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# ANALYSIS OF THE SIRS MODEL OF THE SPREAD OF DENGUE HEMORRHAGIC FEVER USING RUNGE-KUTTA METHOD AND GENETIC ALGORITHM

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*Abstract –Dengue Hemorrhagic Fever is a contagious disease that often occurs in Indonesia. Dengue Hemorrhagic Fever, caused by the Dengue Virus, has four serotypes : DEN-1, DEN-2, DEN-3 and DEN-4. Someone can be infected four times, once for each serotype. After recovering from one serotype, a person gets a lifetime of immunity against that serotype. In this paper a model will be created for modeling the spread of Dengue Hemorrhagic Fever with assumption there are only two serotypes, namely DEN-1 and DEN-2. Model formed based on SIR Model (Susceptible, Infected, Recovered) and SIRS Model (Susceptible, Infected, Recovered, Susceptible). The changes in populations over time are written into a system of differential equations. The system of differential equations is then used to do an equilibrium point analysis. The numerical solution for the system of differential equations can be found using the Runge-Kutta Method. Genetic Algorithm are used to find the values of parameters in the model that are unknown. A series of simulations are performed to get the combination that produces the Genetic Algorithm system that will produce the best approximation solution. The combination includes population size, selection value, crossover value and mutation value. This best combination then will produce an approximation solution with the smallest error.*

***Keywords**: Epidemiological model, Equilibrium point, Runge-Kutta, Genetic Algorithm*

Abstrak – Demam Berdarah Dengue merupakan penyakit menular yang sering terjadi di Indonesia. Demam Berdarah Dengue, yang disebabkan oleh Virus Dengue, memiliki empat serotipe: DEN-1, DEN-2, DEN-3 dan DEN-4. Seseorang dapat terinfeksi empat kali, sekali untuk setiap serotipe. Setelah sembuh dari satu serotipe, seseorang mendapat kekebalan seumur hidup terhadap serotipe tersebut. Pada makalah ini akan dibuat suatu model untuk pemodelan penyebaran Demam Berdarah Dengue dengan asumsi hanya ada dua serotipe yaitu DEN-1 dan DEN-2. Model dibentuk berdasarkan Model SIR (Susceptible, Infected, Recovered) dan Model SIRS (Susceptible, Infected, Recovered, Susceptible). Perubahan populasi dari waktu ke waktu ditulis ke dalam sistem persamaan diferensial. Sistem persamaan diferensial ini kemudian digunakan untuk melakukan analisis titik setimbang. Solusi numerik untuk sistem persamaan diferensial dapat ditemukan dengan menggunakan Metode Runge-Kutta. Algoritma Genetika digunakan untuk mencari nilai parameter dalam model yang tidak diketahui. Serangkaian simulasi dilakukan untuk mendapatkan kombinasi yang menghasilkan sistem Algoritma Genetika yang akan menghasilkan solusi aproksimasi terbaik. Kombinasi tersebut meliputi ukuran populasi, nilai seleksi, nilai crossover dan nilai mutasi. Kombinasi terbaik ini kemudian akan menghasilkan solusi aproksimasi dengan error terkecil.

**Kata Kunci:** Model epidemiologi, Titik kesetimbangan, Runge-Kutta, Algoritma Genetika

## INTRODUCTION

Dengue Hemorrhagic Fever is still one of the major health problems in Indonesia [1]. Dengue fever is mosquito-borne tropical disease with severe flu-like symptoms, caused by the Dengue Virus spreads through bites of infected mosquitoes. That mosquito infected can transmit dengue virus for the rest of its life [2]. There are four serotypes of Dengue Fever, namely: Dengue Virus 1 (DEN-1 or DENV-1), Dengue Virus 2 (DEN-2 or DENV-2), Dengue Virus 3 (DEN-3 or DENV-3) and Dengue Virus 4 (DEN-4 or DENV-4). After recovering from certain serotype Dengue Fever, individuals get lifelong immunity life against the serotype dan temporary immunity to three other serotypes [2]. The spread of Dengue Fever can be made in the form of mathematical models. There are various mathematical

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models that can be used for epidemics, the simplest was discovered by Kernack and McKendrick in 1927, SIR model (Susceptible, Infected, Recovered). Finding certain parameter values from a model can be done in many ways. In this paper, Genetic Algorithms will be used. Genetic Algorithm (Genetic Algorithms) was first introduced by John Holland in years 1960s and later developed by Holland and colleagues as well his students at the University of Michigan in the 1960s and 1970s. Algorithm Genetics is a method that uses a set of "chromosomes" to create new populations using "natural selection". Each chromosome consists of "genes". Selected chromosomes can produce offspring, where chromosomes with a higher fitness value tend to produce better offspring [3].

