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SEIRI Model analysis using the mathematical graph as a solution for Hepatitis B disease in Makassar

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Abstract. The research objective were to build a mathematical model for Hepatitis B; Determine and analyse the equilibrium point of the model; Conduct a model simulation to predict the number of Hepatitis B cases and determine the solution for the spread of Hepatitis B in Makassar City. This research stage examines and builds a mathematical model on the spread of Hepatitis B which is a Susceptible-Exposed-Infected-Recovered-Infected (SEIRI) model; analysis of SEIRI model in Hepatitis B using mathematical Graph method; Model simulation using Maple Software with data assuming the number of Hepatitis B cases, then perform further analysis of the model. The result obtained is the SEIRI model for the spread of Hepatitis B, which is a non-linear differential equation model with 4 dimensions. Mathematical graph is used to determine the status of Hepatitis B, which is a disease-free or endemic case.

1. INTRODUCTION

Hepatitis B is an infectious disease that has a high level of spread. Based on epidemiological reports, around 400 million people worldwide are infected by Hepatitis B Viruses (HBV) and about 170 people live in Asia Pacific. The most endemic area for infection is China, where about 93 million people are infected. Indonesia is ranked third after China and India with a prevalence of 5-17% [1]. The Association of Indonesian Liver Researchers in collaboration with the Gastroentero-Hepatology Section of Internal Medicine, Hasanuddin University Medical Faculty, held a free hepatitis vaccine injection for the people of Makassar City. In Makassar, he said, according to data from the Regional Wahidin Hospital Makassar, during 2007-2009, out of 146 hospitalized patients with chronic liver disease, 10 were positive for hepatitis C and 59 were infected with hepatitis B [2].

Mathematical modeling of infectious and non-communicable diseases such as Hepatitis B, dengue fever, tuberculosis, diabetes, typhoid and covid-19 has been done by [3-18]. Mathematical modeling is an offer of solutions in controlling and controlling disease because model simulations can predict the number of cases, so that the government can take early prevention and treatment. Research on hepatitis B has been conducted by [12,16] but has not used mathematical graphs in determining the basic reproduction number. Therefore, this research will build and analyze the SEIRI model using the mathematical graph method, then analysis and simulation will be carried out using data on the number of Hepatitis B cases in Makassar city using Maple software.

2. METHOD

This research is theoretical and applied [17,18]. This study examines the theory and application of mathematical graphs in analyzing the spread of hepatitis B in Makassar City. The first part of this study is to build a SEIRI model for Hepatitis B transmission, then perform a model analysis using mathematical graphs to determine the existence, stability and status of Hepatitis B. The model uses the suspected, exposed, infected and recovered compartments. Model analysis uses mathematical graph method and uses assumption data for the number of hepatitis B cases and parameter values. Model simulation uses Maple to predict the number of hepatitis B cases in Makassar City.

3. RESULT AND DISCUSSION

The changes that occur in each human population in the transmission of Hepatitis B for the SEIRI model can be interpreted in the form of Figure 1.
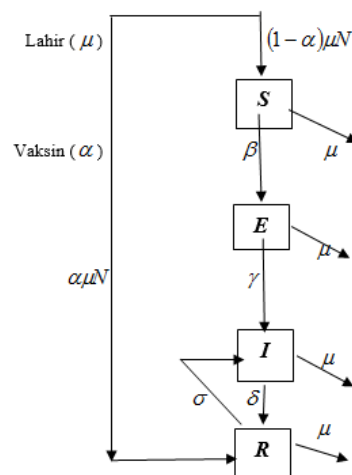

Figure 1. Schematic of SEIRI model of Hepatitis B transmission

Based on Figure 1, the rate of change in the human population in the spread of Hepatitis B over time can be interpreted in the form of the following equation (1) - (4):

$$\frac{dS}{dt} = (1-\alpha)\mu NS - \beta\frac{SI}{N} - \mu S \tag{1}$$

$$\frac{dE}{dt} = \beta\frac{SI}{N} - (\gamma+\mu)E \tag{2}$$

$$\frac{dI}{dt} = \gamma E + \sigma R - (\delta+\mu)I \tag{3}$$

$$\frac{dR}{dt} = \alpha\mu NS + \delta I - (\sigma+\mu)R \tag{4}$$

with $N(t) = S(t) + E(t) + I(t) + R(t)$ (5)

or $R(t) = N(t) - (S(t) + E(t) + I(t))$ (6)

