EQUILIBRIUM APPROACH ON SEIR MODEL ON DENGUE DISEASE

[1]Pappu Mahto,[2]Smita Dey
[1]Assistant Professor,[2]Associate Professor
[1] Department of Mathematics,
[1] St. Xavier's College, Ranchi, India.

Abstract: Dengue is a mosquito – borne, human viral disease found in tropical and subtropical areas. Dengue is an epidemic disease across Asia, Africa and North America and taken many human lives. In this paper we analyses for disease - free equilibrium and Endemic equilibrium by using mathematical model on the SEIR model. Here we focus on how to calculate the basic reproduction number($\mathcal{R}_0$). Whenever the basic reproduction number($\mathcal{R}_0$) is less than or equal to one then disease- free equilibrium is globally stable and the disease dies out. But when the basic reproduction number ($\mathcal{R}_0$) is larger than unity then there exist the endemic equilibrium which is stable and hence disease will persist in the system. The analysis reveals that increasing the treatment rate at an early period of the outbreak will reduce the basic reproduction number. The stability analysis is done by using the Routh – Hurwitz Stability Criterion.

Key Words **- SEIR Model, Endemic, Basic reproduction number, Equilibrium, Stability Analysis.**

I. Introduction

Dengue fever is high on the list of mosquito – borne disease that increases very rapidly with global warming [1]. Dengue virus(DV) belong to the family of flaviviridae, and there are four serotypes of the virus referred as DV – 1, DV – 2, DV – 3 and DV – 4[2]. Dengue is transmitted mainly by the infected Aedes Aegypti mosquito and also by Aedes Albopictus. Dengue Virus infection results in a broad spectrum of clinical presentations ranging from a classic dengue fever(DF) to a severe presentations such as dengue hemorrhagic fever(DHF) or dengue shock syndrome (DSS) which is often fatal [2, 3], death usually results from circulatory collapse due to massive plasma leakage [2, 3]. There is no specific treatment of DHF or DSS although with proper clinical diagnosis and management fatality rate less than 1% [4]. Fatality rates vary between 0.5% to 3.5% in Asian countries [5]. Dengue is the fastest spreading vector – borne viral disease now endemic in over 100 countries. At present half of the world population is living in areas at risk for dengue [6]. The first record of a case of probable dengue is in a Chinese medical encyclopedia from the Jin Dynasty (265 – 420 AD) which referred to a "water poison" associated with flying insects [2, 7]. There have been descriptions of epidemics in the 17th century, but the most plausible early reports of dengue epidemics are from 1779 and 1780, when an epidemic swept across Asia, Africa and North America. From that time until 1940, epidemics were infrequent [2]. A standard program used in many countries to control the spread of the disease in the control of the main disease vector by fuming or fogging. Many studies show that this program was not fully effective [1].

A simple SIR model for dengue disease transmission has been studied by many researchers [8, 9]. Now a day's researchers are going on towards the invention of vaccine for dengue disease. The effects of vaccination on the transmission of infectious disease are studied by many researchers [10, 11]. In India, dengue was first documented in Kolkata (Calcutta) in 1824, and severe epidemics took place in the city during the years 1836, 1906, 1911 and 1972 (affecting 40% of the city population) [12]. Mathematical modeling is a powerful tool to test and compare different intervention strategies. The various mathematical models help us conceptualize the transmission dynamics in a quantitative way as well as allow us to test different hypothesis to understand their importance [13]. In this paper, equilibrium analysis has been done for disease - free equilibrium and endemic equilibrium through Ordinary differential equations using Routh – Hurwitz Stability Criterion [14].

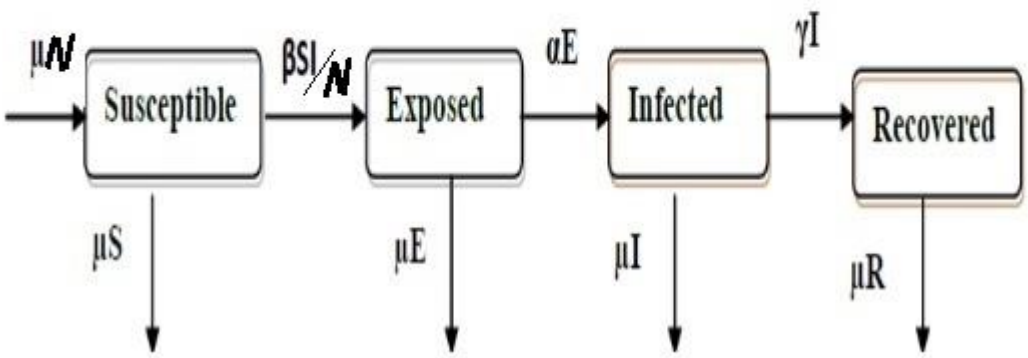
II.THE MATHEMATICAL MODEL -

The SEIR Mathematical Model for dengue disease, in which the total population is divided into four compartments such as the Susceptible (S), Exposed (E), Infectious (I) and Recovered (R).

