On the Reproduction Ratio of Dengue Incidence in Semarang, Indonesia 2015-2018

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Abstract

Dengue is one of the mosquito-borne diseases caused by dengue viruses (DENV), which has become endemic in most tropical and subtropical countries, including Indonesia. Since there is a lot of dengue incidence on children of age less than fourteen years old in Semarang, Indonesia, it is the interest here to analyze the different rates of infection among different age groups. A SIR-UV mathematical model with age structure in human the population is constructed to describe dengue transmission in Semarang from 2015 to 2018. In this study, we separated the human population into four age classes: children (0-4 years), youngster (5-14 years), productive adults (15-60 years) and non-productive adults (over 60 years). We use Particle Swarm Optimization to obtain optimal parameters for the transmission rates based on the yearly incidence. The basic reproduction ratio (R_0) is derived from the Next Generation Matrix and is evaluated by using the optimal parameters for data Semarang in 2015-2018. Numerical simulation results show that the number of dengue incidence is in a good agreement with the actual data in Semarang for 2015-2018.

Keywords: age structure, dengue transmission model, estimation parameter, basic reproduction ratio
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1. INTRODUCTION

Dengue is an infectious diseases transmitted by mosquitoes that carry the dengue virus (DENV). There are four serotypes of dengue virus, namely DENV-1, DENV-2, DENV-3 and DENV-4, where all serotypes have been widely circulating in most of urban Indonesia [1]. Dengue virus is transmitted by the infected female mosquito of the species *Aedes aegypti* and *Aedes albopictus* [2], [3].

Demographical and societal change contribute to the increased of incidence and geographical spread of dengue virus [4]. The report of incidence rate of dengue fever in Indonesia increases from 0.05 per 100000 population in 1968, when the first cases were found, to nearly 35–40 per 100000 population in 2013 [5], [6]. It has been reported in [1] that more than half of children between the age 1–18 years, in 30 urban Indonesian subdistricts, had been exposed to more than one dengue serotype. Moreover, study in [6] reported that the dengue incidence in Indonesia in the last 45 years has been increasing rapidly with high incidences shifting from children between the age $5-14$ years to older age groups (over 15 years). This study used a database of the national disease surveillance system run by the Communicable Disease Center of the Indonesian Ministry of Health that covers 33 provinces with all age categories, namely less than 1 year, $1-4$ years, $5-14$ years, and older than 15 years.

Several mathematical approaches to study the dengue transmission dynamics which include an age structure in human population have been presented. Pongsumpun et al. [7] proposed a mathematical model of Dengue Hemorrhagic Fever (DHF) transmission in a two-age structure in the human population, namely Juveniles class and adults class. In [8], Sungchasit et al. [8] further extends the model by incorporating the presence of two type of mosquitoes: Aedes aegypti and Aedes albopictus. Furthermore, Tasman et al. [9] also developed a two-age-class model, consisting child and adult classes, by considering immigration vaccination strategy, as an anticipative study before the vaccine exists. Kristiani et al. [10] proposed an SIR-SI model with age-structured human population for estimating the relative risk of dengue transmission in Bandung, Indonesia, taking into account stochastic factors. The human population is also divided into two classes, namely juvenile and adult classes. Recently, Ganegoda et al. [11] introduced a PDE-ODE model with 14 class age structure

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in human population. In the study, characterization of parameter regimes is used for constructing the basic reproduction ratio, using the data for the period 2009-2014. As a validation, they used incidence data of the Semarang city, Indonesia, for parameter estimation.

In this study, we propose a SIR-SI mathematical model for dengue transmission with age structure in human population that consist of children ($0-4$ years), youngster ($5-14$ years), productive adults ($15-60$ years) and non-productive adults (over 60 years). Different from previous models, the transmission rates of dengue are estimated using Particle Swarm Optimization. Here, we used dengue incidence data from the city of Semarang. Furthermore, we derive the yearly basic reproduction ratio (R_0) using the estimated parameters, which represent the endemic ratio of the disease during the period.