SEIRI mathematical model for Hepatitis B transmission in equations (1) - (4) is a 4-D system of non-linear ordinary differential equations. The result of SEIRI model can be simplified by supposing the following fractions:

$$x(t) = \frac{S}{N} \tag{7}$$

$$y(t) = \frac{I}{N} \tag{8}$$

$$z(t) = \frac{R}{N} \tag{9}$$

$$u(t) = \frac{E}{N} \tag{10}$$

Based on these assumptions, the SEIRI model of human population in Hepatitis B transmission in equations (1) - (4) can be simplified as in the following equation system:

$$\frac{dx}{dt} = (1-\alpha)\mu N - \beta xy - \mu x \tag{11}$$

$$\frac{du}{dt} = \beta xy - (\gamma + \mu)u \tag{12}$$

$$\frac{dy}{dt} = \gamma u + \sigma z - (\delta + \mu)y \tag{13}$$

$$\frac{dz}{dt} = \alpha\mu N + \delta y - (\sigma + \mu)z \tag{14}$$

3.1. Analysis of The SEIRI Model for The Spread of Hepatitis B

Based on equations (11) - (14), a stability analysis is performed to determine the disease-free equilibrium point (K_0) and the endemic equilibrium point (K_1). To determine these two equilibrium points, each equation in the subsystem must be equal to zero, $\frac{dx}{dt} = 0$ $\frac{du}{dt} = 0$, $\frac{dy}{dt} = 0$ and $\frac{dz}{dt} = 0$. Then, found the values of x, u, y and z to determine the point of equilibrium as in equations (15) - (18).

$$z = \frac{\alpha\mu N + \delta y}{\sigma + \mu} \tag{15}$$

$$y = \frac{\gamma u + \sigma z}{\delta + \mu} \tag{16}$$

$$u = \frac{\beta xy}{\gamma + \mu} \tag{17}$$

$$x = \frac{(1-\alpha)\mu N}{\beta y + \mu} \tag{18}$$

Thus, the endemic equilibrium point is obtained

$$x = \frac{(1-\alpha)\mu DN}{\beta C + \mu D} \tag{19}$$

$$y = \frac{C}{D} \tag{20}$$

$$u = \frac{(1-\alpha)\mu NB}{A\mu + B(\gamma + \mu)} \tag{21}$$

$$z = \frac{\alpha\mu ND + \delta C}{D(\sigma + \mu)} \tag{22}$$

with

$$C = (1-\alpha)(\sigma + \mu)\,\mu\gamma NB + \alpha\mu\sigma N\big(A\mu + B(\gamma + \mu)\big)$$
$$D = \mu(\sigma + \delta + \mu)\big(A\mu + B(\gamma + \mu)\big)$$

Based on the equilibrium point, the jacobian matrix is obtained as follows:

$$J = \begin{pmatrix} -\beta y - \mu & 0 & \beta x & 0 \\ \beta y & -(\gamma + \mu) & \beta x & 0 \\ 0 & \gamma & -(\delta + \mu) & \sigma \\ 0 & 0 & \delta & -(\sigma + \mu) \end{pmatrix} \tag{23}$$

Then an evaluation is carried out for the equilibrium point to determine the stability of the model, where the stability is determined by the eigenvalues that are searched by using the formula:

$$|\lambda I - J(X)| = 0 \tag{24}$$

3.2. Stability Analysis for SEIRI Model of Endemic Case

Substitute the equilibrium point obtained in (19) - (22) to the matrix (23) so that:

$$J(K_1) = \begin{bmatrix} -\dfrac{\beta C}{D} - \mu & 0 & \dfrac{\beta(1-\alpha)\mu DN}{BC+\mu D} & 0 \\ \dfrac{\beta C}{D} & \dfrac{\beta C}{D} & \dfrac{\beta(1-\alpha)\mu DN}{BC+\mu D} & 0 \\ 0 & \gamma & -(\delta+\mu) & \sigma \\ 0 & 0 & \delta & -(\sigma+\mu) \end{bmatrix} \tag{25}$$

with

$$T = \frac{\beta(1-\alpha)\mu DN}{BC+\mu D} \quad \text{and} \quad V = \frac{\beta C}{D}$$

