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AN OVERVIEW OF SOME BIOMATHEMATICAL MODELS OF DENGUE FEVER VIRUS TRANSMISSION

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Abstract:

Dengue fever is a viral disease transmitted to humans by the bite of infected Aedes mosquitoes. In recent years, the illness has grown to be a significant public health burden. Dengue sickness has no effective therapy and no vaccination. Therefore, raising people's awareness of how diseases spread can be extremely important in halting the development of the illness. The paper discusses creating a compartmental diagram for human and mosquito populations, developing mathematical models for dengue fever transmission, defining variables, and parameters. Using compartmental mathematical models with ordinary differential equations for both human and mosquito populations, the dynamics of the disease are investigated. The stability of the equilibrium points of the SIR, SEIR, SIR-SI, and SEIR-SI models was analyzed by considering that recovered patients could be reinfected with dengue. Using the Mathematica program, the stability conditions were discussed, and we used some numerical values for the various variables mentioned in some previous studies to determine the equilibrium points for each model and clarify whether these equilibrium points were stable or unstable.

Key Words: Dengue fever; SEIR-SI model; Endemic; Aedes mosquitoes; Stability.

1. **Introduction**: Dengue fever is a viral infection transmitted by the bite of a mosquito that occurs mostly in tropical and subtropical regions. It spreads especially rapidly in urban, suburban, and poor rural areas (Esteva & Vargas, 1998). The first recorded incidence of dengue was most likely in a Chinese medical encyclopedia during the Jin era (265-420), referred to as "water poison" and linked to an aircraft bug (Gubler,1998). The major carrier, the Egyptian Aedes, spread outside of Africa between the 15th and 19th centuries as a result of rising globalization and the slave trade (Simmons et al,2012) Physician and founding father of the United States Benjamin Rush used the term "breaking bone fever" or "painful bone fever" in a 1789 report to refer to dengue fever. The term dengue fever did not come into general use until after 1828 (Halstead,2007). There are references to epidemics in the seventeenth century, but the first plausible outbreaks occurred in 1779 and 1780 when the disease raced through Asia, Africa, and North America. From then until 1940, outbreaks were uncommon. Aedes confirmed disease transmission in 1906, and dengue disease was identified as the second disease after yellow fever in 1907. Henchal and Putnak conducted research that led to a better knowledge of disease transmission (Henchal,1990). The Second World War saw a notable outbreak of dengue due to environmental issues. This serious kind of illness was initially identified in the Philippines in 1953, and in the 1970s, it was a leading cause of infant mortality in the Americas and the Pacific. In 1981, cases of type 2 dengue virus were reported in Central and South America, where cases of type 1 virus infection had been reported several years earlier (Gould & Solomon,2008). This marked the first reports of dengue hemorrhagic fever and dengue shock syndrome, also the disease began to appear in 1994 in Saudi Arabia and was recorded annually but not at a high rate. Since 2000, infection rates have increased eight times worldwide, primarily due to increased urbanization and travel due to climate change. Although many cases were not reported, there were 2,809,818 dengue cases in total in 2022, including 1,290 deaths. In the Americas, there were 243,342 cases of dengue fever reported between January 1, 2023, and March 4, 2023, with 86 deaths. Bolivia recorded the highest cumulative incidence of dengue fever cases during that time, with 264.4 cases per 100,000 people. Nicaragua came in second with 196.8 cases per 100,000 people, and Belize came in third with 145.6 cases per 100,000 people (PAHO,2023). Furthermore, due to ideal weather for mosquito spread, higher transmission rates are anticipated in the southern hemisphere in the upcoming months. Urbanization, population growth, increased international travel, and global warming are thought to be contributing factors to this increase [(Normile, 2013), (Whitehorn & Farrar, 2010)]. The majority of dengue fever patients

recover fully and without any further complications. The death rate varies from 1% to 5%, but in cases of appropriate treatment, it is less than 1%, and the death rate for individuals with severe hypotension is 26% (Ranjit & Kissoon,2011). Dengue infection is caused by four types of viruses named: DEN-1, DEN-2, DEN-3, and DEN-4. Each of these viruses has different interactions with antibodies found in human blood serum. Despite these differences, infection with any of these viruses causes the same disease and the same set of clinical symptoms. Like other viruses, the dengue virus is a microscopic structure that can only replicate inside a host organism (Rodenhuis-Zybert et al., 2010). Mosquitoes are considered a means of transmitting the virus from one person to another. The virus grows inside the mosquito's intestines and settles in the salivary glands during an 8–12 day incubation phase, after which it starts to spread the disease for the duration of the mosquito's life. It seems that the virus does not affect the life of the mosquito, as she remains infected with it for her whole life (Patel et al.,2018). The infection is transmitted from person to person by the bite of the Aedes aegypti mosquito, where a healthy mosquito acquires the virus when it feeds on the blood of an infected person, and when it is transmitted to feed on the blood of a healthy person, she transmits the virus to him [(Wilder-Smith et al., 2009), (Stramer et al., 2009)]. Symptoms begin to appear 4-10 days after infection with the bite of a mosquito infected with the virus.These symptoms are similar to the symptoms of influenza, but they are severe. Infection is suspected when the temperature rises (above 40 degrees Celsius) and two of the following symptoms appear: severe headache and pain behind the eyes, muscle and joint pain, nausea, vomiting, and skin rash. To prevent infection with this disease, the vaccine is permitted in some countries for those between the ages of 9 and 45 years who live in areas where the disease is widespread. Prevention of dengue depends largely on control of the Aedes aegypti mosquito, which transmits the disease. It has been found that the best way to prevent it is to avoid mosquito bites:

i. Eliminate places where mosquitoes gather, such as water basins, whether inside or outside the home.

ii. Cover, empty, and clean all water tanks and basins weekly.

iii. Use insect-repellent skin creams inside and outside the home.

iv. Cover the body with long-sleeved clothes.

v. Ensure that the window mesh is secure and that there are no holes that allow insects to enter (Reiter,2010). The disease may develop into severe dengue fever, in which blood vessels are damaged and fluid leaks through them, and the number of platelets decreases, which leads to severe bleeding and a sudden drop in blood pressure, or failure of one of the body's systems and then death (Carod-Artal et al., 2013). There

is no specific drug to treat people with dengue fever, so prevention is the most important step to follow. When infected, it is therefore recommended: Taking a break, Fluid intake, Take painkillers, avoid blood thinners such as aspirin, and avoid exposure to mosquito bites; to prevent the spread of disease. In the case of severe dengue fever, medical care and replacement of lost fluids help prevent the development of the disease and preserve the patient's life (Chen & Wilson,2010). The World Health Organization classified dengue fever in 1997 into undifferentiated fever and dengue hemorrhagic fever. Dengue hemorrhagic fever is divided into 4 degrees: the first degree is the presence of easy bruising or a positive tourniquet test in a person with fever, the second degree is the presence of continuous bleeding in the skin and anywhere else, the third degree is the presence of clinical evidence of shock, and the fourth degree is a shock so severe that neither blood pressure nor pulse can be detected (Lee et al., 2018). Mathematical models describing dengue fever epidemiological dynamics have been found back from 1970 (Fischer & Halstead,1970). In the field of disease control, the use of mathematical models to comprehend the dynamics of viral infection has long been beneficial [(Adekunle et al.,2019), (Almeida et al., 2019), (Bliman et al.,2019)]. The SIR model is utilized to describe the dynamics of dengue virus transmission [(Derouich et al.,2003), (Almeida et al., 2019),(Nuraini et al.,2007)], emphasizing symptoms, transmission through infected mosquitoes, and regions prone to the disease like Egypt. Since severe dengue cases result mostly from re-infection with different serotypes, disease-induced mortality in this single-serotype model was not epidemiologically relevant [(Halstead,2009), (Vaughn,2000)]. A thorough evaluation of deterministic dengue modeling was published in 2012 (Andraud et al., 2012), which came after a review of dengue models to evaluate the impact of upcoming dengue vaccines published in 2011 (Johansson et al., 2011). where the host-to-host and vector-host transmission models were the two primary methods that were taken into consideration. Both extrinsic and intrinsic incubation periods play a significant role in the dynamics of dengue disease. So, many mathematical studies of dengue disease have been made using the compartment of the incubation period. Side and Noorani proposed the SEIR model of dengue disease by taking exposed classes of both vector and host populations (Syafruddin & Noorani,2012) Pongsumpun examined the dengue illness transmission dynamics both with and without the extrinsic incubation period influence (Pongsumpun,2006). Chan and Johansson studied the extrinsic and intrinsic incubation periods in mosquitoes and humans respectively (Chan & Johansson,2012). Phaijoo and Gurung studied the impact of temperature and human movement on the persistence of dengue disease using the SEIR model in the