The organization of the rest of this paper is as follows. In section 2, we construct the mathematical model of dengue infection with age-structured in human population. Section 3 presents estimation of the force of infections. While in section 4, we propose the numerical simulation. Finally, section 4 presents the conclusions.

2. Mathematical Model

Dengue transmission model with age structure in human population will be constructed in this section. We derive a Susceptible, Infected and Recovered (SIR) model for human population and Susceptible and Infected (SI) model for mosquito population based on Kermack and McKendrick model [12]. In this study, we denote Susceptible and Infected mosquito population by U and V, respectively. The human population is divided into four age-structures, that is children ($0-4$ years) with two compartments: Susceptible children (S_1) and Infected children (I_1), youngster ($5-14$ years) with two compartments: Susceptible youngster (S_2) and Infected youngster (I_2), productive adults ($15-60$ years) with two compartments: Susceptible productive adults (S_3) and Infected productive adults (I_3), and non-productive adults (over 60 years) with two compartments: Susceptible non-productive adults (S_4) and Infected non-productive adults (I_4). Here, we assume that the recovered humans have permanent immunity for dengue. So, the total human population as a function of time is given by

$$N_h(t) = S_1(t) + I_1(t) + S_2(t) + I_2(t) + S_3(t) + I_3(t) + S_4(t) + I_4(t) + R(t). \tag{1}$$

The mosquito population is divided into two compartments: Susceptible mosquitoes (U) and Infected mosquitoes (V). We have the total mosquito population as follows:

$$N_m(t) = U(t) + V(t). \tag{2}$$

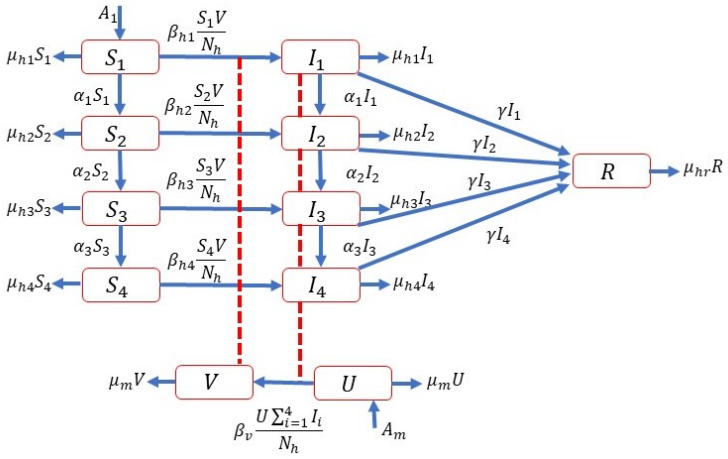


Figure 1: Dengue Transmission Diagram with Age Structure in Human Population

Table 1: Parameter Definition and Value.

Parameter	Definition	Value	Reference
A_1	Human recruitment rate ($Week^{-1}$)	-	Data
A_m	Mosquito recruitment rate ($Week^{-1}$)	$\mu_m \times N_m$	Assumption
α_1	Transition rate from children to youngster ($Week^{-1}$)	$\frac{1}{5\times52}$	-
α_2	Transition rate from youngster to productive adults ($Week^{-1}$)	$\frac{1}{10\times52}$	-
α_3	Transition rate from productive adults to non-productive adults ($Week^{-1}$)	$\frac{1}{46\times52}$	-
β_{h1}	Transmission rate from mosquitoes to children	Estimated	-
β_{h2}	Transmission rate from mosquitoes to youngster	Estimated	-
β_{h3}	Transmission rate from mosquitoes to productive adults	Estimated	-
β_{h4}	Transmission rate from mosquitoes to non-productive adults	Estimated	-
β_v	Transmission rate from humans to mosquitoes	Estimated	-
μ_{h1}	Natural death rate of children ($Week^{-1}$)	-	Data
μ_{h2}	Natural death rate of youngster ($Week^{-1}$)	$\frac{1}{65\times52}$	[13], [14]
μ_{h3}	Natural death rate of productive adults ($Week^{-1}$)	$\frac{1}{65\times52}$	[13], [14]
μ_{h4}	Natural death rate of non-productive adults ($Week^{-1}$)	$\frac{1}{65\times52}$	[13], [14]
μ_m	Natural death rate of mosquitoes ($Week^{-1}$)	$\frac{1}{6}$	[15]
γ	Recovery rate of infected humans ($Week^{-1}$)	1	[16], [17]

