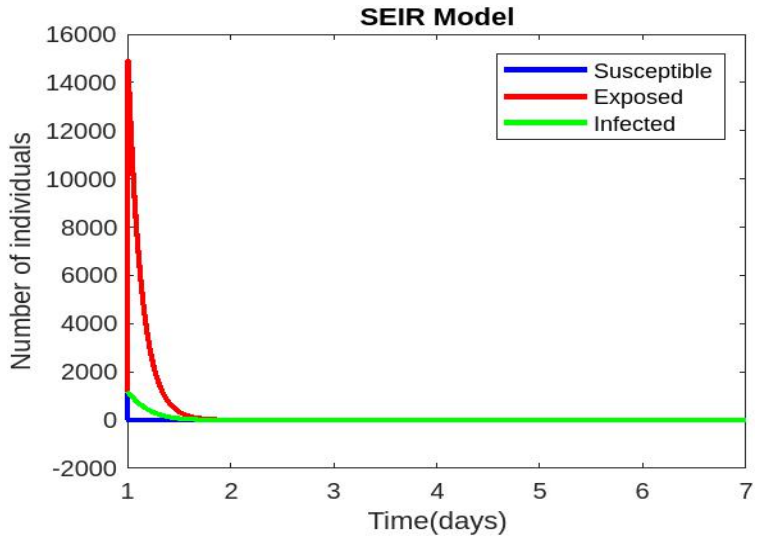


Figure 1: SEIR Model

In above graph, MATLAB represent the combine growth of the epidemic disease. Where S means number of suspectable reduces the total number of cases with respect to time, E means number of exposed cases reduces recorded cases with respect to time, I mean number of infected cases reduces the total number of infected cases with respect to time and R means number of recovered cases.

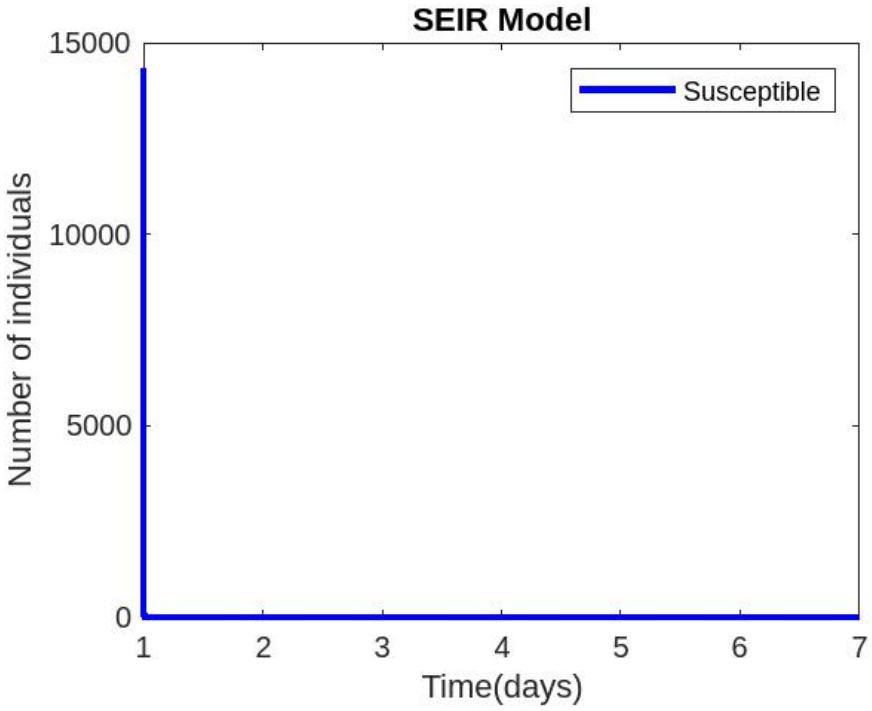


Figure 2: SEIR Model

In above graph, MATLAB represent S & S means number of suspectable reduces the total number of cases with respect to time.