multi-patch environment (Phaijoo & Gurung, 2016) Chanprasopchai et al. (2017) proposed a SEIR (susceptible-exposed-infected-recovered) model for Thailand and the analysis was based on Routh-Hurwitz criteria to establish the local asymptotic stability of the equilibrium points (Chanprasopchai et al., 2017) Recently, many mathematical models of dengue disease have been proposed to analyze and control the disease [(Jia et al., 2016), (Vyhmeister et al., 2022), (Liu-Helmersson et al., 2019)]. Previous studies that used the SIR, SEIR, SIR-SI, and SEIR-SI models to describe the spread of dengue virus assumed that patients who have recovered from dengue become immune so that they will not get infected with dengue fever. Current facts show that many patients who have recovered are infected with dengue. Accordingly, in the present study we constructed the SEIRS model, SIRS-SI model, and SEIRS-SI model as a modification of the SEIR model, SIR-SI model, and SEIR-SI model by taking into account that recovered patients could be reinfected with dengue fever.

2. The Theoretical Framework:

2.1 SIR Model for Transmission of Dengue Fever:

2.1.1 The Flow Diagram for the SIR Model:

A mathematical model called SIR is used to simulate how serotype I of the dengue virus spreads between people. The SIR model was the first model introduced in 1927 by Kermack and McKendrick (Kermack & McKendrick, 1927). This SIR model is based on a well-established concept in epidemiology called Susceptible, Infected, and Recovered [(Pongsumpun & Tang, 2001), (Soewone & Supriatna, 2005), (Derouich & Boutayeb, 2006), (Yaacob, 2007), (Side & Noorani, 2013)]. These models have only checked the formulation. The population in this model is divided into three categories: the Susceptible group represents individuals who are susceptible to the disease but haven't caught it yet, and the infectious group represents individuals infected with the disease and who can transmit the infection to others. Those who have recovered from the illness and are no longer able to spread the infection are represented by the recovered group.

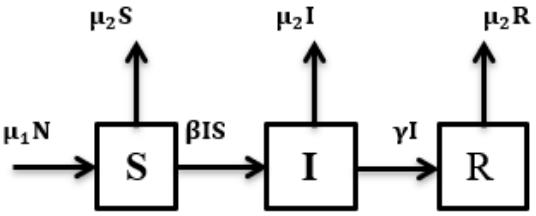

Figure (1): Flow diagram of SIR model

Explanation of model variables and parameters:

(S) The number of susceptible humans at time t.

(I) The number of infectious humans at time t.

(R) The number of recovered humans at time t.

(β) Infection rate.

(γ) Recovery rate.

(N) Total number of human population.

(μ_1) Birth rate.

(μ_2) Death rate.

2.1.2 The Mathematical Model:

The compartmental diagram in Figure (1) can be converted into a mathematical model in the form of non-linear differential equations as shown below:

$$\frac{ds}{dt} = \mu_1 N - \mu_2 S - \beta SI \qquad (1)$$

$$\frac{dI}{dt} = \beta SI - \mu_2 I - \gamma I \qquad (2)$$

$$\frac{dR}{dt} = \gamma I - \mu_2 R \qquad (3)$$

2.1.3The Equilibrium Points for the SIR Model

To find the equilibrium points we must putting

$$\frac{ds}{dt} = 0, \qquad \frac{dI}{dt} = 0, \qquad \frac{dR}{dt} = 0.$$

Then we get

$$\mu_1 N - \mu_2 S - \beta SI = 0 \qquad (4)$$

$$\beta SI - \mu_2 I - \gamma I = 0 \qquad (5)$$

$$\gamma I - \mu_2 R = 0 \qquad (6)$$

These equations can be solved in Mathematica using the following command:

Solve[{$\mu_1 N - \mu_2 S - \beta SI == 0, \beta SI - \mu_2 I - \gamma I == 0, \gamma I - \mu_2 R == 0$}, {S, I, R}]

Thus, the equilibrium points of the system (1)-(3) are:

The first is the disease-free equilibrium point

$$E_0 = (S_0, I_0, R_0)$$

where, $S_0 = \frac{N\mu_1}{\mu_2}, \qquad I_0 = 0, \qquad R_0 = 0.$

The second is the full endemic equilibrium point

$$E_1 = (S_1, I_1, R_1)$$

where $S_1 = \frac{\gamma+\mu_2}{\beta}$, $I_1 = \frac{-N\beta\mu_1+\gamma\mu_2+{\mu_2}^2}{-\beta\gamma-\beta\mu_2}$,

$R_1 = -\frac{\gamma(N\beta\mu_1-\gamma\mu_2-\mu_2^2)}{-\beta\gamma\mu_2-\beta\mu_2^2}$.

2.1.4 The Eigenvalues for SIR Model:

To study the stability of the system (1)-(3), we must find the Jacobian matrix of the system as the following:

We put the system in the form

$$\frac{ds}{dt} = \mu_1 N - \mu_2 S - \beta SI = f_1(S, I, R), \qquad (7)$$

$$\frac{dI}{dt} = \beta SI - \mu_2 I - \gamma I = f_2(S, I, R), \qquad (8)$$

$$\frac{dR}{dt} = \gamma I - \mu_2 R = f_3(S, I, R). \qquad (9)$$

The Jacobian matrix of the system is

$$J = \begin{pmatrix} f_{1S} & f_{1I} & f_{1R} \\ f_{2S} & f_{2I} & f_{2R} \\ f_{3S} & f_{3I} & f_{3R} \end{pmatrix} \qquad (10)$$

$$J = \begin{pmatrix} -\mu_2 - \beta I & -\beta S & 0 \\ \beta I & \beta S - \mu_2 - \gamma & 0 \\ 0 & \gamma & -\mu_2 \end{pmatrix} \qquad (11)$$

The eigenvalues of the Jacobian matrix are determined from the following characteristic equation $|J - \lambda \mathbb{I}| = 0$

, where λ is the eigenvalues of J.

Using the Mathematica, we have

$$\text{Det}[J - \lambda\, \text{IdentityMatrix}[3]] == 0, \qquad (12)$$

which gives the characteristic equation

$$(-\lambda - \mu_2)(I\beta\gamma - S\beta\lambda + I\beta\lambda + \gamma\lambda + \lambda^2 - S\beta\mu_2 + I\beta\mu_2 + \gamma\mu_2 + 2\lambda\mu_2 + \mu_2^2) = 0 \qquad (13)$$

This can be solved in Mathematica using the following command:

Solve[$(-\lambda - \mu_2)(I\beta\gamma - S\beta\lambda + I\beta\lambda + \gamma\lambda + \lambda^2 - S\beta\mu_2 + I\beta\mu_2 + \gamma\mu_2 + 2\lambda\mu_2 + \mu_2^2) == 0, \lambda$]

Thus, the eigenvalues are

$$\lambda_1 = \frac{1}{2}(S\beta - I\beta - \gamma - 2\mu_2 - \sqrt{S^2\beta^2 - 2SI\beta^2 + I^2\beta^2 - 2S\beta\gamma - 2I\beta\gamma + \gamma^2})$$

$$\lambda_2 = \frac{1}{2}(S\beta - I\beta - \gamma - 2\mu_2 + \sqrt{S^2\beta^2 - 2SI\beta^2 + I^2\beta^2 - 2S\beta\gamma - 2I\beta\gamma + \gamma^2}) \quad (14)$$

$$\lambda_3 = -\mu_2$$

The eigenvalues at the first equilibrium point $E_0 = (S_0, I_0, R_0)$ are

$$\lambda_1 = -\gamma + \frac{N\beta\mu_1}{\mu_2} - \mu_2,\ \lambda_2 = -\mu_2,\ \lambda_3 = -\mu_2$$