A flow diagram of dengue transmission in humans with age structure and within mosquitoes is given in Fig. 1. The definitions of all parameters are given in Table 1. We derive the dengue transmission model with age structure in human population as follows:

$$\frac{dX}{dt} = F(X), X = (S_1, S_2, S_3, S_4, I_1, I_2, I_3, I_4, R, U, V)^T, \tag{3}$$

written in detail

$$\begin{aligned}
\frac{dS_i}{dt} &= A_i + \alpha_{i-1}S_{i-1} - \alpha_i S_i - \frac{\beta_{hi}S_iV}{N_h} - \mu_{hi}S_i \\
\frac{dI_i}{dt} &= \alpha_{i-1}I_{i-1} - \alpha_i I_i - \frac{\beta_i S_i V}{N_h} - \gamma I_i - \mu_{hi}I_i \\
\frac{dR}{dt} &= \sum_{i=1}^{4}\gamma I_i - \mu_{hr}R \\
\frac{dU}{dt} &= A_m - \beta_v \sum_{i=1}^{4}\frac{UI_i}{N_h} - \mu_m U \\
\frac{dV}{dt} &= \beta_v \sum_{i=1}^{4}\frac{UI_i}{N_h} - \mu_m V,
\end{aligned} \tag{4}$$

$$N_h(t) = S_1(t) + I_1(t) + S_2(t) + I_2(t) + S_3(t) + I_3(t) + S_4(t) + I_4(t) + R(t),$$

for $i = 1, 2, 3, 4$, where $\alpha_0 = \alpha_4 = 0$ and $A_i = 0$ for $i = 2, 3, 4$. We assumed that the death rate of youngster and adults human are same i.e. $\mu_{hi} = \mu_{hr} = \mu_h, i = 2, 3, 4$. The natural death rate for adults is $\mu_h = \frac{1}{65\times52}$, corresponding to a lifetime average of 65 years for adults. While, the natural death rate of children for every year $(\mu_{h1}(t))$ is obtained by dividing the number of deaths at time t, as seen in Table 2, by the total population of children at time t, as seen in Table 3.

The disease free equilibrium is obtained as

$$\begin{aligned}
DFE &= \Bigg\{R = 0, U = \frac{A_v}{\mu_v}, V = 0, I_1 = 0, I_2 = 0, I_3 = 0, I_4 = 0, S_1 = \frac{A_1}{\alpha_1 + \mu_{h1}}, \\
&\quad S_2 = \frac{A_1\alpha_1}{(\alpha_2 + \mu_h)(\alpha_1 + \mu_{h1})}, S_3 = \frac{\alpha_1\alpha_2 A_1}{(\alpha_3 + \mu_h)(\alpha_2 + \mu_h)(\alpha_1 + \mu_{h1})}, \\
&\quad S_4 = \frac{\alpha_3\alpha_2\alpha_1 A_1}{\mu_h(\alpha_3 + \mu_h)(\alpha_2 + \mu_h)(\alpha_1 + \mu_{h1})}\Bigg\}
\end{aligned}$$