In this model, Susceptible (S) is used to represent the number of individuals not yet infected with the dengue disease or that Susceptible to the dengue disease. The Exposed (E) is those individuals who infected with dengue disease with no positive

symptoms. The infectious (I) denotes the number of individuals who have been infected with the disease and the Recovered (R) is the compartment used for those individuals who have been infected and then removed from the disease, either due to immunization or due to death. Those in this category are not able to be infected again.

- A flow diagram for the SEIR model can be represented as;



The individuals enter to the given SEIR Model with μN in the susceptible (S) compartment. The Susceptible individual goes to the next Exposed (E) compartment with βSI and the Exposed individual once infected then it transfer to the next Infectious (I) compartment with αE.The individual then move to the Recovered (R) compartment with the proper immunity against the dengue disease with γI. The μS, μE, μI and μR are the group of peoples, who passed away from S, E, I and R classes respectively.

Let –

DV – Dengue Virus

S(t) – The number of individuals susceptible to the dengue disease at time t

E(t) – The number of individuals of latently infected individuals at time t

I(t) - The number of individuals infected by the dengue disease at time t

R(t) – The number of individuals who get the proper immunity and have recovered from the infection at time t.

α – The rate at which susceptible individual becomes latently infected with the dengue disease

β - The rate at which latently infected individual become actively infected with the dengue disease

γ – The rate at which the infected individual recovered from the dengue disease with immunity.

Here we suppose that the disease is in the closed population with equal birth or death rate (μ). By these assumptions the following differential equations represents the rate of change from one compartment to other compartment.

The system of differential equation is:-

$$\frac{dS}{dt} = \mu N - \mu S - \frac{\beta SI}{N}$$

$$\frac{dE}{dt} = \frac{\beta SI}{N} - (\mu + \alpha)E$$

…….. (i)

$$\frac{dI}{dt} = \alpha E - (\mu + \gamma)I$$

$$\frac{dR}{dt} = \gamma I - \mu R$$

Now introducing new variable by assuming $S = Ns$, $E = Ne$, $I = Ni$, R= Nr, where 's' is the proportion of susceptible population, 'e' is the exposed proportion of the population, 'i' is the proportion of infectious population and 'r' is the proportion of the recovered population gives the equation below -

$$\frac{de}{dt} = \beta si - (\mu + \alpha)e$$

$$\frac{di}{dt} = \alpha e - (\gamma + \mu)\, i \qquad \ldots\ldots\ldots\ldots \quad \text{(ii)}$$

$\frac{ds}{dt} = \mu - (\mu + \beta i)s$

$\frac{dr}{dt} = \gamma i - \mu r$

Where, s + e + i + r = 1, but since r = 1 – s – e – i, and the variable r does not appear in the first three equations of (ii) so, it is enough to study the system given below [15] –

$\frac{ds}{dt} = \mu - (\mu + \beta i)s$

$\frac{de}{dt} = \beta is - (\mu + \alpha)e$ …… (iii)

$\frac{di}{dt} = \alpha e - (\gamma + \mu)\, i$

Computation of Basic Reproduction number ($\mathcal{R}_0$) –

Basic reproduction number is the average number of secondary infectious produced by one infectious individual in a completely susceptible population at disease – free equilibrium [16, 17].