The system is stable at the equilibrium point E_0 if all the eigenvalues λ_1, λ_2 and λ_3 are negative, then the equilibrium point E_0 is stable if λ_1 is negative.

$$\text{i.e. } \lambda_1 < 0 \implies -\gamma + \frac{N\beta\mu_1}{\mu_2} - \mu_2 < 0$$
$$\implies -\gamma\,\mu_2 + N\beta\mu_1 - {\mu_2}^2 < 0$$
$$\implies N\beta\mu_1 < \mu_2(\mu_2 + \gamma)$$
$$\implies \frac{N\beta\mu_1}{\mu_2(\mu_2 + \gamma)} < 1$$

The eigenvalues at the second equilibrium point $E_1 = (S_1, I_1, R_1)$ are

$$\lambda 1 = -\frac{N\beta\mu_1}{2(\gamma + \mu_2)} - \frac{\sqrt{N^2\beta^2\mu_1^2 - 4N\beta\mu_1(\gamma + \mu_2)^2 + 4\mu_2(\gamma + \mu_2)^3}}{2(\gamma + \mu_2)},$$

$$\lambda 2 = -\frac{N\beta\mu_1}{2(\gamma + \mu_2)} + \frac{\sqrt{N^2\beta^2\mu_1^2 - 4N\beta\mu_1(\gamma + \mu_2)^2 + 4\mu_2(\gamma + \mu_2)^3}}{2(\gamma + \mu_2)},$$

$$\lambda 3 = -\mu_2,$$

The system is stable at the equilibrium point E_1 if λ_2 is negative.

$$\text{i.e. } \lambda_2 < 0 \implies \frac{\mu_2(\gamma + \mu_2)}{N\beta\mu_1} < 1$$

2.2 SEIR Dengue Fever Transmission Model:

In the SEIR model, the latent period is included as an additional variable to examine the prevalence of dengue fever. The latent period is very important and crucial due to unpredictable climate change as one of the effects of global warming at present. In this model, we study mathematical analysis by reviewing fixed points and eigenvalues to determine the dynamic behavior of the system. Simulations were performed on the model using some numerical values for the system parameters, which were mentioned in some previous studies for many countries.

2.2.1 The Flow Diagram for the SEIR Model:

In this model, the human population is divided into four groups: people who may have the potential to get infected by the dengue virus (Susceptible; S), people who show exposure to virus infection (Exposed; E), people who are infected (Infected; I) and people who have recovered (Removed; R).

The SEIR Model is represented by the following diagram:

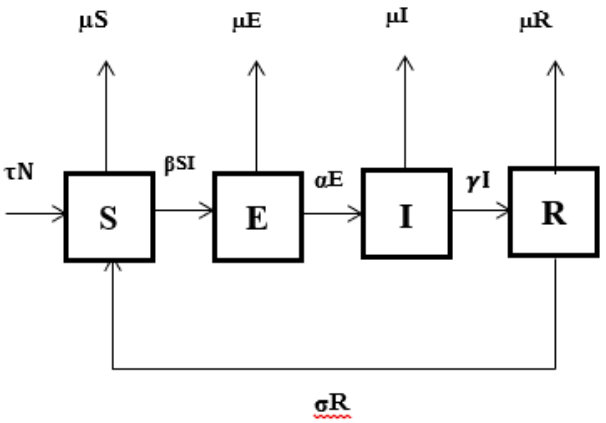

Figure (2) Flow diagram of the SEIR model

Explanation of the model parameters:

(α) The disease spread rate.

(γ) The recovery rate.

(β) The infection rate.

(μ) The death rate.

(τ) The birth rate.

(σ) The immunity loss rate.

(N) The total human population.

$$N = S + E + I + R$$

2.2.2 The Mathematical Model:

The compartmental diagram in Figure (2) can be converted into a mathematical model in the form of non-linear differential equations as shown below:

$$\frac{ds}{dt} = \tau N - \beta SI - \mu S + \sigma R \qquad (15)$$

$$\frac{dE}{dt} = \beta SI - \alpha E - \mu E \qquad (16)$$

$$\frac{dI}{dt} = \alpha E - \gamma I - \mu I \qquad (17)$$

$$\frac{dR}{dt} = \gamma I - \mu R - \sigma R \qquad (18)$$

Assuming that $\mu = \tau$, and using the condition $N = S + E + I + R$

$$\Rightarrow R = N - S - I - E,$$

we get

$$\frac{dS}{dt} = (\mu + \sigma)(N - S) - \beta SI - I\sigma - E\sigma \qquad (19)$$

Assuming that: $S = NX$, $E = NY$, $I = NZ$

Then equations (19), (16) -(18) become

$$\frac{dX}{dt} = (\mu + \sigma)(1 - X) - N\beta XZ - \sigma Z - \sigma Y$$

$$\frac{dY}{dt} = \beta NXZ - (\alpha + \mu)\, Y \qquad (20)$$

$$\frac{dZ}{dt} = \alpha Y - Z(\gamma + \mu)$$

Which can be written in the form

$$\frac{dX}{dt} = B1(1 - X) - B2\, XZ - \sigma\, Z - \sigma\, Y$$
$$= F1(X, Y, Z),$$

$$\frac{dY}{dt} = B2\, XZ - B3\, Y = F2(X, Y, Z), \qquad (21)$$

$$\frac{dZ}{dt} = \alpha Y - ZB4 = F3(X, Y, Z),$$

where, $B1 = \mu + \sigma$, $B2 = \beta N$, $B3 = \alpha + \mu$, $B4 = \gamma + \mu$.

2.2.3 The Equilibrium Points for the SEIR Model:

The equilibrium points are given by equations

$$\frac{dX}{dt} = \frac{dy}{dt} = \frac{dZ}{dt} = 0\ .$$

Then we get

$$B5\,(1 - X) + B6\, XZ - Z - Y = 0,$$
$$B7\, X\, Z - Y = 0, \qquad (22)$$
$$Y + B8\, Z = 0,$$

where, $B5 = \frac{B1}{\sigma}$, $B6 = -\frac{B2}{\sigma}$, $B7 = \frac{B2}{B3}$, $B8 = -\frac{B4}{\alpha}$

This can be solved in Mathematica using the following command:

Solve[{B5 (1 − X) + B6 XZ − Z − Y ==
0, B7 X Z − Y == 0, Y + B8 Z == 0}, {X, Y, Z}]

Thus, The equilibrium points of the system are:

$$E_0 = (X_0, Y_0, Z_0) \qquad (23)$$

where, $X_0 = 1, Y_0 = 0, Z_0 = 0$

$$E_1 = (X_1, Y_1, Z_1) \quad (24)$$

$$X_1 = \frac{(\alpha+\mu)(\gamma+\mu)}{N\alpha\beta},$$

$$Y_1 = \frac{(\gamma+\mu)\big(N\alpha\beta - (\alpha+\mu)(\gamma+\mu)\big)(\sigma+\mu)}{N\alpha\beta((\gamma+\mu)(\sigma+\mu)+\alpha(\gamma+\mu+\sigma)},$$

$$Z_1 = \frac{(N\alpha\beta - (\alpha+\mu)(\gamma+\mu))(\mu+\sigma)}{N\beta((\gamma+\mu)(\sigma+\mu)+\alpha(\gamma+\mu+\sigma))},$$

2.2.4 The Eigenvalues for the SEIR Model:

To study the stability of the system (21), we must find the Jacobian matrix of the system as the following:

The Jacobian matrix of the system is

$$J = \begin{pmatrix} \frac{\partial F_1}{\partial X} & \frac{\partial F_1}{\partial Y} & \frac{\partial F_1}{\partial Z} \\ \frac{\partial F_2}{\partial X} & \frac{\partial F_2}{\partial Y} & \frac{\partial F_2}{\partial Z} \\ \frac{\partial F_3}{\partial X} & \frac{\partial F_3}{\partial Y} & \frac{\partial F_3}{\partial Z} \end{pmatrix} \quad (25)$$

$$J = \begin{pmatrix} -B1 - B2\,Z & -\sigma & -B2\,X - \sigma \\ B2\,Z & -B3 & B2\,X \\ 0 & \alpha & -B4 \end{pmatrix} \quad (26)$$

The eigenvalues of the Jacobian matrix are determined from the following characteristic equation $|J - \lambda\mathbb{I}| = 0$

$$\Rightarrow \left| \begin{pmatrix} -B1 - B2\,Z & \sigma & -B2\,X - \sigma \\ B2\,Z & -B3 & B2\,X \\ 0 & \alpha & -B4 \end{pmatrix} - \lambda \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix} \right| \quad (27)$$

$$\begin{vmatrix} (-B1 - B2)\,Z - \lambda 1 & \sigma & -B2\,X - \sigma \\ B2\,Z & -B3 - \lambda 2 & B2\,X \\ 0 & \alpha & -B4 - \lambda 3 \end{vmatrix} = 0$$

This can be solved in Mathematica using the following command:

$$\text{Det}[J - \lambda\,\text{IdentityMatrix}[3]] == 0, \quad (28)$$

The corresponding characteristic equation is

$$\lambda^3 + B9\,\lambda^2 + B10\,\lambda + B11 = 0 \quad (29)$$

Where,

$$B9 = -B1 - B2\,Z - B3 - B4,$$

$$B10 = -B1B3 - B1B4 - B2B3\,Z - B2B4\,Z + \alpha\,B2\,X - B2\,\sigma\,Z - B3B4,$$

$$B11 = \alpha\,B1B2\,X - B1B3B4 - B2B3B4\,Z,$$

Equation (29) can be solved in Mathematica using the following command:

$$\text{Solve}[\lambda^3 + B9\,\lambda^2 + B10\,\lambda + B11 == 0, \lambda]$$

Thus, the eigenvalues are:

$$\lambda_1 = -\frac{B9}{3} - \frac{2^{1/3}(3B10 - B9^2)}{3B13} + \frac{B13}{32^{1/3}},$$

$$\lambda_2 = -\frac{B9}{3} + \frac{(1+i\sqrt{3})(3B10 - B9^2)}{32^{2/3}B13} - \frac{(1-i\sqrt{3})B13}{62^{1/3}}, \quad (30)$$

$$\lambda_3 = -\frac{B9}{3} + \frac{(1-i\sqrt{3})(3B10 - B9^2)}{32^{2/3}B13} - \frac{(1+i\sqrt{3})B13}{62^{1/3}}.$$

where, $B12 = -B10^2B9^2 - 18B10B11B9 + 4B10^3 + 27B11^2 + 4B11B9^3,$

$$B13 = \sqrt[3]{9B10B9 - 27B11 + 3\sqrt{3}\sqrt{B12} - 2B9^3},$$

The eigenvalues at the first equilibrium point $E_0 = (1,0,0)$ are

$$\lambda 1 = -\frac{1}{2}\sqrt{\alpha^2 - 2\alpha\gamma + \gamma^2 + 4\alpha\beta N} - \frac{1}{2}(\alpha + \gamma + 2\mu),$$

$$\lambda 2 = \frac{1}{2}\sqrt{\alpha^2 - 2\alpha\gamma + \gamma^2 + 4\alpha\beta N} - \frac{1}{2}(\alpha + \gamma + 2\mu), \quad (31)$$

$$\lambda 3 = -\mu - \sigma,$$

The system is stable at the equilibrium point E_0 if all the eigenvalues λ_1, λ_2 and λ_3 are negative, then the equilibrium point E_0 is stable if λ_1 is negative.

i.e. $\lambda_2 < 0$

$$\Rightarrow \sqrt{\alpha^2 - 2\alpha\gamma + \gamma^2 + 4\alpha\beta N} < \alpha + \gamma + 2\mu$$

$$\Longrightarrow \quad \alpha\beta N < (\alpha+\mu)(\gamma+\mu).$$

The eigenvalues at the second equilibrium point $E_1 = (X_1, Y_1, Z_1)$ are

$$\lambda 1 = -\frac{\sqrt[3]{2}(3B15 - B14^2)}{3B17} - \frac{B14}{3} + \frac{B17}{3\sqrt[3]{2}},$$

$$\lambda 2 = \frac{(1+i\sqrt{3})(3B15 - B14^2)}{32^{2/3}B17} - \frac{B14}{3} - \frac{(1-i\sqrt{3})B17}{6\sqrt[3]{2}}, \qquad (32)$$

$$\lambda 3 = \frac{(1-i\sqrt{3})(3B15 - B14^2)}{32^{2/3}B17} - \frac{B14}{3} - \frac{(1+i\sqrt{3})B17}{6\sqrt[3]{2}},$$

where, $B14 = \alpha + \gamma + 3\mu + \beta NZ1 + \sigma,$

$$B15 = \alpha\gamma + 2\alpha\mu + \alpha\sigma + 2\gamma\mu + \gamma\sigma + 3\mu^2 - \alpha\beta NX1 + \alpha\beta NZ1 + \beta\gamma NZ1 + 2\beta\mu NZ1 + 2\mu\sigma + \beta N\sigma Z1,$$

$$B16 = \alpha\gamma\mu + \alpha\gamma\sigma + \alpha\mu^2 + \alpha\mu\sigma + \gamma\mu^2 + \gamma\mu\sigma - \alpha\beta N\sigma X1 + \alpha\beta\gamma NZ1 + \alpha\beta\mu NZ1 + \alpha\beta N\sigma Z1 + \beta\gamma\mu NZ1 + \beta\gamma N\sigma Z1 + \beta\mu^2 NZ1 + \beta\mu N\sigma Z1 + \mu^3 + \mu^2\sigma - \alpha\beta\mu NX1,$$

$$B17 = (-2B14^3 + 9B14B15 - 27B16 + 3\sqrt{3}B18)^{\frac{1}{3}},$$

$$B18 = (4B14^3B16 - B14^2B15^2 - 18B14B15B16 + 4B15^3 + 27B16^2)^{\frac{1}{2}},$$

2.3 SIR–SI Model for Transmission of Dengue Fever:

In this model, it is assumed that some people in the population have already been infected by the virus while others have not. Additionally, it is believed that although there is a consistent population of mosquitoes, the virus is still spreading across it. As the vector, mosquito populations are assumed to be stable. Both people and mosquitoes are categorized into one group at a time.

2.3.1 The Flow Diagram for the SIR–SI Model:

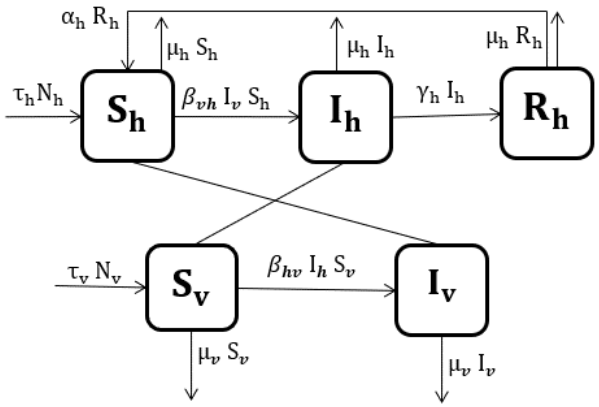

Figure (3) Flow diagram of the SIR-SI model

Explanation of the model variables and parameters:

S_h	Susceptible human at time t.
I_h	Infected human at time t.
R_h	Recovered human at time t.
S_v	Susceptible mosquito at time t.
I_v	Infected mosquito at time t.
N_h	Total number of human population.
N_v	Total number of mosquitoes.
τ_h	Human recruitment rate.
τ_v	Mosquito recruitment rate.
μ_h	The death rate for the human population.
μ_v	The death rate for the mosquito population.
γ_h	The recovery rate of an infected human.
β_{vh}	Probability of viral transmission from an infected mosquito to a susceptible human.
β_{hv}	Probability of viral transmission from an infected human to a susceptible mosquito.
α	Decline rate in human immunity to disease.