and the corresponding next generation matrix is

$$NGM = \begin{bmatrix} 0 & 0 & 0 & 0 & \frac{\mu_h \beta_{h1}}{(\mu_h+\alpha_1)\mu_m} \\ \frac{\alpha_1}{\alpha_1+\mu_{h1}+\gamma} & 0 & 0 & 0 & \frac{\alpha_1 \mu_h \beta_{h2}}{(\alpha_2+\mu_h)(\mu_h+\alpha_1)\mu_m} \\ 0 & \frac{\alpha_2}{\alpha_2+\mu_h+\gamma} & 0 & 0 & \frac{\alpha_1 \alpha_2 \mu_h \beta_{h3}}{(\alpha_2+\mu_h)(\alpha_3+\mu_h)(\mu_h+\alpha_1)\mu_m} \\ 0 & 0 & \frac{\alpha_3}{\alpha_3+\mu_h+\gamma} & 0 & \frac{\alpha_1 \alpha_2 \alpha_3 \beta_{h4}}{(\alpha_2+\mu_h)(\alpha_3+\mu_h)(\mu_h+\alpha_1)\mu_m} \\ \frac{A_m \beta_v}{Q\mu_m(\alpha_1+\mu_{h1}+\gamma)} & \frac{A_m \beta_v}{Q\mu_m(\alpha_2+\mu_h+\gamma)} & \frac{A_m \beta_v}{Q\mu_m(\alpha_3+\mu_h+\gamma)} & \frac{A_m \beta_v}{Q\mu_m(\mu_h+\gamma)} & 0 \end{bmatrix} \quad (5)$$

where $Q = \frac{(\alpha_1+\mu_{h1})\mu_h}{A_1(\mu_h+\alpha_1)}$. The basic reproduction ratio (R_0) is equal to the spectral radius of the next generation matrix [18], i.e. the largest eigen value of characteristic polynomial

$$P(\lambda) = a_5\lambda^5 + a_3\lambda^3 + a_2\lambda^2 + a_1\lambda + a_0, \quad (6)$$

where

$$\begin{aligned}
a_0 &= -A_m\alpha_1\alpha_2\alpha_3\beta_{h1}\beta_v\mu_h^2\left(\alpha_3+\mu_h\right)\left(\alpha_2+\mu_h\right)\left(\alpha_1+\mu_{h1}\right) \\
a_1 &= -A_m\alpha_1\alpha_2\beta_v{\mu_h}^2\left(\alpha_3+\mu_h\right)\left(\alpha_1+\mu_{h1}\right)\left(\left(\alpha_2+\mu_h\right)\left(\mu_h+\gamma\right)\beta_{h1}+\alpha_3\left(\alpha_1+\mu_{h1}+\gamma\right)\beta_{h2}\right) \\
a_2 &= -A_m\alpha_1\left(\alpha_1+\mu_{h1}\right){\mu_h}^2\beta_v\big(\left(\alpha_3+\mu_h\right)\left(\mu_h+\gamma\right)\left(\alpha_3+\mu_h+\gamma\right)\left(\alpha_2+\mu_h\right)\beta_{h1}+\alpha_2\left(\alpha_3+\mu_h\right) \\
&\quad \left(\mu_h+\gamma\right)\left(\alpha_1+\mu_{h1}+\gamma\right)\beta_{h2}+\alpha_3\alpha_2\left(\alpha_2+\mu_h+\gamma\right)\left(\alpha_1+\mu_{h1}+\gamma\right)\beta_{h3}\big) \\
a_3 &= -A_m\left(\alpha_1+\mu_{h1}\right)\mu_h\beta_v\big(\mu_h\left(\alpha_3+\mu_h\right)\left(\alpha_2+\mu_h\right)\left(\mu_h+\gamma\right)\left(\alpha_3+\mu_h+\gamma\right)\left(\alpha_2+\mu_h+\gamma\right)\beta_{h1}+ \\
&\quad \alpha_1\mu_h\left(\alpha_3+\mu_h\right)\left(\mu_h+\gamma\right)\left(\alpha_3+\mu_h+\gamma\right)\left(\alpha_1+\mu_{h1}+\gamma\right)\beta_{h2}+\alpha_1\alpha_2\mu_h\left(\mu_h+\gamma\right)\left(\alpha_2+\mu_h+\gamma\right) \\
&\quad \left(\alpha_1+\mu_{h1}+\gamma\right)\beta_{h3}+\alpha_1\alpha_2\alpha_3\left(\alpha_3+\mu_h+\gamma\right)\left(\alpha_2+\mu_h+\gamma\right)\left(\alpha_1+\mu_{h1}+\gamma\right)\beta_{h4}\big) \\
a_5 &= A_1{\mu_m}^2\left(\mu_h+\alpha_1\right)^2\left(\alpha_3+\mu_h\right)\left(\alpha_2+\mu_h\right)\left(\mu_h+\gamma\right)\left(\alpha_3+\mu_h+\gamma\right)\left(\alpha_2+\mu_h+\gamma\right)\left(\alpha_1+\mu_{h1}+\gamma\right).
\end{aligned}$$

Analytical form of R_0 is not possible to obtained for the characteristic polynomial (6). Numerical estimate of R_0 in each year will be obtained for (6) with the estimation of infection rates in Section 3. For simplification, in the numerical simulation in each year, the total human population is assigned with the yearly population data.