It is assumed that 's' is near disease – free equilibrium. Hence from equation (iii), for the exposed and infectious results -

$(A - B) = \begin{bmatrix} 0 & \beta \\ 0 & 0 \end{bmatrix} - \begin{bmatrix} \mu + \alpha & 0 \\ -\alpha & \gamma + \mu \end{bmatrix}$

Where, A = matrix of infection,

And B = matrix of transmission, such that

A = $\begin{bmatrix} 0 & \beta \\ 0 & 0 \end{bmatrix} and\ B = \begin{bmatrix} \mu + \alpha & 0 \\ -\alpha & \gamma + \mu \end{bmatrix}$

But |B|= $(\mu + \alpha)(\gamma + \mu)$,

Then $B^{-1} = \frac{1}{(\mu+\alpha)(\gamma+\mu)} \begin{bmatrix} (\gamma + \mu) & 0 \\ \alpha & (\mu + \alpha) \end{bmatrix} = \begin{bmatrix} \frac{1}{\mu+\alpha} & 0 \\ \frac{\alpha}{(\mu+\alpha)(\gamma+\mu)} & \frac{1}{\mu+\gamma} \end{bmatrix}$

Then $AB^{-1} = \begin{bmatrix} 0 & \beta \\ 0 & 0 \end{bmatrix} \begin{bmatrix} \frac{1}{\mu+\alpha} & 0 \\ \frac{\alpha}{(\mu+\alpha)(\gamma+\mu)} & \frac{1}{\mu+\gamma} \end{bmatrix} = \begin{bmatrix} \frac{\alpha\beta}{(\mu+\alpha)(\gamma+\mu)} & \frac{\beta}{\gamma+\mu} \\ 0 & 0 \end{bmatrix}$

Thus the basic reproduction number is the dominant eigenvalue of $AB^{-1}\ i.e.\ \mathcal{R}_0 = \frac{\alpha\beta}{(\mu+\alpha)(\gamma+\mu)}$ ……..(iv)

III. Equilibrium point –

Two equilibrium points are considered in this study: disease – free equilibrium and endemic equilibrium points. To obtain these points the equation (iii) are set to zero and the values of the proportions (s, e and i) are to be solved.

$\mu - (\mu + \beta i)\ s = 0$

$\beta is - (\mu + \alpha)e = 0$ …… (v)

$\alpha e - (\gamma + \mu)\, i = 0$

IV. Disease free equilibrium point and stability –

Here we assume that there is no disease or infection in the system, hence putting i = 0 and e = 0 in the equation (v), we get,

$\mu - \mu s + \beta s \times 0 = 0$

$\beta s \times 0 - (\mu + \alpha) \times 0 = 0$

$\alpha \times 0 - (\gamma + \mu) \times 0 = 0$

After simplification, we get,

$\mu - \mu s = 0$

$\Rightarrow s = 1$

so,at this disease – free equilibrium point is (s, e, i) = (1, 0, 0), since the virth rate and death rates are equal.

Now, for the stability of the disease free equilibrium, first we calculate the Jacobian matrix.

The Stability of the Equilibrium point –

Let us suppose equation (iii) as

$k(t) = \mu - \mu s(t) - \beta i(t)s(t)$

$l(t) = \beta s(t)i(t) - (\mu + \alpha)e(t)$ ……..*(vi)*

$m(t) = \alpha e(t) - (\gamma + \mu)i(t)$

Now the Jacobian matrix is –

$$J = \begin{bmatrix} \frac{\partial k}{\partial s} & \frac{\partial k}{\partial e} & \frac{\partial k}{\partial i} \\ \frac{\partial l}{\partial s} & \frac{\partial l}{\partial e} & \frac{\partial l}{\partial i} \\ \frac{\partial m}{\partial s} & \frac{\partial m}{\partial e} & \frac{\partial m}{\partial i} \end{bmatrix} = \begin{bmatrix} -\mu - \beta i & 0 & -\beta s \\ \beta i & -(\alpha + \mu) & \beta s \\ 0 & \alpha & -(\gamma + \mu) \end{bmatrix}$$

Stability of the disease – free equilibrium point –

Theorem 1 – The disease -free equilibrium point of the system of equation (v) is asymptotically stable if and only if $\mathcal{R}_0 \leq 1$, and unstable if $\mathcal{R}_0 > 1$.

Proof – For the disease free – equilibrium, the Jacobian matrix about the point was obtained as (s, e, i) = (1, 0, 0)

Then from (v), the disease free point is (s, e, i) = (1, 0, 0).

Thus, $J = J_0 = \begin{bmatrix} -\mu & 0 & -\beta \\ 0 & -(\alpha + \mu) & \beta \\ 0 & \alpha & -(\gamma + \mu) \end{bmatrix}$

Where J_0 be the Jacobian matrix about the disease free equilibrium and solve the characterstics equation as follows.
Let λ is the eigen value and I is the identity matrix of order 3. Then the characteristic equation is Det $[J_0 - \lambda I] = 0$.