2.3.2 Model Equations:

The compartmental diagram in Figure (3) can be converted into a mathematical model based on the interaction between the hosts and vectors model which is in the form of non-linear differential equations as shown below .

Human population model:

$$\frac{dS_h}{dt} = \tau_h N_h - \beta_{vh} I_v S_h - \mu_h S_h + \alpha R_h , \quad (33)$$

$$\frac{dI_h}{dt} = \beta_{vh} I_v S_h - \mu_h I_h - \gamma_h I_h, \quad (34)$$

$$\frac{dR_h}{dt} = \gamma_h I_h - \mu_h R_h - \alpha R_h, \quad (35)$$

Vector population model

$$\frac{dS_v}{dt} = \tau_v N_v - \beta_{hv} I_h S_v - \mu_v S_v, \quad (36)$$

$$\frac{dI_v}{dt} = \beta_{hv} I_h S_v - \mu_v I_v, \quad (37)$$

Assuming that:

$$\tau_h = \mu_h , \tau_v = \mu_v , S_h + I_h + R_h = N_h$$

$$\Longrightarrow R_h = N_h - S_h - I_h, \quad (38)$$

and $S_v + I_v = N_v \quad \Longrightarrow S_v = N_v - I_v.$ (39)

From (38) in (33)-(35), we get

$$\frac{dS_h}{dt} = \mu_h N_h - \beta_{vh} I_v S_h - \mu_h S_h + \alpha(N_h - S_h - I_h)$$

$$= N_h(\mu_h + \alpha) - \beta_{vh} I_v S_h - S_h(\mu_h + \alpha) - \alpha I_h$$

$$\frac{dS_h}{dt} = (\mu_h + \alpha)(N_h - S_h) - \beta_{vh} I_v S_h - \alpha I_h \quad (40)$$

$$\frac{dI_h}{dt} = \beta_{vh} I_v S_h - \mu_h I_h - \gamma_h I_h \quad (41)$$

From (39) in (37), we get

$$\frac{dI_v}{dt} = \beta_{hv} I_h (N_v - I_v) - \mu_v I_v$$

$$\frac{dI_v}{dt} = \beta_{hv} I_h N_v - \beta_{hv} I_h I_v - \mu_v I_v \quad (42)$$

Assuming that: $S_h = N_h X,\ I_h = N_h Y,\ I_v = N_v Z$

Then equations (40)-(42) become

$$\frac{dX}{dt} = C_1(1 - X) - C_2 X Z - \alpha Y \quad (43)$$

$$\frac{dY}{dt} = C_2 X Z - C_3 Y \quad (44)$$

$$\frac{dZ}{dt} = C_4(Y - Y Z) - \mu_v Z \quad (45)$$

where, $c1 = \alpha + \mu_h,\ c2 = N_v \beta_{vh},$

$$c3 = \gamma_h + \mu_h, c4 = N_h \beta_{hv}.$$

2.3.3 The Equilibrium Points for SIR-IR Model:

To find the equilibrium points we must putting $X` = Y` = Z` = 0$ then we get:

$$C_1(1 - X) - C_2 X Z - \alpha Y = 0$$
$$C_2 X Z - C_3 Y = 0$$
$$C_4(Y - Y Z) - \mu_v Z = 0 \quad (46)$$

This can be solved in Mathematica using the following command:

Solve [{$C_1(1 - X) - C_2 X Z - \alpha Y == 0,\ C_2 X Z - C_3 Y == 0, C_4 Y (1 - Z) - \mu_v Z == 0$}, {X, Y, Z}]

Thus, the equilibrium points are:

The first is the disease-free equilibrium

$$E_0 = (X_0, Y_0, Z_0) = (1, 0, 0) \quad (47)$$

The second is the full-endemic equilibrium

$$E_1 = (X_1, Y_1, Z_1) ,$$

where,

$$X_1 = \frac{c5c7 + (c6 - c7)c8}{c7(c5 - c6 + c7)},$$

$$Y_1 = \frac{c5(c7 + c8)}{c5 - c6 + c7} , \quad (48)$$

$$Z_1 = \frac{c5(c7 + c8)}{c5c7 + c6c8 - c7c8} ,$$

where,

$$c5 = \frac{c1}{\alpha}, c6 = -\frac{c2}{\alpha}, c7 = \frac{c2}{c3}, c8 = -\frac{\mu_v}{c4} , \quad (49)$$

2.3.4 The Eigenvalues for SIR-SI Model:

We put the system of equations (43)-(45) in the form

$$\frac{dX}{dt} = C_1(1 - X) - C_2 X Z - \alpha Y = F_1(X, Y, Z),$$

$$\frac{dY}{dt} = C_2 X\, Z - C_3 Y = F_2(X, Y, Z), \qquad (50)$$
$$\frac{dZ}{dt} = C_4 Y(1 - Z) - \mu_v Z = F_3(X, Y, Z),$$

Therefore, we can analyze the stability by finding the eigenvalues of the following Jacobian matrix

$$J = \begin{pmatrix} \frac{\partial F_1}{\partial X} & \frac{\partial F_1}{\partial Y} & \frac{\partial F_1}{\partial Z} \\ \frac{\partial F_2}{\partial X} & \frac{\partial F_2}{\partial Y} & \frac{\partial F_2}{\partial Z} \\ \frac{\partial F_3}{\partial X} & \frac{\partial F_3}{\partial Y} & \frac{\partial F_3}{\partial Z} \end{pmatrix} \qquad (51)$$

At the equilibrium points, we have

$$J = \begin{pmatrix} -C_1 - C_2 Z & -\alpha & -C_2 X \\ C_2 Z & -C_3 & C_2 X \\ 0 & C_4 - C_4 Z & -C_4 Y - \mu_V \end{pmatrix}$$

The eigenvalues are obtained from

$|J - \lambda I| = 0$ where I is the identity matrix.

$$\left| \begin{pmatrix} -C_1 - C_2 Z & -\alpha & -C_2 X \\ C_2 Z & -C_3 & C_2 X \\ 0 & C_4 - C_4 Z & -C_4 Y - \mu_V \end{pmatrix} - \lambda \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix} \right| = 0$$

Using a Mathematica, we get

$$\text{Det}[J - \lambda\ \text{IdentityMatrix}[3]] == 0$$
$$\lambda^3 + C_9\,\lambda^2 + C_{10}\,\lambda + C_{11} = 0, \qquad (52)$$

which is the characteristic equation,

where,

$$c9 = c1 + c2\,z\ + c3 + c4\,y + \mu_v,$$
$$c10 = \mu_v(c1 + c2z + c3) + c1(c3 + c4y)$$
$$+c2(z(\alpha + c3) + c4z(x + y) - c4x) + c3c4y,$$
$$c11 = c4(c1(c2x(z - 1) + c3y)$$
$$+c2yz(\alpha + c3)) + \mu_v(c1c3 + c2z(\alpha + c3)),$$

Equation (52) can be solved in Mathematica using the following command:

$$\text{Solve}[\lambda^3 + C_9\,\lambda^2 + C_{10}\,\lambda + C_{11} == 0, \lambda]$$

The eigenvalues are:

$$\lambda 1 = -\frac{\sqrt[3]{2}(3c10 - c9^2)}{3c13} + \frac{c13}{3\sqrt[3]{2}} - \frac{c9}{3},$$

$$\lambda 2 = \frac{(1 + i\sqrt{3})(3c10 - c9^2)}{32^{2/3}c13} - \frac{(1 - i\sqrt{3})c13}{6\sqrt[3]{2}} - \frac{c9}{3}, \qquad (53)$$

$$\lambda 3 = \frac{(1 - i\sqrt{3})(3c10 - c9^2)}{32^{2/3}c13} - \frac{(1 + i\sqrt{3})c13}{6\sqrt[3]{2}} - \frac{c9}{3},$$

where,

$$c12 = 4c10^3 - c10^2c9^2 - 18c10c11c9 + 27c11^2 + 4c11c9^3,$$
$$c13 = \sqrt[3]{9c10c9 - 27c11 + 3\sqrt{3}\sqrt{c12} - 2c9^3}$$