3. ESTIMATION OF THE FORCE OF INFECTIONS

In this study, we use observed data from Semarang in yearly basis as given in Table 2 and Table 3 [19]–[24], to estimate the transmission rates, β_i and β_v for $i = 1, 2, 3, 4$. First, we define relations among the mean number of infections per week for class i, $\frac{\beta_i V}{N_h}$, that describes the force of infections, and proportion of an infection in class i, ρ_i, as follows:

$$\frac{\beta_i V}{N_h} \approx \rho_i, \quad (7)$$

where $\rho_i = \frac{I_i(t)}{N_i(t)}$. $I_i(t)$ is dengue incidence data for class i in year t and $N_i(t)$ denotes the number of population for class i in year t. So, the comparison for each class is given by

$$\beta_1 : \beta_2 : \beta_3 : \beta_4 \approx \rho_1 : \rho_2 : \rho_3 : \rho_4.$$

We can then rewrite the infection rates as a function of proportion ρ_i as follows:

$$\beta_i = a\rho_i(1 \pm \epsilon_i), \quad (8)$$

where $a \in \mathbb{R}^+$ is a multiplicative factor and ϵ_i is the variation ratio in each age group. Thus, we have five parameters, β_i and β_v for $i = 1, 2, 3, 4$, that will be estimated using Particle Swarm Optimization (PSO) based on data.

Table 2: Birth and Mortality Data of Semarang

Age Structure	Number of Birth $A_1(t)$				Number of Mortality			
	2015	2016	2017	2018	2015	2016	2017	2018
Children	22609	22202	21517	21517	283	232	228	187

Table 3: Incidence Data of Semarang

j	Age Structure	Dengue Incidence Data ($I_j^{data}(t)$) [19]				Number of Population ($N_j(t)$) [20]				Comparison of ρ_j			
		2015	2016	2017	2018	2015	2016	2017	2018	2015	2016	2017	2018
1	Children	301	135	46	15	128160	130294	124501	140261	11	10	7	5
2	Youngster	706	376	172	46	250836	264618	242897	297583	13	14	13	8
3	Productive	463	177	69	33	1104239	1192819	1081931	1250963	2	2	1	1
4	Non-productive	25	14	6	3	112031	141697	106655	151189	1	1	1	1
	Total	1495	702	293	97	1595266	1729428	1555984	1839996				

Furthermore, we define a optimization problem which is expressed by the following objective function:

$$\begin{array}{lll} \underset{\{\beta_i,\beta_v\}}{\text{minimize}} & : & F(X,\tau,\beta_i,\beta_v) = \sqrt{\sum_{j=1}^{4}\left(I_j^{data}(\tau)-\hat{I}_j(\tau)\right)^2}, \\ \text{subject to} & : & \frac{dX}{dt} = F(X,t), \\ \text{with} & : & \beta_i,\beta_v \geq 0, i=1,2,3,4, \end{array}$$

where $\hat{I}_j(\tau)$ denote the dengue incidence simulation for class j in year τ. In this case, the available dengue data is annual-based data, whereas we want more detailed weekly simulation results on the dynamics of dengue transmission in Semarang. Therefore, the objective function that we defined above is a representation of minimizing errors between dengue annual data and simulations. We then solved the optimization problem using PSO. The value of $\hat{I}_j(\tau)$ is computed as an accumulative infected human every week in the year as follows:

$$\hat{I}_j(\tau) = \sum_{t=1}^{52}\sum_{i=1}^{4} I_i(t), \tag{9}$$

where $I_j(t)$ denote the numerical solution of infected compartment for class j. Eq. (9) is an accumulative number of dengue cases per year (accumulated for 52 weeks) per age structure. In another word, it represents the number of dengue cases per year.