Then $\text{Det}|J_0 - \lambda I| = \begin{vmatrix} -\mu - \lambda & 0 & -\beta \\ 0 & -(\alpha + \mu) - \lambda & \beta \\ 0 & \alpha & -(\gamma + \mu) - \lambda \end{vmatrix}$

$= (-\mu - \lambda)\{(-\alpha - \mu - \lambda)(-\gamma - \mu - \lambda) - \alpha\beta\}$
$= \lambda^3 + \lambda^2(\alpha + \gamma + 3\mu) + \lambda[\mu(\alpha + \gamma + 2\mu) + (\alpha + \mu)(\gamma + \mu) - \alpha\beta] + \mu[(\alpha + \mu)(\gamma + \mu) - \alpha\beta]$ …….(vii)

Suppose that, $\text{Det}|J_0 - \lambda I| = c_0\lambda^3 + c_1\lambda^2 + c_2\lambda^1 + c_3\lambda^0$

Then from equation (vii), we get,
$c_0 = 1$
$c_1 = \alpha + \gamma + 3\mu$
$c_2 = \mu(\alpha + \gamma + 2\mu) + (\alpha + \mu)(\gamma + \mu) - \alpha\beta$
$c_3 = \mu[(\alpha + \mu)(\gamma + \mu) - \alpha\beta]$

From Routh – Hurwitz stability criterion,
For all i ϵ {0, 3}; $c_i > 0$ and $\frac{c_1c_2 - c_0c_3}{c_1} > 0$ holds,
then all the eigenvalue of the characteristic equation have negative real part hence the disease – free equilibrium point is stable [14]. When $\mathcal{R}_0 \leq 1$, then the disease - free equilibrium is stable and unstable if $\mathcal{R}_0 > 1$.

V. Endemic equilibrium point and Stability –

This point indicates that the disease or infection will persist in the system. The system of ordinary differential equation in (v) are solved for s, e and i. But for easy identification let s = s^* , e = e^*, i = i*.

From equation (v), we get the endemic point as -

$\alpha e - (\gamma + \mu)\, i = 0$

$\Rightarrow i = \frac{\alpha e}{(\gamma + \mu)}$

So, $i^* = \frac{\alpha e}{(\gamma + \mu)}$

Also, $\beta i s - (\mu + \alpha) e = 0$

$\Rightarrow s = \frac{(\mu+\alpha)e}{\beta i}$

Putting the value of e, we get,

$s = \frac{(\mu+\alpha)(\gamma+\mu)}{\alpha\beta}$

So, $s^* = \frac{(\mu+\alpha)(\gamma+\mu)}{\alpha\beta}$

Also, from $\beta i s - (\mu + \alpha) e = 0$

$\Rightarrow \beta i s = (\mu + \alpha) e$

Putting this into $\mu - (\mu + \beta i)\, s = 0$

$\Rightarrow \mu - \mu s - (\mu + \alpha) e = 0$

$\Rightarrow (\mu + \alpha) e = \mu - \mu s$

Since, $s = \frac{(\mu+\alpha)(\gamma+\mu)}{\alpha\beta}$

$\Rightarrow (\mu + \alpha) e = \mu - \mu \frac{(\mu+\alpha)(\gamma+\mu)}{\alpha\beta}$

$= \frac{\mu\alpha\beta - \mu(\mu+\alpha)(\gamma+\mu)}{\alpha\beta}$

$\Rightarrow e = \frac{\mu\alpha\beta - \mu(\mu+\alpha)(\gamma+\mu)}{\alpha\beta(\mu+\alpha)}$

So, $e^* = \frac{\mu\alpha\beta - \mu(\mu+\alpha)(\gamma+\mu)}{\alpha\beta(\mu+\alpha)}$

Also, from, $i = \frac{\alpha e}{(\gamma + \mu)}$

Putting the value of e here, we get,

$i = \frac{\mu\alpha\beta - \mu(\mu+\alpha)(\gamma+\mu)}{\beta(\mu+\alpha)(\gamma+\mu)}$

So, $i^* = \frac{\mu\alpha\beta - \mu(\mu+\alpha)(\gamma+\mu)}{\beta(\mu+\alpha)(\gamma+\mu)}$

Then the endemic equilibrium point is –

$(s^*, e^*, i^*) = \left\{\frac{(\mu+\alpha)(\gamma+\mu)}{\alpha\beta}, \frac{\mu\alpha\beta - \mu(\mu+\alpha)(\gamma+\mu)}{\alpha\beta(\mu+\alpha)}, \frac{\mu\alpha\beta - \mu(\mu+\alpha)(\gamma+\mu)}{\beta(\mu+\alpha)(\gamma+\mu)}\right\}$.