The eigenvalues at the first equilibrium point $E_0 = (1,0,0)$ are

$$\lambda 1 = -\alpha - \mu_h,$$
$$\lambda 2 = \frac{(-\gamma_h - \mu_h - \mu_v)}{2} - \frac{1}{2}\sqrt{(\gamma_h + \mu_h + \mu_v)^2 - 4(-N_h\beta_{hv}N_v\beta_{vh} + \gamma_h\mu_v + \mu_h\mu_v)}, \qquad (54)$$
$$\lambda 3 = \frac{(-\gamma_h - \mu_h - \mu_v)}{2} + \frac{1}{2}\sqrt{(\gamma_h + \mu_h + \mu_v)^2 - 4(-N_h\beta_{hv}N_v\beta_{vh} + \gamma_h\mu_v + \mu_h\mu_v)}$$

The system is stable at the equilibrium point $E_0 = (1,0,0)$ if all the eigenvalues λ_1, λ_2 and λ_3 are negative, it is clear that λ_1, and λ_2, are negative, then the equilibrium point E_0 is locally asymptotically stable if λ_3 is negative

i.e. $\lambda_3 < 0$

$$\Rightarrow \quad \frac{N_h\,\beta_{hv}\,N_v\,\beta_{vh}}{\mu_v\,(\gamma_h + \mu_h)} < 1 \qquad (55)$$

The eigenvalues at the second equilibrium point $E_1 = (X_1, Y_1, Z_1)$ are

$$\lambda 1 = -\frac{\sqrt[3]{2}(3c15 - c14^2)}{3c18} - \frac{c14}{3} + \frac{c18}{3\sqrt[3]{2}},$$
$$\lambda 2 = \frac{(1 + i\sqrt{3})(3c15 - c14^2)}{32^{2/3}c18} - \frac{(1 - i\sqrt{3})c18}{6\sqrt[3]{2}}$$

$$-\frac{c14}{3}, \qquad (56)$$

$$\lambda 3 = \frac{(1-i\sqrt{3})(3c15-c14^2)}{32^{2/3}c18} - \frac{(1+i\sqrt{3})c18}{6\sqrt[3]{2}} - \frac{c14}{3},$$

where,

$$c14 = c1 + c2z1 + c3 + c4y1 + \mu_v,$$
$$c15 = c1c3 + c1c4y1 + c1\mu_v + c2c3z1 + c2c4x1z1 - c2c4x1 + c2c4y1z1 + c2z1\mu_v + \alpha c2z1 + c3c4y1 + c3\mu_v,$$
$$c16 = c1c2c4x1z1 - c1c2c4x1 + c1c3c4y1 + c1c3\mu_v + c2c3c4y1z1 + c2c3z1\mu_v + \alpha c2c4y1z1 + \alpha c2z1\mu_v, \qquad (57)$$
$$c17 = 3\sqrt{3}\,(4c14^3c16 - c14^2c15^2 - 18c14c15c16 + 4c15^3 + 27c16^2)^{\frac{1}{2}}$$
$$c18 = \sqrt[3]{-2c14^3 + 9c14c15 - 27c16 + c17},$$

2.4 SEIR–SI Model for Transmission of Dengue Fever:

The SEIR-SI model describes how diseases spread between humans and mosquitoes, and using mathematical equations the rate of change (increase or decrease) in the variables (S, E, I, R) at any moment is calculated. We can also set equilibrium points for the system, which express the absence of change in the values of the variables (S, E, I, R) for humans and S, I for mosquitoes. Dengue virus is transmitted and spread by mosquito bites. There are three agents of transmission of dengue virus: humans, viruses, and intermediate vectors (Tyas, 2019). There are two types of dengue transmission such as horizontal and vertical transmissions. Horizontal transmission means humans can be infected by biting infected female Aedes mosquitoes. Vertical transmission is the process by which HIV can also spread from an infected female vector to her progeny (Lequime & Lambrechts, 2014). In 2015, a dengue transmission model was modeled with two mosquito species and population age structure. Aedes aegypti and Aedes albopictus mosquitoes were the two mosquito species studied for dengue infection transmission using the SIR model (Sungchasit et al., 2015). Shahrud and Noorani studied the system of differential equations for the dynamics of the SEIR model for more detailed prediction of the epidemic (Syafruddin & Noorani, 2012). Provided a quantitative framework for making allocation decisions in the presence of different externalities associated with control measures such as vaccination or antibiotic treatment (Althouse et al., 2010). With approximately 400 million dengue infections occurring each year, several mathematical models describing the transmission of dengue viruses have been proposed to explain the erratic behavior of dengue epidemics [(Bhatt et al., 2013), (Side & Noorani, 2013), (Rangkuti, et al. 2014), (Li & Wanf,2006)]. The current model is considered a modification of previous models, as it takes into account that recovered patients can become infected with dengue again.

2.4.1 The Flow Diagram for the SEIR–SI Model:

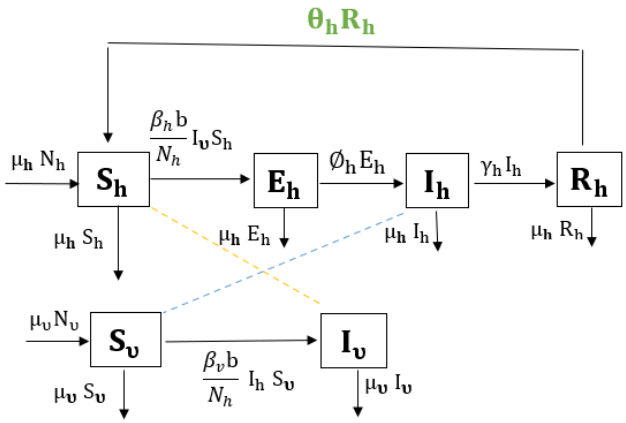

Figure (4) Flow diagram of the SEIR-SI model

Explanation of model variables and parameters:

S_h	The number of suspected population.
E_h	The number of exposed populations.
I_h	The number of infected population.
R_h	The number of recovered population.
S_υ	The number of suspected vectors.
I_υ	The number of infected vectors.
N_h	The total human population.
θ_h	The rate of loss of acquired immunity.
φ_h	The rate of suspected humans who have not been infected by the dengue virus.
γ_h	The rate of recovered humans from infection
β_h	The rate of individuals who have been infected with suspected mosquitoes.
b	The number of times a mosquito bites a human.
μ_h	The rate of deaths in the human population.