The algorithm of PSO is shown below [25], [26].

1) Initialization:
   a) Set the number of particles (M), dimension of the optimized problem, maximum iteration, upper and lower bound for initial of the particle, the cognitive (individual) learning rate (c_1) and the social (group) learning rate (c_2).
   b) Randomly initialize particle position, $X_k(0)$ and velocities $V_k(0)$, for $k = 1, 2, ..., M$.
2) Evaluate the objective value of each particles, $F(X_k(0))$. Set $s = 1$.
3) In the sth iteration, find the two important parameters for each particle k:
   a) P_{best}, k denote the historical best value of $X_k(s)$ with the lowest value of the objective function $F(X_k(s))$, encountered by particle k in all the previous iterations; and G_{best} denote the historical best value of $X_k(s)$ with the lowest value of the objective function $F(X_k(s))$, encountered in all the previous iterations by any of the M particles.
   b) Update the velocity of particle k in sth iteration using the following equation:

$$V_k(s) = \theta V_k(s-1) + c_1 r_1 (P_{best}, k - X_k(s-1)) + c_2 r_2 (G_{best} - X_k(s-1)); \; k = 1, 2, ..., M, \tag{10}$$

with

$$\theta(s) = \theta_{max} - \left(\frac{\theta_{max} - \theta_{min}}{s_{max}}\right) s, \tag{11}$$

where θ is an inertia weight to reduce the velocity, $\theta_{max} = 0.9$ and $\theta_{min} = 0.4$ are commonly used. The value of r_1 and r_2 are uniformly distributed random numbers within the range 0 and 1.

c) Update position of kth particle in kth iteration using the following equation:

$$X_k(s) = X_k(s-1) + V_k(s);\ k = 1, 2, ...M. \tag{12}$$

Furthermore, evaluate the objective values corresponding to the particles as $F(X_1(s))$,$F(X_2(s))$,...,$F(X_M(s))$.

4) Terminate criteria: If the position of all particle converge to the same set of values then stop. Otherwise, set $s = s + 1$ and return to step 3.

4. NUMERICAL SIMULATION

The numerical simulations of the dengue transmission model in Eq. (5) for every year using parameter values as given in Table 1 are represented in this section. We used initial values to solve the model for Data Semarang for every year as given in Table 4. Whereas, initial values for mosquito compartments are assumed to be proportional to the human compartments.

Here, we obtain the estimated parameters for every year using PSO algorithm with $M = 1000$, maximum iteration 1000, upper and lower bound $[0\,1]$ and $c_1 = c_2 = 1$ as given in Table 4. The objective function values of the best particle in every iteration can be seen in Fig. 2. We also obtain the basic reproduction ratio (R_0) value for every year as shown in Table 4. All of the R_0 value using the estimated parameters is bigger than 1. It means that the dengue infection will outbreak in the long run.

Table 4: Initial values, estimated parameters and basic reproduction number

Year	Initial values		Estimated parameters					R_0
			β_1	β_2	β_3	β_4	β_v	
2015	$S_1(0) = 128149$,	$I_1(0) = 11$,	0.681	0.833	0.126	0.056	0.753	1.007
	$S_2(0) = 250823$,	$I_2(0) = 13$,						
	$S_3(0) = 1104237$,	$I_3(0) = 2$,						
	$S_4(0) = 112030$,	$II_4(0) = 1$,						
	$R(0) = 0$,							
	$U(0) = 1595239$,	$V(0) = 27$.						
2016	$S_1(0) = 130284$,	$I_1(0) = 10$,	0.552	0.799	0.086	0.047	0.804	1.013
	$S_2(0) = 264604$,	$I_2(0) = 14$,						
	$S_3(0) = 1192817$,	$I_3(0) = 2$,						
	$S_4(0) = 141696$,	$I_4(0) = 1$,						
	$R(0) = 0$,							
	$U(0) = 1729401$,	$V(0) = 27$.						
2017	$S_1(0) = 124500$,	$I_1(0) = 1$,	0.390	0.717	0.069	0.054	1.027	1.029
	$S_2(0) = 242890$,	$I_2(0) = 7$,						
	$S_3(0) = 1081931$,	$I_3(0) = 0$,						
	$S_4(0) = 106655$,	$I_4(0) = 0$,						
	$R(0) = 0$,							
	$U(0) = 1555976$,	$V(0) = 8$.						
2018	$S_1(0) = 140260$,	$I_1(0) = 1$,	1.177	1.746	0.318	0.220	0.270	1.008
	$S_2(0) = 297581$,	$I_2(0) = 2$,						
	$S_3(0) = 1250963$,	$I_3(0) = 0$,						
	$S_4(0) = 151189$,	$I_4(0) = 0$,						
	$R(0) = 0$,							
	$U(0) = 1839993$,	$V(0) = 3$.						