## EPIDEMIOLOGICAL MODELS

The model used is the epidemiological model, namely the SIR model and SIRS model. This research assumes that there are only two serotypes, which are means when an individual suffers from Dengue Fever for the first time, a model the SIRS model is used. When individuals suffer from Dengue Fever for the second time, the SIR model was used, which means the individual will never has Dengue Fever again all his/her life because she/he has gained immunity lifetime for both serotypes. The population is divided into four groups [4]:

1. Susceptible Individuals are not infected with pathogens, but have low immunity against the disease.
2. Exposed Individuals who interact with other individuals who have contracted with the pathogen.
3. Infected Individuals from the susceptible group who have high levels of parasites in the body as well as being able to transmit diseases to other individuals within susceptible group.
4. Recovered Individuals whose immune system has eliminated all parasites in the body and are no longer able to transmit disease to other individuals within susceptible group.

Based on the group, the SEIR model was formed. In order to make the simpler model, SIR model, where the exposed groups are ignored. Besides SIR, there are also SI model that are commonly found on plants, SIS model that are commonly found in sexually transmitted diseases, and SIRS model where immunity is temporary.

The equation for the SIR model in general is as (1) [4]:

$$\begin{cases} \frac{ds}{dt} = \mu - \beta IS - \mu S \\ \frac{dI}{dt} = \beta IS - \gamma I - \mu I \\ \frac{dR}{dt} = \gamma I - \mu R \end{cases} \quad (1)$$

The parameter $\beta$ is the transmission rate, $\gamma$ is the removal or recovery rate and $\mu$ is the rate individuals suffer natural mortality and also the birth rate.
The equation for the SIRS model in general is as (2) [4]:

$$\begin{cases} \frac{ds}{dt} = \mu - \beta IS - \mu S + \omega R \\ \frac{dI}{dt} = \beta IS - \gamma I - \mu I \\ \frac{dR}{dt} = \gamma I - \mu R - \omega R \end{cases} \quad (2)$$

The parameter $\omega$ is the rate at which immunity is lost. The equation for the SIR and SIRS model for dengue fever is as (3). Mosquito vector and human vector model are shown in Fig.1 and Fig.2. Red line represents output of each process. The Description and value of each variabel is tabulated in Table 1.

$$\begin{cases} \frac{ds}{dt} = \upsilon - \Omega\left(\frac{\beta_h b}{N_h} I_\upsilon S\right) - (1-\Omega)\left(\frac{\beta_h b}{N_h} I_\upsilon S\right) - \mu_S S \\ \frac{dI_1}{dt} = \Omega\left(\frac{\beta_h b}{N_h} I_\upsilon S\right) - \gamma_1 I_1 - \mu_{I_1} I_1 \\ \frac{dR_1}{dt} = \gamma_1 I_1 - \omega_1 R_1 - \mu_{R_1} R_1 \\ \frac{dR_2}{dt} = \gamma_2 I_2 - \omega_2 R_2 - \mu_{R_2} R_2 \\ \frac{dS_1}{dt} = \omega_1 R_1 - \left(\frac{\beta_h b}{N_h} I_\upsilon S_1\right) - \mu_{S_1} S_1 \\ \frac{dS_2}{dt} = \omega_2 R_2 - \left(\frac{\beta_h b}{N_h} I_\upsilon S_2\right) - \mu_{S_2} S_2 \\ \frac{dI_{12}}{dt} = \left(\frac{\beta_h b}{N_h} I_\upsilon S_1\right) + \left(\frac{\beta_h b}{N_h} I_\upsilon S_2\right) - \gamma_{12} I_{12} - \mu_{I_{12}} I_{12} \\ \frac{dR_{12}}{dt} = \gamma_{12} I_{12} - \mu_{R_{12}} R_{12} \\ \frac{dS_\upsilon}{dt} = \mu - \frac{\beta_\upsilon b}{N_h}(I_1 + I_2 + I_3) S_\upsilon - \mu_{S_\upsilon} S_\upsilon \\ \frac{dI_\upsilon}{dt} = \frac{\beta_\upsilon b}{N_h}(I_1 + I_2 + I_3) S_\upsilon - \mu_{I_\upsilon} I_\upsilon \end{cases} \quad \text{... (3)}$$