2.4.2 The Mathematical Model:

Human population model:

$$\frac{dS_h}{dt} = \mu_h N_h - \frac{\beta_h b}{N_h} I_\upsilon S_h - \mu_h S_h + \theta_h R_h \quad (58)$$

$$\frac{dE_h}{dt} = \frac{\beta_h b}{N_h} I_\upsilon S_h - (\mu_h + \varphi_h) E_h \quad (59)$$

$$\frac{dI_h}{dt} = \varphi_h E_h - (\mu_h + \gamma_h) I_h \quad (60)$$

$$\frac{dR_h}{dt} = \gamma_h I_h - (\mu_h + \theta_h) R_h \quad (61)$$

Vector population model:

$$\frac{dS_\upsilon}{dt} = \mu_\upsilon N_\upsilon - \frac{\beta_\upsilon b}{N_h} I_h S_\upsilon - \mu_\upsilon S_\upsilon \quad (62)$$

$$\frac{dI_\upsilon}{dt} = \frac{\beta_\upsilon b}{N_h} I_h S_\upsilon - \mu_\upsilon I_\upsilon \quad (63)$$

Both host and vector populations are considered constant. So, $N_h = S_h + E_h + I_h + R_h$

$$\Rightarrow R_h = -S_h - E_h - I_h + N_h ,$$

and $N_\upsilon = S_\upsilon + I_\upsilon \Rightarrow S_\upsilon = N_\upsilon - I_\upsilon$

Substituting in the equations (58)-(63), we get the following system of equations:

$$\frac{dS_h}{dt} = (\mu_h + \theta_h)(N_h - S_h) - \frac{\beta_h b}{N_h} I_\upsilon S_h - \theta_h E_h - \theta_h I_h \quad (64)$$

$$\frac{dE_h}{dt} = \frac{\beta_h b}{N_h} I_\upsilon S_h - E_h(\mu_h + \varphi_h) \quad (65)$$

$$\frac{dI_h}{dt} = \varphi_h E_h - I_h(\mu_h + \gamma_h) \quad (66)$$

$$\frac{dI_\upsilon}{dt} = \frac{\beta_\upsilon b}{N_h} I_h (N_\upsilon - I_\upsilon) - \mu_\upsilon I_\upsilon \quad (67)$$

Setting $S_h = N_h x$, $E_h = N_h y$, $I_h = N_h z$, and $I_\upsilon = N_\upsilon w$, we get

$$\frac{dx}{dt} = (\mu_h + \theta_h)(1 - x) - \frac{\beta_h b}{N_h} N_\upsilon x w - \theta_h y - \theta_h z \quad (68)$$

$$\frac{dy}{dt} = \frac{\beta_h b}{N_h} N_\upsilon w x - (\mu_h + \varphi_h) y \quad (69)$$

$$\frac{dz}{dt} = \varphi_h y - (\mu_h + \gamma_h) z \quad (70)$$

$$\frac{dw}{dt} = \beta_\upsilon b z - \beta_\upsilon b z w - \mu_\upsilon w \quad (71)$$

2.4.3 The Equilibrium Points for SEIR–SI Model:

The equilibrium points are given by equations

$$\dot{x} = \dot{y} = \dot{z} = \dot{w} = 0$$

Then we get

$$d1(1 - x) - d2\, x\, w - \theta_h\, y - \theta_h z = 0 \quad (72)$$

$$d2\, w\, x - d3\, y = 0 \quad (73)$$

$$\varphi_h\, y - d4\, z = 0 \quad (74)$$

$$d5\, z - d5\, z\, w - \mu_\upsilon\, w = 0 \quad (75)$$

Which can be written in the form

$$d6(1 - x) - x\, w + d7 y + d7\, z = 0, \quad (76)$$

$$d8\, w\, x - y = 0, \quad (77)$$

$$d9\, y - z = 0, \quad (78)$$

$$z\,(1 - w) + d10\, w = 0, \quad (79)$$

```
Solve[{d6(1 − x) − x w + d7y + d7z == 0,
      d8 w x − y == 0, d9 y − z == 0,
      z(1 − w) + d10 w == 0}, {x, y, z, w}]
```

Thus, the equilibrium points of this system are:

The first is the disease-free equilibrium point

$$E_0 = (x_0, y_0, z_0, w_0) = (1, 0, 0, 0) \quad (80)$$

The second is the full-endemic equilibrium point $E_1 = (x1, y1, z1, w1)$

where,

$$x1 = -\frac{d6d8d9 + d10(-1 + d7d8(1 + d9))}{d8d9(-1 - d6 + d7d8(1 + d9))},$$

$$y1 = -\frac{d6(d10 + d8d9)}{d9(-1 - d6 + d7d8(1 + d9))}, \quad (81)$$

$$z1 = \frac{d6(d10 + d8d9)}{1 + d6 - d7d8(1 + d9)},$$

$$w1 = \frac{d6(d10 + d8d9)}{d6d8d9 + d10(-1 + d7d8(1 + d9))}.$$

where, $d1 = \mu_h + \theta_h$, $d2 = \frac{\beta_h b}{N_h} N_\upsilon$, $d3 = \mu_h + \varphi_h$, $d4 = \mu_h + \gamma_h$, $d5 = \beta_\upsilon b$, $d6 = \frac{d1}{d2}$, $d7 = -\frac{\theta_h}{d2}$, $d8 = \frac{d2}{d3}$, $d9 = \frac{\varphi_h}{d4}$, $d10 = -\frac{\mu_\upsilon}{d5}$.

Equations (76)-(79) can be solved in Mathematica using the following command:

$$\frac{dx}{dt} = d1(1 - x) - d2\, x\, w - \theta_h\, y - \theta_h\, z = F_1(x, y, z, w), \quad (82)$$

$$\frac{dy}{dt} = d2\, w\, x - d3\, y = F_2(x, y, z, w), \quad (83)$$

$$\frac{dz}{dt} = \varphi_h\, y - d4\, z = F_3(x, y, z, w), \quad (84)$$

$$\frac{dw}{dt} = d5\, z - d5\, z\, w - \mu_\upsilon\, w = F_4(x, y, z, w), \quad (85)$$

2.4.4 The Eigenvalues for SEIR–SI Model:

To find the eigenvalues of the system of equations (68)-(71), we must find the Jacobian matrix of the system as the following:

We put the system of equations (68)-(71) in the form

Thus, the Jacobian matrix of the system is

$$J = \begin{pmatrix} \frac{\partial F_1}{\partial X} & \frac{\partial F_1}{\partial Y} & \frac{\partial F_1}{\partial Z} & \frac{\partial F_1}{\partial W} \\ \frac{\partial F_2}{\partial X} & \frac{\partial F_2}{\partial Y} & \frac{\partial F_2}{\partial Z} & \frac{\partial F_2}{\partial W} \\ \frac{\partial F_3}{\partial X} & \frac{\partial F_3}{\partial Y} & \frac{\partial F_3}{\partial Z} & \frac{\partial F_3}{\partial W} \\ \frac{\partial F_4}{\partial X} & \frac{\partial F_4}{\partial Y} & \frac{\partial F_4}{\partial Z} & \frac{\partial F_4}{\partial W} \end{pmatrix} \quad (86)$$

$$J = \begin{pmatrix} -d1 - d2\, w & -\theta_h & -\theta_h & -d2\, x \\ d2\, w & -d3 & 0 & d2\, x \\ 0 & \varphi_h & -d4 & 0 \\ 0 & 0 & d5 - d5\, w & -d5\, z - \mu_\upsilon \end{pmatrix}$$

The eigenvalues of the Jacobian matrix are determined from the following characteristic equation $|J - \lambda \mathbb{I}| = 0$

$$\Rightarrow \left| \begin{pmatrix} -d1 - d2\ w & -\theta_h & -\theta_h & -d2\ x \\ d2\ w & -d3 & 0 & d2\ x \\ 0 & \varphi_h & -d4 & 0 \\ 0 & 0 & d5 - d5\ w & -d5\ z - \mu_\upsilon \end{pmatrix} - \lambda \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix} \right| = 0$$

$$\begin{vmatrix} -d1 - d2\ w - \lambda & -\theta_h & -\theta_h & -d2\ x \\ d2\ w & -d3 - \lambda & 0 & d2\ x \\ 0 & \varphi_h & -d4 - \lambda & 0 \\ 0 & 0 & d5 - d5\ w & -d5\ z - \mu_\upsilon - \lambda \end{vmatrix} = 0 \quad (87)$$