Fig.3 shows the comparison between the incidence dengue data and the incidence dengue simulation using the estimated parameters. High dengue incidence in Semarang occur in youngster class for every year. This is relevant with the simulation results as shown in Fig. 3.

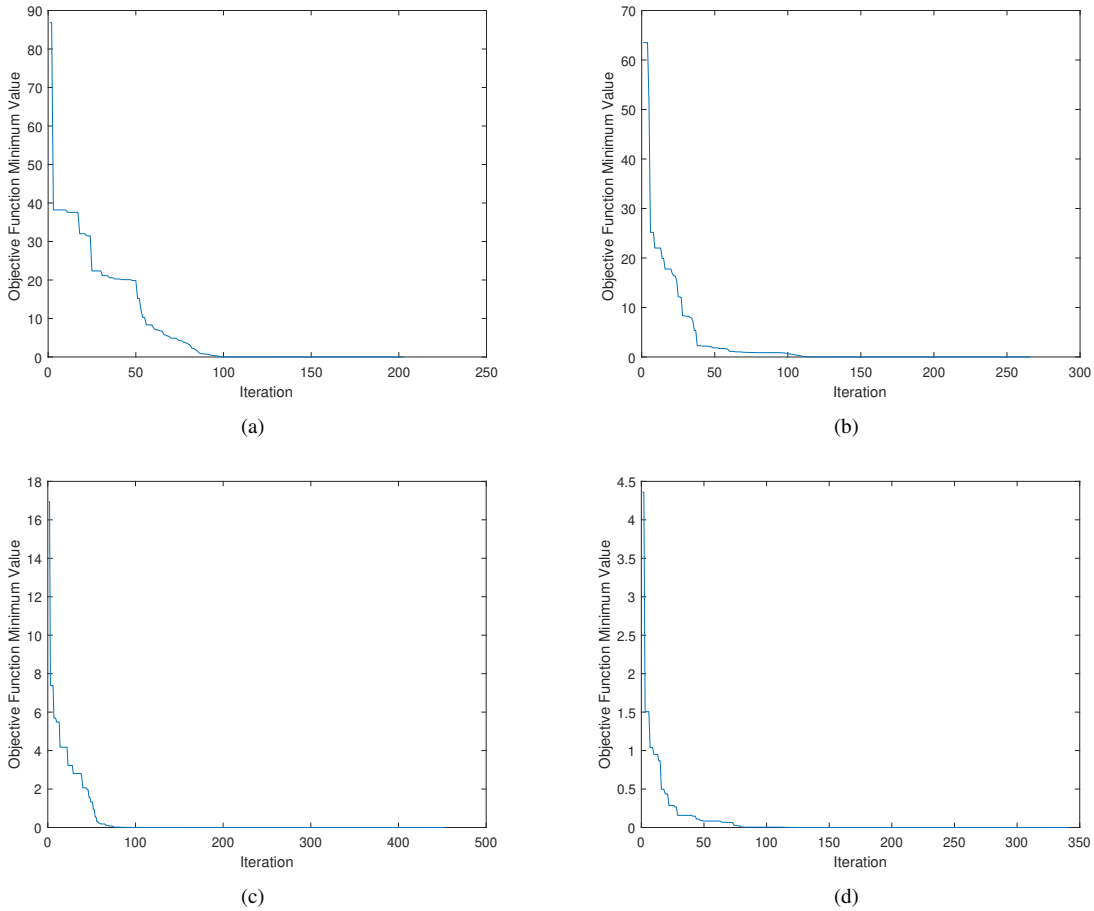
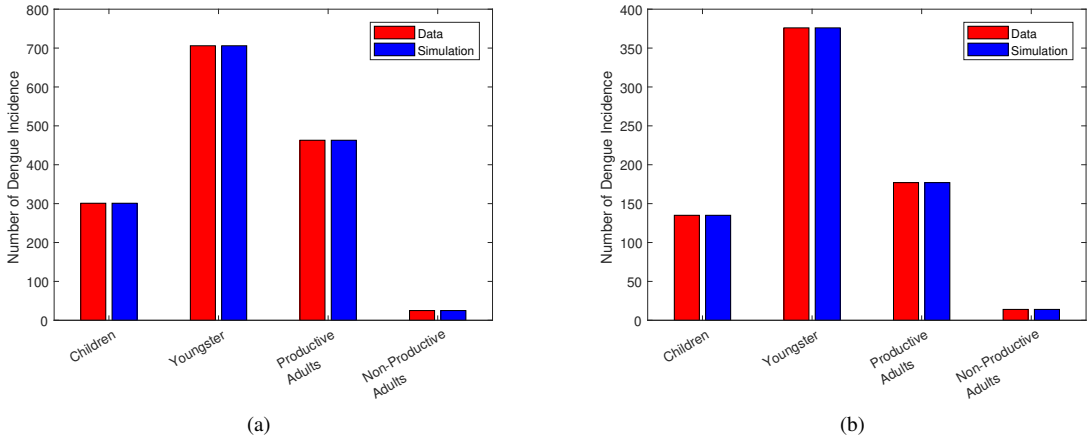


