Analysis of Epidemic model for Dengue by Simulation

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Abstract

Mathematical models have a profound contribution in the field of epidemiological research, which became more prominent after the outspread of Coronavirus. In this paper, with the aid of mathematical modeling we propose a method of recovery for the humans affected by dengue. According to WHO, dengue is a dangerous disease. This disease is caused in humans through the bite of female mosquito, especially Aedes Aegypti/ Yellow Fever Mosquito. When an infected mosquito with any four types of virus strain denoted by DENV-1 to DENV-4 bites humans, they may get this disease. For, this we proposed a SIHRV (Susceptible Infectious Hospital Recovery Vaccine) model, which is an extension of SIR model. By using Jacobian and Routh- Hurwity criterion we find the threshold number R_0. If $R_0 > 1$ model is unstable and if $R_0 < 1$ the model is stable. We also find Disease free equilibrium point and Endemic equilibrium point, which is useful for better recovery. For the better representation of the model, we have used matlab to make graphs.

Key word : *Mathematical model; vaccination; Endemic equilibrium; Routh-Hurwitz criteria*

1.Introduction : In tropical and subtropical areas of many industrialized and developing nations, dengue fever is a serious issue. The World Health Organization (WHO) reports millions of cases each year from all around the world. The female Aedes Aegypti/Yellow Fever Mosquito is the primary carrier of this disease. Humans can contract this disease from mosquito bites carrying any of the four virus strains, designated by DENV-1 through DENV4. Once bitten by a dengue strain, humans get a lifelong immunity to that strain but only a transient cross-immunity to the other strains.

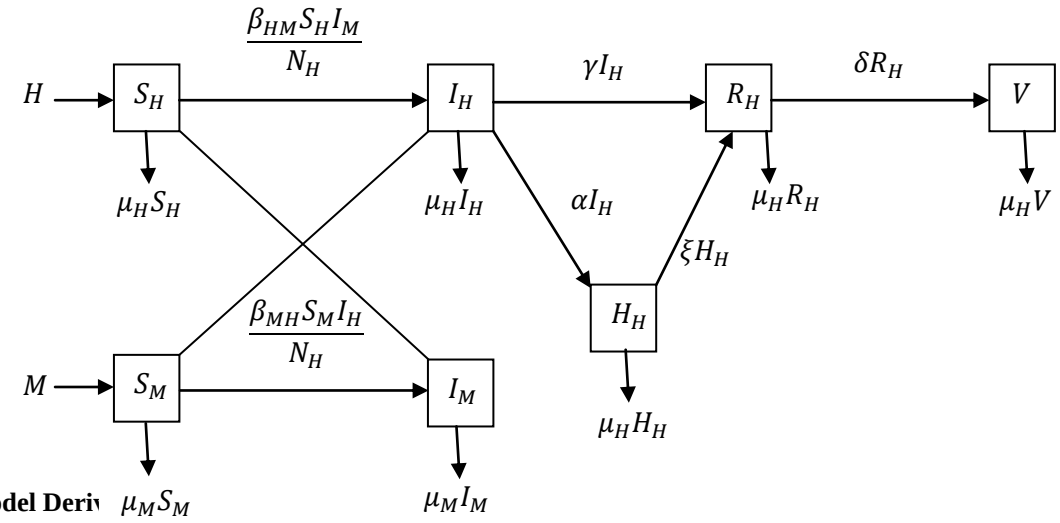
Dengue symptoms can continue up to a week or two after the virus enters the bloodstream of the bitten individual and typically manifest 4–10 days later. By getting the New Serotype Dengue Fever Vaccine, dengue fever is currently avoidable. The other, essentially expensive or impractical, method of remaining unaffected is prevention.

The proposed Dengue Epidemic Model is derived in this paper using generalized fractional order derivatives. When modeling biological, economic, and social systems where memory effects are significant, fractional order equations are shown to be more appropriate than integer order equations. As a result, it is common for mosquitoes to select humans based on their past interactions with them—particularly on their location and level of defense. Based on the evaluation of the transmission history and fractional order calculus, a perfect model to enable a nation to be disease free can thus be created. Many Authors [1,2] discussed the different type of model, which is used for calculation.

