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Modelling the Dynamics of Dengue Fever Transmission: An Empirical Analysis

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Abstract

Objectives: The aim of this study is to obtain SIRI model for dengue fever (DHF) transmission, conduct analysis, and simulation of SIRI model in disease-free and endemic and also to predict the number of DHF cases. **Methods/statistical analysis**: Dengue fever is caused by a virus carried by the *Aedes aegypti* and *Aedes albopictus* mosquitoes, the SIRI model is a modification of the SIR model. Analysis of the SIRI model use the Lyapunov function method, then the data used in the simulation are assuming to show two possible dengue status are disease free and endemic status. The simulation also using the number of dengue case in Makassar city for showing the status of dengue fever transmission in Makassar city. Simulation models using Maple software are to predict the number of dengue cases in the following months. **Findings:** The results of this study are the SIRI model of the transmission of dengue fever with variables that have recovered can be re-infected with dengue fever, analysis of the SIRI model of dengue transmission provides information that the equation system in the SIRI model which is asymptotically stable, it means that dengue cases always exist at a certain time and certain region. The simulation results of the SIRI model in this study illustrate the number of dengue cases in the following months. While the first simulation found the basic reproduction number is $R_0 = 0.0366 \le 1$ this means that dengue transmission is at an alarming stage, but the second simulation finds the basic reproduction number $R_0 = 31.2733 > 1$, this means that, a person infected with dengue causes eight individuals will be infected with dengue fever, so that it is in the endemic stage, and the last simulation using data of the number

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of dengue case in Makassar city found = 1, that means, Makassar city is a free disease case for dengue fever transmission. **Application/ improvements:** SIRI model for DHF transmission is a mathematical health application. Model analysis guarantees existence, disease-free Dengue.

Indexed keywords: SIRI Model, Dengue Fever, Model Analysis, Simulation, Free Disease, Endemic

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1. Introduction

he World Health Organization [1] states that the number of dengue fever (DHF) cases in the world has increased 30-fold over the past 50 years, and was named the fastest growing disease in the world and more than half of the world's research results are related quality. In cites, one to one million people were admitted in hospitals to diagnose DHF every year [1]. More than patients were children and 2.5 percent of them eventually died. Data from around the world [1] show that Asia determines the first place in the number of dengue fever patients each year. Meanwhile, starting in 1968 until 2016, Indonesia was the highest country with Dengue Fever in Southeast Asia [1]. Makassar city is one of the districts in South Sulawesi with the highest number of dengue cases. According to the Health Department Makassar City, the number of dengue cases in Makassar in 2016 is 142 cases, 2017 is 248 cases and January to February 2018 is 62 cases [2].

Mathematical modeling to detect and predict the number of dengue cases, namely the SIR and SEIR models have been carried out [3–17]. The models assume that the recovered population is immune, but the current facts show that recovered populations can be re-infected. Based on this, this study will build a SIRI model as a modification of the SIR model that has been carried out by researchers [9–10], then this model is analyzed and then simulated to predict the number of cases in the following years in Makassar city, South Sulawesi which can be a solution to prevent dengue fever.

2. Material and Method

2.1. Study Area and Data

The case of dengue in tropic country every year becomes a problem for the government. The study area in this study is several cities which are high DHF cases each year; the data used are data on the number of dengue cases in Makassar city. In addition, there are assumptions for parameter and initial values are simulation data for free disease and endemic status.

2.2. Methods

The SIRI model in this study is a modification of the SIR model. Analysis of the SIRI model uses the Lyapunov function method [9], and then the data used in the simulation are assuming data to show two possible dengue statuses are disease free and endemic status.

The simulation of the model also using the number of dengue cases data in Makassar city by the Department of Health in South Sulawesi. Simulation models using Maple 18 to predict the number of dengue cases in Makassar city in the following month.

3. Results and Discussion

3.1. S IRI Model for Dengue Fever Disease

Changes that occur in each human population and vector population of SIRI model for the transmission of dengue disease can be interpreted in Figure 1.

According to Figure 1, SIRI model for dengue fever transmission can be interpreted in system (1):

□□□dSdth □□h hN □□□□□Nhhb Iv □□h □□□Sh

□□dIh □□hb I Sv h □□□□Nh vI bh □□□Rh □□□
□h □ h□Ih
□ dt Nh □
□

□□□dRh □□h hI □□□□h □□Nh vI bh □□□Rh
(1) dt □

□□□dSdt^v □□v vN □□N^v$_h$b I S$_h$ $_v$ □□v vS

□□dIdtv □□Nv$_h$b I Sh v □□v vI

□
□

Sh Ih Rh Sv Iv

Simplify system (1) with S_h = ; I_h = ; R_h = ; S_v = ;*and* I_v =___

Nh Nh Nh Nv Nv

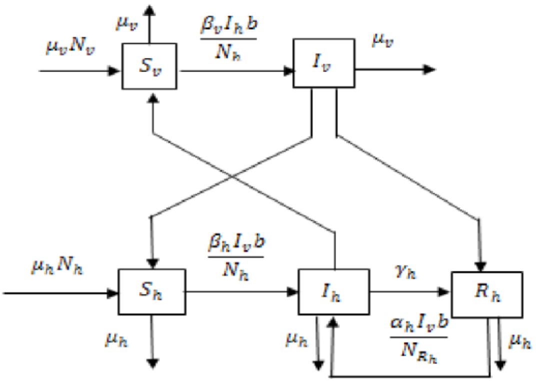

FIGURE 1. SIRI model for dengue fever transmission.