Figure 2: Objective function values for each iteration, based on β_i and β_v parameters generated by Particle Swarm Optimization in (a) 2015; (b) 2016; (c) 2017; and (d) 2018.



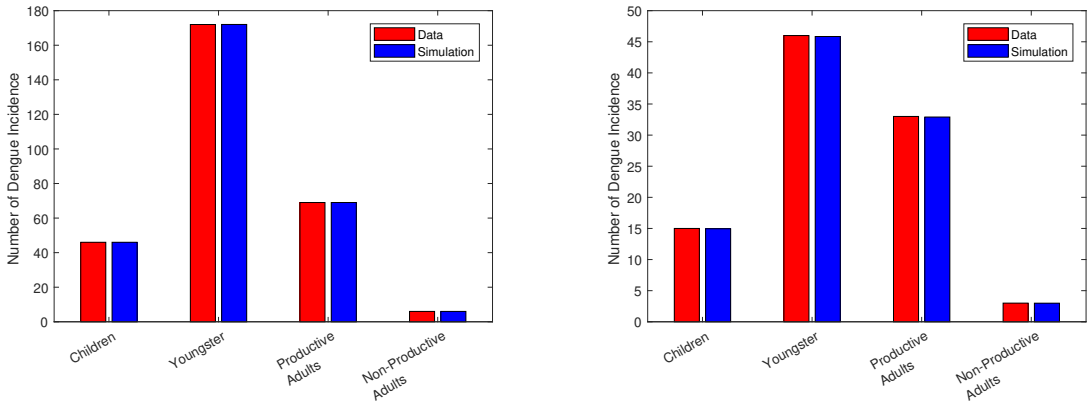


Figure 3: Comparison of dengue incidence data and simulation from Semarang in (a) 2015; (b) 2016; (c) 2017; and (d) 2018.

5. Conclusion

In this study, we consider a mathematical model of dengue transmission with age structure that focuses on estimating the parameters of transmission rate using Particle Swarm Optimization. We derive the Next Generation Matrix to obtain the basic reproduction ratio (R_0). The optimal parameters are used to calculate the R_0. It is shown that the numerical simulations of the dengue incidence are in agreement with the actual data of dengue incidence in Semarang for 2015-2018.

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