Sulami [5] The fractional order dengue epidemic model is the topic of this research. Study is done on the stability of positive fixed points and disease-free fixed points.The system of differential equations has been solved and simulated using the Adams-Bashforth-Moulton technique.

Hamdam [6] Discuss SIR modle with the next-generation matrix technique, where the threshold quantity value R0, which is comparable to the fundamental reproduction number.

Defterli [7] author examine how temperature affects the transmission of the vector-host transmitted dengue disease, a dengue epidemic model with fractional order derivative is developed. The model is made up of a set of differential equations of fractional order that are expressed within the Caputo fractional operator.



2. Model Deriv

For Human :

$$\frac{dS_H}{dt} = H - \mu_H S_H - \beta_{HM}\frac{S_H I_M}{N_H}$$
$$\frac{dI_H}{dt} = \beta_{HM}\frac{S_H I_M}{N_H} - \mu_H I_H - \alpha I_H - \gamma I_H$$
$$\frac{dR_H}{dt} = \gamma I_H - \xi H_H - \mu_H R_H - \delta R_H$$
$$\frac{dH_H}{dt} = \alpha I_H - \xi H_H - \mu_H H_H$$
$$\frac{dV}{dt} = \delta R_H - \mu_H V$$

For Mosquitoes :

$$\left.\begin{aligned}\frac{dS_M}{dt} &= M - \beta_{MH}\frac{S_M H}{N_H} - \mu_M S_M \\ \frac{dI_M}{dt} &= \beta_{MH}\frac{S_M I_H}{N_H} - \mu_M I_M\end{aligned}\right\} \quad \ldots. \quad (1)$$

Condition : $S_H + I_H + R_H + H_H + V = N_H$

where,

H is influx rate which is assumed to be susceptible

N_H is the total population of Human

M is the total population of Mosquito

S_H is the total number of susceptible Human population

I_H is the total number of infective Human population

R_H is the total number of recovered Human population

H_H is the total number of hospitalized Human population

V is the total number of vaccinated Human population

μ_H death rate in Human population

S_M is the total number of susceptible Mosquito population

I_M is the total number of infective Mosquito population

μ_M death rate in Mosquito population

α is the hospitalized rate by infective Human population

γ is the recovery rate by infective Human population

δ is the vaccinated rate by recovered Human population

ε is the recovery rate by hospitalized Human population

β_{HM} transmission probability from Human to Mosquito

β_{MH} transmission probability from Mosquito to Human

Many definitions of fractional derivatives [3,4] are used. The Riemann –Liouville derivatives of ith order is defined as

$$ {}_{RL}\mathcal{D}^{i}_{0+}f(t) = \frac{1}{\Gamma(n-i)}\left(\frac{d}{dt}\right)^{n}\int_{0}^{t}\frac{f(s)}{(t-s)^{i-n+1}}ds \text{ where}, n=[i]+1 \quad \ldots (2)$$

An alternative definition by Caputo was as follows

$$ \mathcal{D}^{i}_{t}f(t) = \frac{1}{\Gamma(n-i)}\int_{0}^{t}\frac{f^{(n)}(s)}{(t-s)^{i-n+1}}ds \text{ where}, n=[i]+1 \quad \ldots (3)$$

In this paper we will use Caputo fractional derivative for the system (1)

$$\left.\begin{aligned}
\mathcal{D}^{i}_{t}S_H &= H-\mu_H S_H-\beta_{HM}\frac{S_H I_M}{N_H}\\
\mathcal{D}^{i}_{t}I_H &= \beta_{HM}\frac{S_H I_M}{N_H}-\mu_H I_H-\alpha I_H-\gamma I_H\\
\mathcal{D}^{i}_{t}R_H &= \gamma I_H-\xi H_H-\mu_H R_H-\delta R_H\\
\mathcal{D}^{i}_{t}H_H &= \alpha I_H-\xi H_H-\mu_H H_H\\
\mathcal{D}^{i}_{t}V &= \delta R_H-\mu_H V\\
\mathcal{D}^{i}_{t}S_M &= M-\beta_{MH}\frac{S_M I_H}{N_H}-\mu_M S_M\\
\mathcal{D}^{i}_{t}I_M &= \beta_{MH}\frac{S_M I_H}{N_H}-\mu_M I_M
\end{aligned}\right\} \quad \ldots (4)$$