□□*dS*^{h} □ □□ □*hI* $S_{v\,h}$ □□*h hS*
□ *dt*

□□□*dIdth* □□*I Sv h* □□ □*h h vR I*□*h* □□□ □*h* □
h□*Ih*

□□*dRh* □□ □*h hI* □ *h hR* □□ □*h h vR I*
(2)

□ *dt* □*h*

□□*dSdtv* □ □□ □*vvbI Sh v* □□*v vS*
□

□□*dIdt*^{v} □□*vbI*
$S_{h\,v}$ □□*v vI* □

*b*β^h*N*^{v}
where η= ______
.
N_h

The system (2) is a SIRI model for dengue fever trasmission.

3.2. G lobal Stability Analysis of SIRI Model for Dengue Fever Disease

3.2.1. Stability Analysis of SIRI Model for Dengue Fever Disease

The stability of the model towards the balance points obtained is determined by eigen values λ as in Table 1.

The types of stability of the system depend on eigen values with the type of stability shown in Table 1. The eigen value is obtained by determining the matrix of system (2) then substituting the fixed point in the case of disease-free, by Maple 18, the eigen value obtained for the system of equation (2) by Jacobian matrix of system (2) is:

□□□*h* o o o □□□
□ □
□ o□□□ □*h* □ *h*□ o o □ □
*J** □□ 0 □*h* □□ □□$_v$ 0 □
□ *h* □
□□*vb*
□ 0 0 0 □
□ 0 □*vb* 0
□□*v*□
□ □

then det □□*I* □ □*J**□ o mm

TABLE 1. Stability types for equilibrium points

Eigen values λ_i; i = 1,2,...	Stability
Real and all positive	Node unstable
Real and all negative	Asymptotic stable nod
Real and different sign	SaddlePoint
Complex, original imaginer	Center
Complex,λη λ± *i*, > o	Focus and unstable
Complex,λη λ± *i*, < o	Focus and asymptotic stable

(λ μ λ μ λ μ λ μ μ γ λ μ μ γ ηβ+ *h*)(+ *h*)(+ *υ*)(² +($_h$ + +*υh*) +($_υ$ ($_h$ + *h*)− *υb*)=o (3)

The eigen value of model is:

−(µ µ γ*h* + +*υh*)+ (μ*h*)2 −2µµ µγ µ*h υ* +2 *h h* +(*υ*)2 +5γμ γ*h υ* +(*h*)2 +4ηβ*υb*

λ_1 = 2 (4)

−(µ µ γ*h* + +*υh*)+ (μ*h*)2 −2µµ µγ µ*h υ* +2 *h h* +(*υ*)2 +5γμ γ*h υ* +(*h*)2 +4ηβ*υb*

λ_2 = 2 (5)

$\lambda \mu_3 {}^{=-} \; h$ (6) $\lambda \mu_4 = - \; v$ (7)

$\lambda \mu \gamma 5 = -(h + h)$ (8)

3.2.2. Basic Reproduction Number

The basic reproduction number is the expected value of the number of infections per time. This infection occurs in a suspectible population infected by an infected individual.

According to the eigen equation (3) of system (2), the basic reproduction number of the SIRI model for dengue fever transmission is:

$R0 = \underline{\eta\beta v b \qquad}$ (9) $\mu \mu \gamma v (h + h)$

3.3. S imulation of SIRI Model for Dengue Fever Transmission in Free Disease Case

The SIRI model simulation by using Maple with initial and parameter values based on the assumptions is presented in Table 2, with basic reproduction number values obtained based on equation (9), namely:

$\underline{R0 = \eta\beta v b}$
$\mu \mu \gamma v (h +$
$h)$

To determine the critical point, with the substitution of parameter values for diseasefree cases in Table 2, system equation (2) is equaled to zero, then the following system of equations (1) is obtained:

□0.0146□0.0245$I \;\; S_v \; h$ □0.0146S_h □ 0
□□0.0245S_h □0.084$I \;\; R_v \; h$ □0.3266I_h □
0
□□0.312I_h □□0.0146 □0.084$I \; R_v$ □ h □ 0
(10)
□□0.043□0.21$I \; S_{h\,v}$ □0.043S_v □ 0
□□0.21$I \; S_{h\,v}$ □0.043I_v □ 0

TABLE 2. Initial and parameter values of the SIRI model for free disease case

Parameter	**Values $R_o \leq 1$**	**Variable**	**Initial value**

β_h 0.006125
(0) 2500 μ_h
0.0146 (0)
1300 b 10
(0) 800 α_h
0.021 (0)

N_h
S_h
I_h
R_h
N_v
S_v
I_v

400 γ_h 0.312 (0) 1000 μ_v 0.043 (0) 700 β_v 0.021 (0)
300

The system (10) provides equilibrium points of the SIRI model for free disease model are:

$$(S\,I\,R_h, {}_h, {}_h, S_v, I_v)=(0.3085;0.0822;0.7737;0.6895;0.3065)$$

The equilibrium points explain that the number of suspected human populations is 3085 people, infected with dengue fever as many as 822 people, the number of people recovering is 7737 people out of the total 10,000 human population.