Then, found the characteristic equation of $J(K_1)$

$$\begin{aligned} |J(K_1) - \lambda I| &= 0 \\ &= (\lambda + G)\left[\lambda^3 + (P+K+L)\lambda^2 + (PK+PL+KL)\lambda + PKL - \delta\sigma(\lambda+K) - H(\lambda+P)\right] \\ &= \lambda^4 + W_8\lambda^3 + (W_9 - W_{10})\lambda^2 + (W_{11} - W_{12})\lambda + W_{13} - W_{14} \tag{26} \end{aligned}$$

According to Descartes' rule, the number of negative solution roots of the equation $f(\lambda) = 0$ is equal to or less than the number of variations (changes) in the coefficient sign $f(-\lambda)$. This means that equation (26) has a maximum of four negative eigenvalues if

$$K(J) = L_6\lambda^4 - L_7\lambda^3 + L_8\lambda^2 - L_9\lambda + L_{10} \tag{27}$$

Then, with condition $L_6, L_7, L_8, L_9,$ and L_{10} are:

$$L_6 = 1 > 0$$
$$L_7 = W_8 > 0$$
$$L_8 = W_9 > W_{10}$$
$$L_9 = W_{11} > W_{12}$$
$$L_{10} = W_{13} > W_{14}$$

According to Descartes' rule, equation (27) has four negative eigenvalues, so the system can be said to be stable.

3.3. The Basic Reproduction Number R_0 Using Graph Method

In determining the basic reproduction number (R_0) using a reduction graph, the SEIRI model of diabetes transmission can be described as shown in Figure 2.
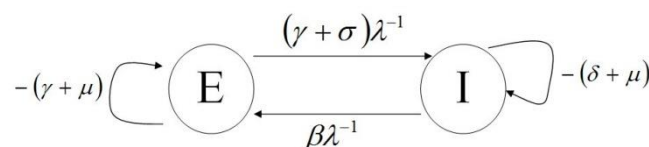

Figure 2. Illustration of SEIRI Graph Model for Hepatitis B

Furthermore, Figures 3 to 5 show the process of reducing the SEIRI Graph Model of Hepatitis B Transmission
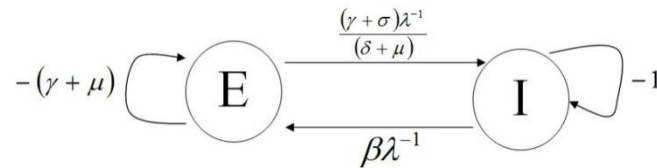

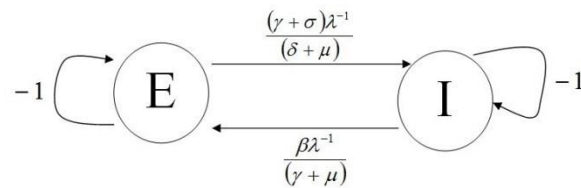**Figure 3**. Create the first trivial point on loop I

Figure 4. Create a second nontrivial point on loop E
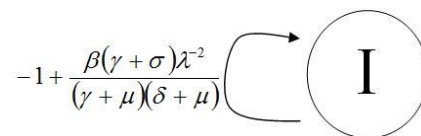

Figure 5. Elimination of the edge through the trivial point E.

The next step is to equate the value of side I with zero and solve for the value of λ, so that it is obtained:

$$-1+\frac{\beta(\gamma+\sigma)\lambda^{-2}}{(\gamma+\mu)(\delta+\mu)}=0$$

$$\frac{\beta(\gamma+\sigma)\lambda^{-2}}{(\gamma+\mu)(\delta+\mu)}=1$$

$$\lambda=\sqrt{\frac{\beta(\gamma+\sigma)}{(\gamma+\mu)(\delta+\mu)}}$$

Then, we found the basic reproduction number from the SEIRI model in Hepatitis B:

$$R_0=\sqrt{\frac{\beta(\gamma+\sigma)}{(\gamma+\mu)(\delta+\mu)}} \qquad (28)$$

3.4. SEIRI Model Simulation for Spread of Hepatitis B

Model simulation is done using Maple. The initial values S (0), E (0), I (0) and R (0) as well as the parameter values of the model based on the assumptions presented used in this simulation are shown in Table 4, with the basic reproduction number value R_0 obtained based on equation (28).