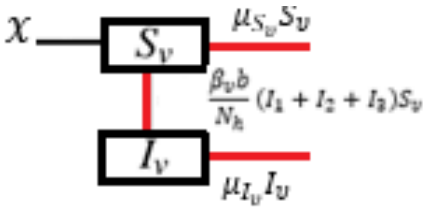


Fig.1 Mosquito Vector Model

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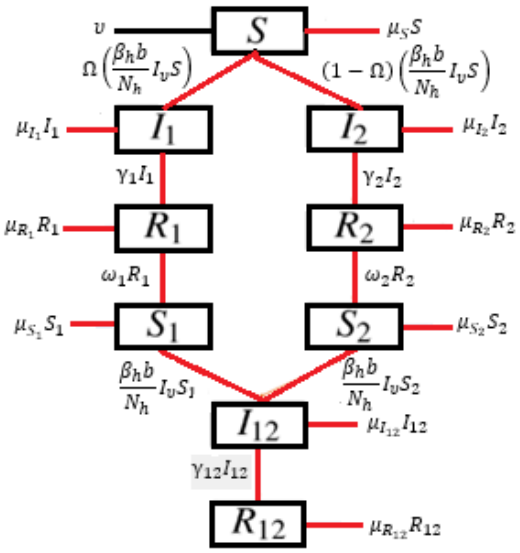

Fig.2 Human Vector Model

**EQUILIBRIUM POINT**

Equilibrium Point will occur when all values in left side of equation [3] are zero [5]. The equation is solved using Maple software progam. It is tabulated in Table 2.

| $X_i$ | $X_1$ | $X_2$ | $X_3$ | $X_4$ |
|---|---|---|---|---|
| $S$ | 110.80 | 23.16 | -454.96 | -290.28 |
| $I_1$ | 0 | 0.24 | 1.15 | 1.10 |
| $I_2$ | 0 | 0,15 | 1 | 0.71 |
| $R_1$ | 0 | 2.71 | 17.57 | 12.45 |
| $R_2$ | 0 | 1.73 | 11.17 | 7.92 |
| $S_1$ | 0 | 0.96 | 352.18 | -463.54 |
| $S_2$ | 0 | 0.60 | 128.54 | 778.98 |
| $I_{12}$ | 0 | 0.03 | -2.68 | -1.96 |
| $R_{12}$ | 0 | 3.80 | -385.19 | -280.84 |
| $S_v$ | 55.00 | 53.86 | 55.37 | 55.41 |
| $I_v$ | 0 | 1.14 | -0.37 | -0.41 |

There are four equilibrium points from table 2. The first equilibrium point, $X_1$ is the equilibrium point when there is no Dengue Fever in the entire population. $X_1$ is the equilibrium point without disease. The second equilibrium point, $X_2$ is the equilibrium point when both serotypes Dengue fever exists in the population. The third equilibrium point, $X_3$ is the "unnatural" equilibrium point, because population values cannot be negative. The fourth equilibrium point, $X_4$ is the "unnatural" equilibrium point, because population values cannot be negative.