Stability of endemic equilibrium point -

Theorem – 2 – The endemic equilibrium of system (v) is also asymptotically stable when when $\mathcal{R}_0 > 1$ and unstable when $\mathcal{R}_0 \leq 1$.

Proof - At the endemic equilibrium, we have,

$$(s^*, e^*, i^*) = \left\{\frac{(\mu+\alpha)(\gamma+\mu)}{\alpha\beta}, \frac{\mu\alpha\beta - \mu(\mu+\alpha)(\gamma+\mu)}{\alpha\beta(\mu+\alpha)}, \frac{\mu\alpha\beta - \mu(\mu+\alpha)(\gamma+\mu)}{\beta(\mu+\alpha)(\gamma+\mu)}\right\}.$$

Then the Jacobian of endemic equilibrium point is –

$$J^* = \begin{bmatrix} -\mu - \beta i^* & 0 & -\beta s^* \\ \beta i^* & -(\alpha + \mu) & \beta s^* \\ 0 & \alpha & -(\gamma + \mu) \end{bmatrix}$$

Let J^* be the Jacobian matrix at the endemic equilibrium and then solve the characterstic equation.

Then, $\text{Det}|J^* - \lambda I| = \begin{bmatrix} -\mu - \beta i^* - \lambda & 0 & -\beta s^* \\ \beta i^* & -(\alpha + \mu) - \lambda & \beta s^* \\ 0 & \alpha & -(\gamma + \mu) - \lambda \end{bmatrix}$

$= (-\mu - \beta i^* - \lambda)\{(-(\alpha + \mu) - \lambda)(-(\gamma + \mu) - \lambda) - \alpha\beta s^*\} - \beta s^*(\alpha\beta i^*)$

Expanding this, we get,

$\text{Det}|J^* - \lambda I| = \lambda^3 + \lambda^2(3\mu + \beta i^* + \alpha + \gamma) + \lambda(2\mu^2 + 2\mu\alpha + \mu\gamma + 2\beta i^*\mu + \beta i^*\alpha + \beta i^*\gamma + \alpha\gamma - \alpha\beta s^*) + (\mu^2 + \alpha\mu^2 + \mu\alpha\gamma - \mu\alpha\beta s^* + \beta i^*\mu^2 + \beta i^*\alpha\mu + \beta i^*\alpha\gamma)$ …….(viii)

Let $\text{Det}|J_1 - \lambda I| = d_0\lambda^3 + d_1\lambda^2 + d_2\lambda^1 + d_3\lambda^0$

So, from equation (viii),

$d_0 = 1$

$d_1 = 3\mu + \beta i^* + \alpha + \gamma$

$d_2 = 2\mu^2 + 2\mu\alpha + \mu\gamma + 2\beta i^*\mu + \beta i^*\alpha + \beta i^*\gamma + \alpha\gamma - \alpha\beta s^*$
$d_3 = \mu^2 + \alpha\mu^2 + \mu\alpha\gamma - \mu\alpha\beta s^* + \beta i^*\mu^2 + \beta i^*\alpha\mu + \beta i^*\alpha\gamma$

Using the Routh – Hurwitz stability criterion,
If all i ϵ {0, 3}; $d_i > 0$ and $\frac{d_1 d_2 - d_0 d_3}{d_1} > 0$ holds.

Then all the eigenvalue of the characteristic equation have negative real part which means the endemic equilibrium point is stable. Hence, the system is asymptotically stable when $\mathcal{R}_0 > 1$ and unstable when $\mathcal{R}_0 \leq 1$.

VI. Conclusion –

The SEIR model exhibit two equilibrium; the disease – free equilibrium and the endemic equilibrium. Disease – free equilibrium is asymptotically stable when the basic reproduction number ($\mathcal{R}_0$) is less than or equal to one (i.e. $\mathcal{R}_0 \leq 1$), So, the disease will disappear from the population. Also the disease – free equilibrium becomes unstable and the endemic equilibrium is stable if $\mathcal{R}_0 > 1$. So, the disease will persist in the population .

VII. References–

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