Table 1. Initial values and parameter values of the Hepatitis B SEIRI model

Symbol	$R_0 > 1$		$R_0 \leq 1$		Variable	Initial Value
	Value 1	Value 2	Value 1	Value 2		
μ	0.25	0.03	0.3	0.4	N(0)	10000
β	0.7	0.2	0.5	0.1	S(0)	6000
γ	0.4	0.1	0.02	0.2	E(0)	3000
σ	0.1	0.3	0.15	0.02	I(0)	400
δ	0.2	0.1	0.52	0.1	R(0)	600
R_0	1.09	2.18	0.57	0.27		

3.5. Simulation of SEIRI Model for Endemic Hepatitis B

Based on Table 1, a graph of each given parameter value is obtained as in Figure 6 and Figure 7:

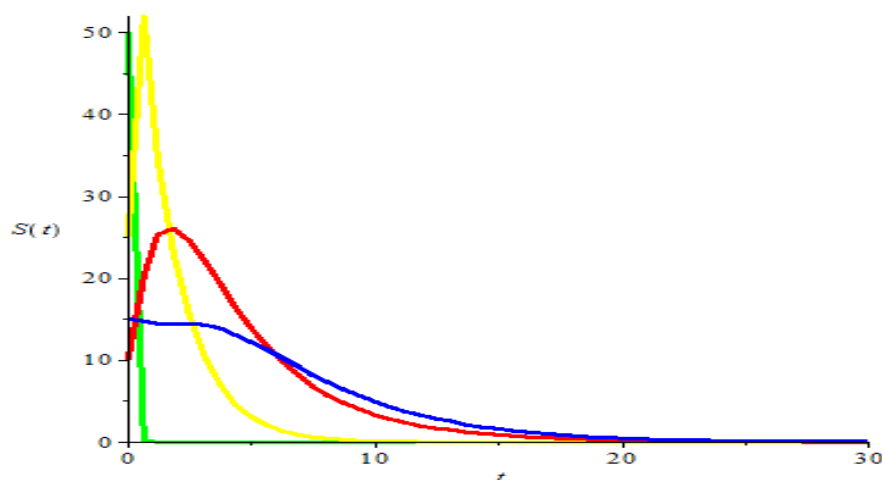*3.5.1. Simulation of parameter value 1*

Figure 6. Simulation results of Hepatitis B spread model in Suspected, Exposed, Infected and Recovered individuals

Figure 6 showed that the number of individuals who are susceptible and recovered each month has continued to decline since the first year, in contrast to the population of exposed and infected individuals which initially increases but a few years later decreases.

3.5.2. Simulation of parameter value 2

Figure 7 shows that the number of individuals who are susceptible and recovered every month has continued to decline since the first year, although individuals who recovered there was an increase starting at year 14, in contrast to the population of exposed and infected individuals which initially increased but a few years later decreased.
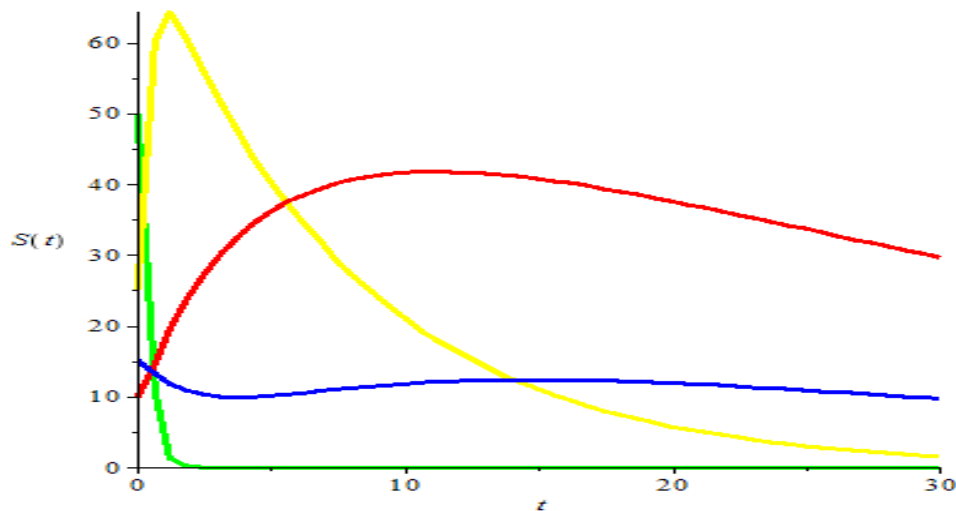
Figure 7. Simulation results of the Hepatitis B spread model in Suspected, Exposed, Infected and Recovered individuals

3.6. Simulation of SEIRI Model for Free Disease case Hepatitis B
Based on Table 1, it is obtained a graph of each given parameter value as in Figure 8 and Figure 9:

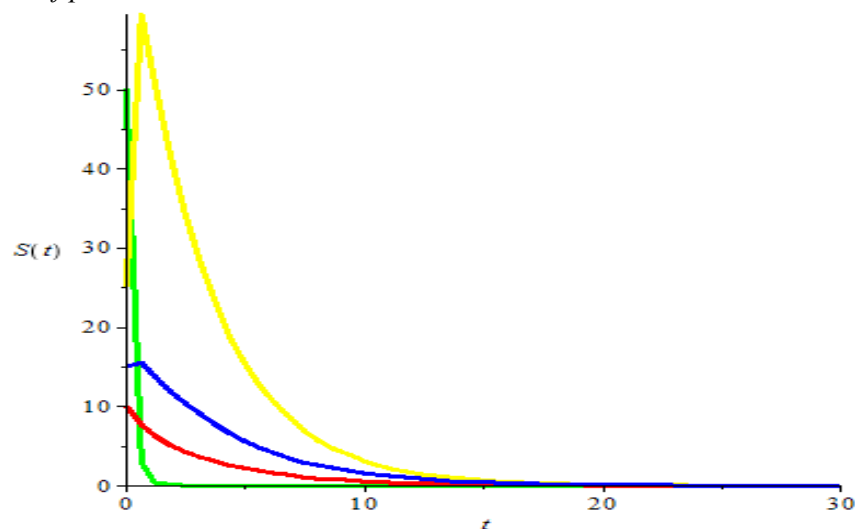*3.6.1. Simulation of parameter value 1*

Figure 8.The simulation results of the Hepatitis B model in Suspected, Exposed, Infected and Recovered individual

   Based on Figure 8, it shows that the number of individuals who are vulnerable, infected and recovered each year continues to decline, in contrast to the population of exposed individuals, which initially increased even though in year 3 it also decreased.
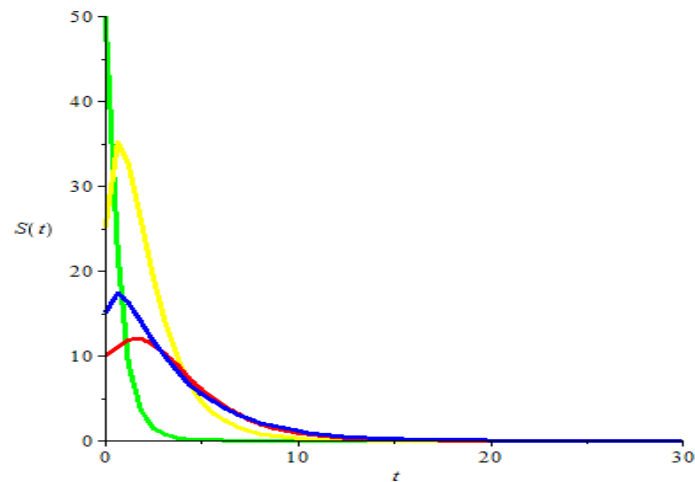
3.6.2. Simulation of parameter value 2

Figure 9. Simulation results of Hepatitis B model in Suspected, Exposed, Infected and Recovered individual

Figure 9 shows that the number of exposed, infected and recovered individuals each year continues to decline even though at the beginning of the year it has increased, in contrast to the population of vulnerable individuals which has continued to decline from the initial year.

4. DISCUSSION

Hepatitis B Mathematical model for Hepatitis B performed by Side *et al*[12] used a model SEIR and simulated using the assumption data for two cases are free disease and endemic case. In addition, [16] found a Hepatitis B virus model with Transmission Applied to Immunization Strategies. This study derived the SEIRI model for Hepatitis B in Makassar. The model analysis using Graph method to found the Basic Reproduction Number. The simulation result of the SEIRI model using Maple for free-disease cases and endemic case. The result of the model simulation provides information and prediction of the number of Hepatitis B in Makassar, so that this model is expected to help improve the strategy of controlling the number of Hepatitis B.

5. CONCLUSION

The conclusions from the research results are: the spread of Hepatitis B can be presented in the SEIRI mathematical model; The results of the analysis of the SEIRI model explain that hepatitis B in Makassar is in a stable state, then the basic reproduction number is obtained using the mathematical graph method and based on the simulation results of the SEIRI model in Hepatitis B using Maple both in disease-free and endemic cases providing predictive information on the number of Hepatitis cases B for disease-free and endemic conditions for Hepatitis B.

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