All parameters are assumed to be non-negative from system (4)

$$\mathcal{D}^{i}_{t}N_H = H-\mu_H N_H \quad \ldots (5)$$

Let $\Omega=\{(S_H,I_H,R_H,H_H,V,S_M,I_M): S_H,I_H,R_H,H_H,V,S_M,I_M \le 0, S_H+I_H+R_H+H_H+V \le H/\mu_H\}$

3. Equilibrium Points :

$$\mathcal{D}^{i}_{t}S_H=0,\ \mathcal{D}^{i}_{t}I_H=0,\ \mathcal{D}^{i}_{t}R_H=0,\ \mathcal{D}^{i}_{t}H_H=0,\ \mathcal{D}^{i}_{t}V=0,\ \mathcal{D}^{i}_{t}S_M=0,\ \mathcal{D}^{i}_{t}I_M=0 \quad \ldots (6)$$

Then $E_0=(H/\mu_H,0,0,0,0,M/\mu_M,0)$

For positive equilibrium point : $E_1=(S'_H,\ I'_H,\ R'_H,\ H'_H,\ V',S'_M,\ I'_M)$

$$S'_H=\frac{H-(\mu_H+\alpha+\gamma)I_H}{\mu_H} \qquad I'_H=\frac{(\mu_H+\delta)(\mu_H+\varepsilon)}{\gamma(\mu_H+\xi)-\alpha\xi}R_H$$

$$R'_H=\frac{\gamma(\mu_H+\xi)-\alpha\xi}{(\mu_H+\delta)(\mu_H+\xi)}I_H \qquad H'_H=\frac{(\mu_H+\delta)(\mu_H+\xi)}{(\mu_H+\xi)\{\gamma(\mu_H+\xi)-\alpha\xi\}}R_H\alpha$$

$$V'=\frac{\delta R_H}{\mu_H} \qquad S'_M=\frac{MN_H}{(\beta_{MH}I_H+\mu_M N_H)} \qquad I'_M=\frac{\beta_{MH}MI_H}{\mu_M(\beta_{MH}I_H+\mu_M H_M)}$$

The Jacobian matrix $J(E_0)$ for system (5) for diseases free equilibrium point is as follows:

$$J(E_0)=\begin{bmatrix}
-\mu_H & 0 & 0 & 0 & 0 & 0 & 0\\
0 & -(\mu_H+\alpha+\gamma) & 0 & 0 & 0 & 0 & 0\\
0 & \gamma & -(\mu_H+\delta) & \xi & 0 & 0 & 0\\
0 & \alpha & 0 & -(\mu_H+\xi) & -\mu_H & 0 & 0\\
0 & 0 & \delta & 0 & 0 & 0 & 0\\
0 & -\beta_{MH}S^0_M/N_H & 0 & 0 & 0 & -\mu_M & 0\\
0 & \beta_{MH}S^0_M/N_H & 0 & 0 & 0 & 0 & -\mu_M
\end{bmatrix}$$

The characteristic root for $|J(E_0)-\lambda I|$ are

$\lambda_1=-\mu_H, \lambda_2=-(\mu_H+\alpha+\gamma), \lambda_3=-\mu_M, \lambda_4=-\mu_M$

The other three roots are determined by the cubic equation

$$(\mu_H+\alpha+\gamma)(\mu_H+\xi+\lambda)\lambda+\xi\mu_H\delta=0$$

$$\Rightarrow \lambda^3+\lambda^2(2\mu_H+\delta+\xi)+\lambda(\mu_H+\delta)(\mu_H+\xi)+\xi\mu_H\delta=0$$

From above cubic equation all the roots are negative. Therefore the point E_0 is disease free equilibrium point.