Table 2. Equilibrium Point

Table 1. Description and value of each variable

| Var | Description | Unit | Value |
|---|---|---|---|
| $\upsilon$ | Per capita birth rate | Per day | 0.01662 |
| $\Omega$ | Percentage of individuals infected Serotype 1 Dengue Fever (DENV-1) | % | 0.61 |
| $\frac{\beta_h b}{N_h}$ | Transmission rate of Dengue Fever for humans | Per day | 0.0005 |
| $\gamma_1$ | Recovery rate of Serotype 1 Dengue Fever (DENV-1) | Per day | 0.033 |
| $\gamma_2$ | Recovery rate of Serotype 2 Dengue Fever (DENV-2) | Per day | 0.033 |
| $\gamma_{12}$ | Recovery individual suffers rate from Dengue Fever for the second time | Per day | 0.033 |
| $\omega_1$ | Immunity lost rate against Serotype 1 Dengue Fever (DENV-1) | Per day | 0.0027 |
| $\omega_2$ | Immunity lost rate against Serotype 2 Dengue Fever (DENV-2) | Per day | 0.0027 |
| $\mu$ | Per capita birth rate for mosquitos vector | Per day | 0.055 |
| $\frac{\beta_v b}{N_h}$ | Transmission rate of Dengue Fever for vectors | Per day | 0.00005 |
| $S$ | Population who have never suffered from Dengue Fever and susceptible to both serotypes | People | - |
| $I_1$ | Population who suffered from Serotype 1 Dengue Fever (DENV-1) | People | - |
| $I_2$ | Population who suffered from Serotype 2 Dengue Fever (DENV-2) | People | - |
| $R_1$ | Population who have cured from Serotype 1 Dengue Fever (DENV-1) | People | - |
| $R_2$ | Population who have cured from Serotype 2 Dengue Fever (DENV-2) | People | - |
| $S_1$ | Population who have never suffered from Serotype 2 Dengue Fever and susceptible to the serotype | People | - |
| $S_2$ | Population who have never suffered from Serotype 1 Dengue Fever and susceptible to the serotype | People | - |
| $I_{12}$ | Population who suffered from Dengue Fever for the second time | People | - |
| $R_{12}$ | Population who have cured from Dengue Fever for the second time | People | - |
| $S_v$ | Population of mosquitoes who have never suffered from Dengue Fever and susceptible to the disease | Head | - |
| $I_v$ | Population of mosquitos who suffered from Dengue Feve | Head | - |
| $\mu_S$ | Per capita death rate for $S$ group | Per day | 0.00015 |
| $\mu_{I_1}$ | Per capita death rate for $I_1$ group | Per day | 0.00030 |
| $\mu_{I_2}$ | Per capita death rate for $I_2$ group | Per day | 0.00025 |
| $\mu_{R_1}$ | Per capita death rate for $R_1$ group | Per day | 0.00022 |
| $\mu_{R_2}$ | Per capita death rate for $R_2$ group | Per day | 0.00024 |
| $\mu_{S_1}$ | Per capita death rate for $S_1$ group | Per day | 0.00020 |
| $\mu_{S_2}$ | Per capita death rate for $S_2$ group | Per day | 0.00021 |

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| | | | |
|---|---|---|---|
| $\mu_{I_{12}}$ | Per capita death rate for $I_{12}$ group | Per day | 0.00040 |
| $\mu_{R_{12}}$ | Per capita death rate for $R_{12}$ group | Per day | 0.00023 |
| $\mu_{S_v}$ | Per capita death rate for $S_v$ group | Per day | 0.00050 |
| $\mu_{I_v}$ | Per capita death rate for $I_v$ group | Per day | 0.00050 |

## GENETIC ALGORITHM

Genetic Algorithm is designed to find out value of eleven parameters out of 21 parameters of equation (3) assuming that other parameters are constants. They are the per capita mortality rate in each group. They are $\mu_S$, $\mu_{I_1}$, $\mu_{I_2}$, $\mu_{R_1}$, $\mu_{R_2}$, $\mu_{S_1}$, $\mu_{S_2}$, $\mu_{I_{12}}$, $\mu_{R_{12}}$, $\mu_{S_v}$ and $\mu_{I_v}$. Each death rate cannot exceed 1, then the death rate must be between 0 and 1. The solutions for the equation of the SIR and SIRS model for dengue fever will be calculated using Runge-Kutta fourth-order method (RK4) with initial conditions $t = 0$ are

$S$= 950, $I_1 = I_2 = R_1 = R_2 = S_1 = 0$,
$S_2 = I_{12} = R_{12} = I_v = 0$, $S_v = 1000$,
time $t$ = 150 and stepsize $h$ = 0.05.

The form of i[th] chromosome is as follows:

$$C(i) = (S, I_1, I_2, R_1, R_2, S_1, S_2, I_{12}, R_{12}, S_\vartheta, I_v)$$

The Genetics algorithm is as follow
Initial population
While condition is true
  Evaluation
  Selection
  Crossover
  Mutation
End
Interprete the solution

Initial population is the first process to have initial population in Genetic Algorithm. That is generate $n$ number of chromosome in random. Since the values of gene are small number and to speed up the processing time of Genetic Algorithm then initial value of each gene in a chromosome is started with multiplying random numbers between 0 and 1 by 0.001. All chromosome is stored in matrix $C$.

Evaluation is done by using fitness function. Fitness function of i[th] chromosome is defined with equation (4)

$$f(i) = 1 - \left(\frac{1}{11}\right)\left(\frac{\sum_{i=1}^{11}(C(i,j)-c\prime(i,j))^2}{\sqrt{\sum_{i=1}^{11} A\prime(i,j)^2}}\right) \qquad (4)$$

$C'(i,j)$ is true solution using Runge-Kutta with values from Table 1.