This can be determined in Mathematica using the following command:

$$\text{Det}[J - \lambda\ \text{IdentityMatrix}[4]] == 0, \quad (88)$$

The corresponding characteristic equation is

$$\lambda^4 + d11\lambda^3 + d12\lambda^2 + d13\lambda + d14 = 0, \quad (89)$$

where,

$$d11 = d1 + d3 + d4 + d2\ w + d5\ z + \mu_\upsilon,$$
$$d12 = d1d3 + d1d4 + d3d4 + d2d3w + d2d4w + d5(d1 + d3 + d4 + d2w)z + d2w\theta_h + (d1 + d3 + d4 + d2w)\mu_\upsilon,$$
$$d13 = d3d4(d1 + d2w) + d5(d3d4 + d1(d3 + d4) + d2(d3 + d4)w)z + (d3d4 + d1(d3 + d4) + d2(d3 + d4)w)\mu_\upsilon - d2d5\ x\phi_h + d2w\theta_h(d4 + d5z + \mu_\upsilon + \phi_h) + d2d5\ w\ x\phi_h$$
$$d14 = d3d4(d1 + d2w)(d5z + \mu_\upsilon) + d1d2d5(-1 + w)x\phi_h + d2w\theta_h(d5z + \mu_\upsilon)(d4 + \phi_h),$$

Equation (64) can be solved in Mathematica using the following command:

$$\text{Solve}[\lambda^4 + d11\lambda^3 + d12\lambda^2 + d13\lambda + d14 == 0, \lambda]$$

Thus, the eigenvalues are:

$$\lambda1 = -\frac{d11}{4} - \frac{1}{2}\sqrt{d22 - \frac{d19}{4\sqrt{d21}}} - \frac{\sqrt{d21}}{2},$$

$$\lambda2 = -\frac{d11}{4} + \frac{1}{12}\sqrt{d23 - \frac{9d19}{\sqrt{d21}}} - \frac{\sqrt{d21}}{2},$$

$$\lambda3 = -\frac{d11}{4} - \frac{1}{2}\sqrt{\frac{d19}{4\sqrt{d21}} + d22} + \frac{\sqrt{d21}}{2},$$

$$\lambda4 = -\frac{d11}{4} + \frac{1}{12}\sqrt{\frac{9d19}{\sqrt{d21}} + d23} + \frac{\sqrt{d21}}{2}, \quad (90)$$

where, $d16 = (27d11^2d14 - 9\ d11\ d12\ d13 + 2d12^3 - 72\ d12\ d14 + 27\ d13^2 + d15)^{\frac{1}{3}},$

$$d17 = \sqrt[3]{2}(-3\ d11\ d13 + d12^2 + 12\ d14),$$
$$d18 = \frac{d11^2}{4} - \frac{2d12}{3},$$
$$d19 = -d11^3 + 4\ d11d12 - 8\ d13,$$
$$d20 = \frac{d17}{3d16}, \quad d21 = \frac{d16}{3\sqrt[3]{2}} + d18 + d20,$$
$$d22 = -\frac{d16}{3\sqrt[3]{2}} + d18 - d20,$$
$$d23 = -62^{2/3}d16 + 36\ d18 - 36\ d20. \quad (91)$$

3. Results of Research:

Here we will use some numerical values that were mentioned in previous research to study the stability of some equilibrium points for some models included in the current study.

For the SEIR model; we will take the values

$$M = 0.2055, \beta = 0.0025, \sigma = 0.03,$$
$$\alpha = 0.1667, \gamma = 0.055, n = 2500.$$

Accordingly, the eigenvalues at the first equilibrium point $E_0 = (1,0,0)$ are:

$$\lambda1 = -0.7059 - 1.1102 \times 10^{-16}\ i,$$
$$\lambda2 = -1.3386 - 5.5511 \times 10^{-17}\ i,$$
$$\lambda3 = -0.2355 + 3.3307 \times 10^{-17}\ i,$$

Since all real parts of the eigenvalues are negative, then the equilibrium point $E_0 = (1,0,0)$ is asymptotically stable.

The eigenvalues at the second equilibrium point $E_1 = (X_1, Y_1, Z_1) = (0.0931,\ 0.5068,\ 0.3243)$

are: $\lambda 1 = -0.3053 - 0.0648\,\mathrm{i},$

$\lambda 2 = -2.2848 - 1.1102 \times 10^{-16}\,\mathrm{i}$

$\lambda 3 = -0.3053 + 0.0648\,\mathrm{i},$

and the equilibrium point $(0.0931,\ 0.5068,\ 0.3243)$ is asymptotically stable.

For the SIR-SI model; we will take the values

$\mu_h = 0.000046; \mu_v = 0.0323;$
$\beta_{\mathrm{hv}} = 4.27 \times 10^{-8}, \beta_{\mathrm{vh}} = 8.55 \times 10^{-8},$
$\gamma_h = 0.328833, N_h = 8771970,$
$\alpha = 0.575, N_v = 1000000.$

Accordingly, The eigenvalues at the first equilibrium point $\mathrm{E}_0 = (1,0,0)$ are:

$\lambda 1 = 0.0518 - 6.9389 \times 10^{-18}\,\mathrm{i},$
$\lambda 2 = -0.575 - 2.7757 \times 10^{-17}\,\mathrm{i},$
$\lambda 3 = -0.413 + 2.7756 \times 10^{-17}\,\mathrm{i},$

Since the real part of $\lambda 1$ is positive, then the equilibrium point$(1,0,0)$ is unstable (called saddle point).

The eigenvalues at the second equilibrium point $\mathbf{E_1 = (0.8061, 0.1233, 0.5885)}$ are:

$\lambda 1 = -0.0491,$
$\lambda 2 = -0.4918 + 0.0932\,\mathrm{i},$
$\lambda 3 = -0.4918 - 0.0932\,\mathrm{i}.$

Since all real parts of the eigenvalues are negative, then $\mathbf{(0.8061, 0.1233, 0.5885)}$ is asymptotically stable.

For the SEIR–SI model;

If we take $\mathbf{\mu_h = 0.046},$

$\mathbf{\gamma_h = 0.3288, N_h = 877197, \theta_h = 0.575,}$
$\mathbf{b\beta_h = 0.75, \phi_h = 0.1667,\ \mu_v = 0.0323,}$
$\mathbf{b\beta_v = 0.375, N_v = 1000000.}$

Then, the eigenvalues at the first equilibrium point $\mathbf{E_0 = (1,0,0,0)}$ are:

$\boldsymbol{\lambda 1 = -0.4081 - 0.3288\,i,}$
$\boldsymbol{\lambda 2 = -0.4081 + 0.3288\,i,}$
$\boldsymbol{\lambda 3 = -0.6014,\ \lambda 4 = 0.1768.}$

Since, the real part of, $\boldsymbol{\lambda 4}$ is positive, then the equilibrium point $\mathbf{E_0 = (1,0,0,0)}$ is unstable (called saddle point).

The eigenvalues at the equilibrium point $\mathbf{E_1 = (0.1709, 0.4934, 0.2195, 0.7181)}$ are:

$\lambda 1 = -0.8687, \lambda 2 = -0.1162,$
$\lambda 3 = -0.4761 - 0.3392\,\mathrm{i}$
$, \lambda 4 = -0.4761 + 0.3392\,\mathrm{i}.$

and the equilibrium point is asymptotically stable.

4. Conclusion

Dengue fever is a global health threat that threatens the future of humanity. Raising public awareness is the only way to eliminate this deadly disease. Therefore, So we studied transmission mechanisms of dengue fever by focusing on understanding the biology of the human body and mosquito vectors, to reduce the impact of dengue epidemics.

In this research, we reviewed several mathematical models for dengue fever. Four models with different estimates and assumptions were considered, and several epidemic scenarios were reviewed. We first modeled the dynamics of transmission of dengue fever using the SIR model, which divided the entire population into three segments: susceptible, infected, and recovering. In the second step in the investigation, we prepared an SEIR model and through it, we added another section of the population: those who carry the disease and have not yet shown symptoms (exposed).

Since the number of infections depended on the interaction between mosquitoes and humans, in the third step we made the SIR-SI model and added another section of the mosquito population: susceptible, and infected. In the next step, we prepared the SEIR-SI model. In each of the previous models, we Adjust the parameters of mathematical models to study the state of stability by solving the system of equations with the Mathematica program, then obtaining equilibrium points, and classifying the predicted scenarios for the period of stability. Finally, we discussed the stability conditions for the first and second models, and in the last three models, we used some numerical values for the various parameters mentioned in some of the previous studies to set the equilibrium points for each model and clarify whether these equilibrium points are stable or unstable.

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