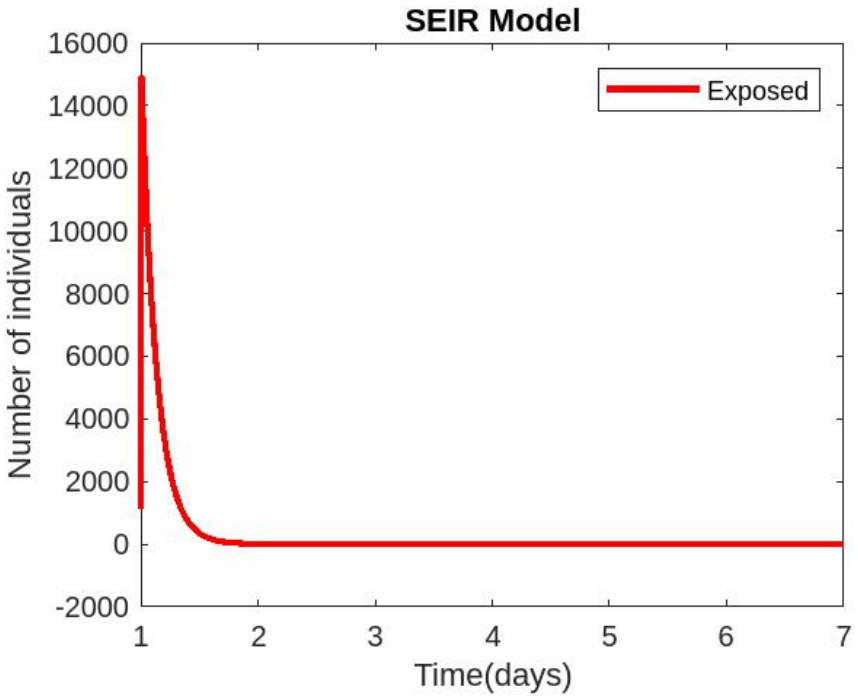


Figure 3: SEIR Model

In above graph, MATLAB represent the E, where E means number of exposed cases reduces recorded cases with respect to time.

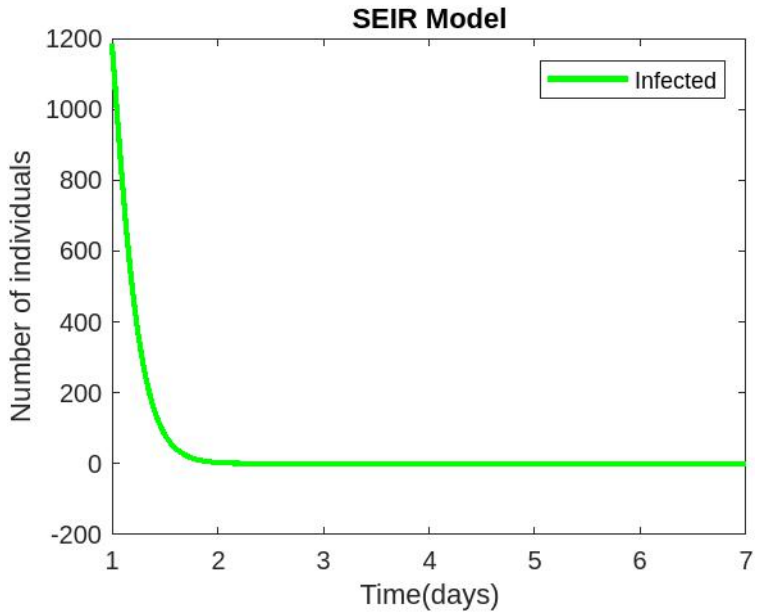


Figure 4: SEIR Model

In above graph, MATLAB represent the I that is I number of infected cases reduces the total number of infected cases with respect to time.

## 3. CONCLUSION:

A mathematical model has been used on epidemiology. By modifying the basic SIR model, we have obtained useful result insight on the effect of viral infection during endemic. According to SIR Model provides the stable situation. This modified mathematical model can possibly allow decision makers to make a better decision on the preventing and controlling of the spread of infectious disease.

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