Selection is done with elitism algorithm by maintaining a number of the best chromosome of every generation [3]. That is sval% × n number of chromosomes in population. Selection is carried out using the following algorithm:

a. Sort the $C$ matrix based on its fitness value with the Quicksort algorithm.
b. Create new ten chromosomes
c. The remainder chromosomes in new population are chosen randomly from previous population.

Crossover is done by two-point crossover, exchanging segments in between two randomly selected crossover point positions [3]. Crossover done is carried out using the following algorithm

a. Determine number of chromosome are going to be crossovered. That is sval% × n number of chromosomes in population.
b. Determine pairs of chromosome are going to be crosovered randomly.
c. Determine two random crossover point positions for each pair parent.
d. Swap segments between two crossover point positions for each parent pair

Mutation is done by changing genes in chromosomes randomly. Mutation is carried out using the following algorithm

a. Determine the number of gene that will undergo mutation. That is mval × 11 × n number of chromosomes in population.
b. Determine the mutated gene randomly.
c. Value of each mutated gene is filled by multiplying 0.001 to random number 0 to 1.

Repetition will stop when at least one of the chromosomes has the fitness value greater than 0.99999.

## RESULT AND DISCUSSION

Experiment is started by determining population size n, selection value sval, crossover value cval and mutation value mval. The goal of experiment is not only to find the best chromosome but also the best combination of genetic parameter that is $\boldsymbol{n}$, $\boldsymbol{sval}$, $\boldsymbol{cval}$ and $\boldsymbol{mval}$. The experimen is to determine what is the best population size with $\boldsymbol{sval} = \boldsymbol{0.4}$; $\boldsymbol{cval} = \boldsymbol{0.7}$ and $\boldsymbol{mval} = \boldsymbol{0.1}$. The experimen result is shown in Table 3. The best population size is $\boldsymbol{n} = \boldsymbol{500}$ because it is not only having the lowest error but also the smallest average generation.

Table 3. Experiment result

| Average | Number of population (n) | | | | |
|---|---|---|---|---|---|
| | 100 | 200 | 300 | 400 | 500 |
| Average Error | 0.64 | 0.41 | 0.41 | 0.50 | 0.22 |
| Lowest Error | 0.27 | 0.27 | 0.26 | 0.18 | 0.15 |
| Average Time (sec) | 857 | 912 | 3394 | 4711 | 3127 |
| Average Generation | 304 | 312 | 394 | 552 | 246 |
| Average tipe perstep (Sec) | 3.23 | 3.01 | 7.94 | 7.61 | 14.18 |

The best chromosome is C=(0.00022, 0.00022, 0.00021, 0.00021, 0.00021, 0.00021, 0.00021,0.00018, 0,00050, 0.00050. 0.00050) with h = 0.05, error = 0.26, t = 5049 sec.

From the experiment can be seen that the average error and the best error is inversely proportional to $n$. This means the results are getting better if the larger population $n$ increase. Incontrary, average time is

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increase while $n$ increase except for $n = 500$.

Figure 3 is the actual solution using Runge-kutta fourth order method and Fig. 4 using Genetic Algorithm.

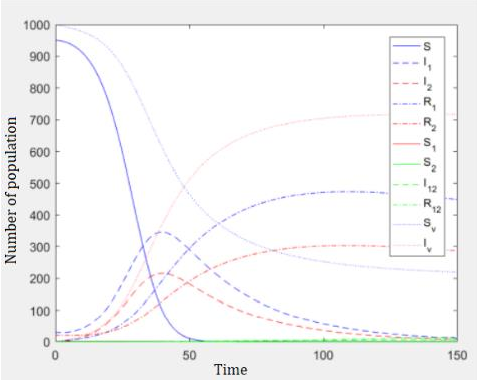


Fig. 3. Actual solution

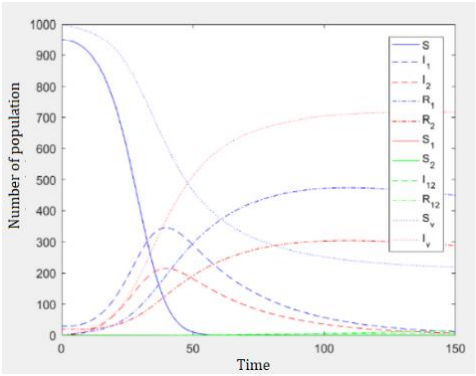


Fig. 4. GA solution

## CONCLUSION

In this paper a mathematical model has been made for the spread of Dengue Fever with two serotypes based on the SIR Model and SIRS Model. The solutions are listed in Table 3 with an error of 0.26.

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