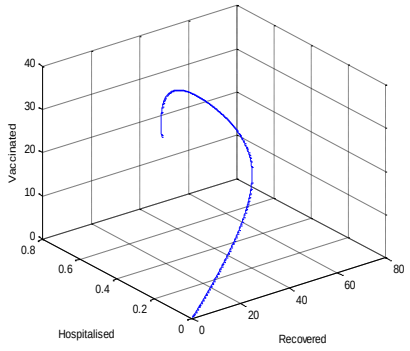


Fig. 1

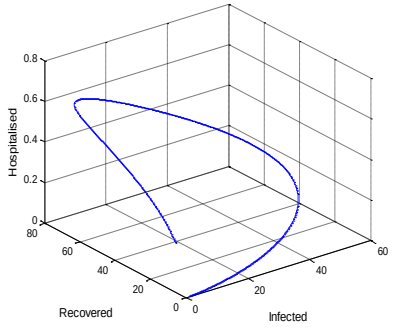


Fig. 2

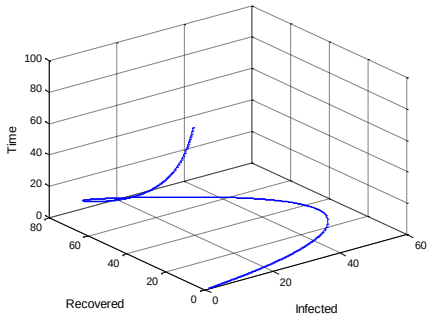


Fig. 3

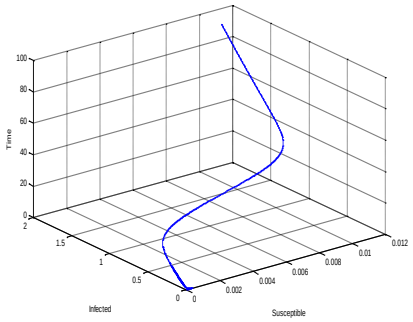


Fig. 4

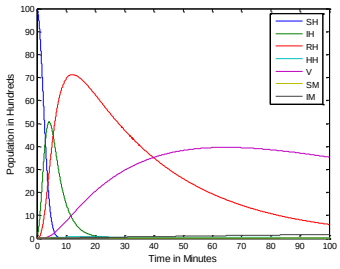


Fig. 5

4.Endemic Equilibrium :

The Jacobian matrix $J(E_1)$ is evaluated for point E_1

$$J(E_1) = \begin{bmatrix} -\mu_H - \beta_{HM}\frac{I'_M}{N_H} & 0 & 0 & 0 & 0 & 0 & -\frac{\beta_{HM}S'_H}{N_H} \\ \beta_{HM}\frac{I'_M}{N_H} & -(\mu_H+\alpha+\gamma) & 0 & 0 & 0 & 0 & \frac{\beta_{HM}S'_H}{N_H} \\ 0 & 0 & -(\mu_H+\delta) & \xi & 0 & 0 & 0 \\ 0 & \alpha & 0 & -(\mu_H+\varepsilon) & 0 & 0 & 0 \\ 0 & 0 & \delta & 0 & -\mu_H & 0 & 0 \\ 0 & -\frac{\beta_{MH}S'_M}{N_H} & 0 & 0 & 0 & -\left(\beta_{MH}\frac{I'_H}{N_H}+\mu_M\right) & 0 \\ 0 & \frac{\beta_{MH}S'_M}{N_H} & 0 & 0 & 0 & \beta_{MH}\frac{I'_H}{N_H} & -\mu_M \end{bmatrix}$$

After solving the characteristic equation all the eigen values of $|J(E_1) - \lambda I| = 0$ are negative, which shows that the system (4) is stable for the endemic equilibrium point E_1.

5. Simulation : All five fig. draw with help of same parameter. In 1st graph we comparing hospitalized and recovered number of patient with using vaccination. In 2nd graph 3D presentation of recovered patient no. with hospitalized and infected no. In 3rd graph we compare the number of recovered patient with infected no. and time. Form first three graph shows the recovery rate are increase as increase with time. In 4th graph shows the comparing between number of susceptible and infected patient with respect to time.

6.Conclusion : In this paper SIRHV epidemic infectious disease model for Dengue. This S model control the spreading of the disease in Human population. By using Routh-Hurwitz Criteria we find all the eigen values for endemic point are negative which shows that the above model SIRHV (Susceptible Infectious Recovered Hospitalization Vacation) is stable. Extending our work, we can also use harmonic mean type incidence rate for better stability and control the disease.

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