Eigen values with parameter in Table 2 of SIRI model for DHF transmission are: $\lambda_1 =-0.0146$, $\lambda_2 =-0.0146$, $\lambda_3 =-0.043$, $\lambda_4 =-0.5682$ and $\lambda_5 =-0.0667$

The values obtained are real and negative, so based on Table 1, then this type of stability at this equilibrium point is asymptotic stable. While the basic reproduction number for dengue fever transmission is , this means that infected individuals cannot transmit to other individuals that cause the disease to disappear from the population or the stage of DHF is disease free disease case.

3.3.1. Simulation Results of SIRI Model for Dengue Fever Transmission in Free Disease Case

The simulation results of the SIRI model of DHF transmission for disease-free cases were obtained by Maple software with the initial values and parameters as in Table 2 shown in Figure 2. The *x*-axis and *y*-axis coordinates represent the time (month) and number of cases for each variables $S\,t\,I_h\,(\ )$, ${}_h\,(t\,R\,t\,S\,t)$, ${}_h\,(\ )$, ${}_v\,(\ )$, and $I_v\,(t)$.

Based on Figure 2, it can be concluded that DHF number cases for infected populations will continue to decline and the disease will disappear in the 12th month, this is caused by the value of R_0 <1, which means that infected individuals cannot transmit the disease to other individuals. Decreasing the number of infected populations also causes suspect populations to continue to increase.

3.4. Simulation of SIRI Model for Dengue Fever Transmission in Endemic Case

The SIRI model simulation by using Maple with initial and parameter values based on the assumptions is presented in Table 3.

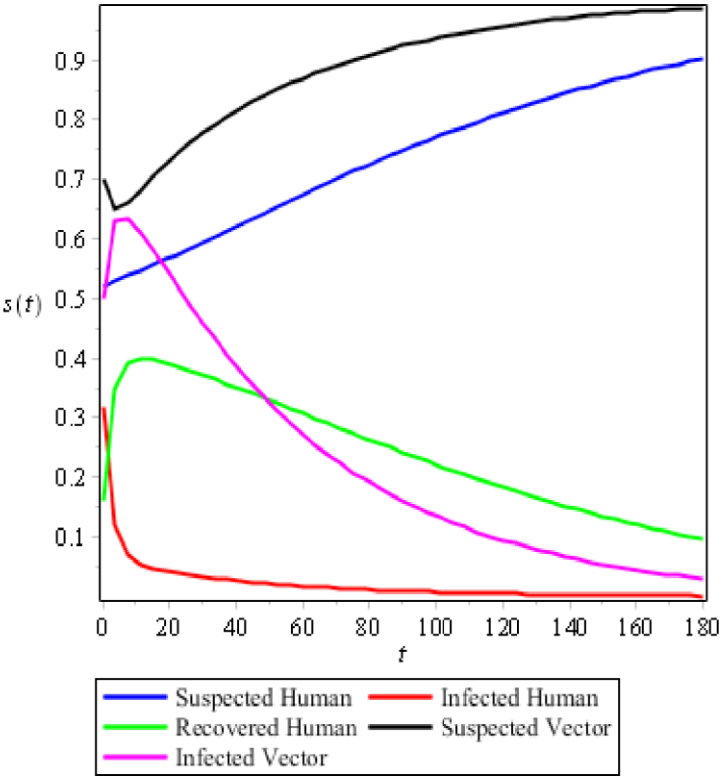

FIGURE 2. Prediction of suspected, infeted, recovered number for free disease case of DHF.

To determine equilibrium point, with the substitution of parameter values for endemic cases in Table 3, system equation (2) is equal to zero, then the following system of equations (11) is obtained: □0.0236□0.312I S_v $_h$ □0.0236S_h □ 0

□□0.312S_h □2.22I R_v $_h$ □0.1796I_h 0□

□□0.156I_h □□0.0236 □2.22I_v □R_h □ 0

(11)

□□0.026 □0.6765I S_h $_v$ □0.026S_v □ 0

□□0.6765I S_h $_v$ □0.026I_v 0□

The equation (11) system provides equlibrium points for SIRI endemic model are:

$(S\,I\,R_{h\,h,,\,h}, S_v, I_v)$=(0.0447;0.7591;0.1962;0.00051;0.9944)

These equilibrium points shown that the number of suspected human populations is 447 people, infected with dengue is 7591 people and the number of recovered is 1962 people out of the total 10,000 human population.

Eigen values with parameter in Table 3 of SIRI model for DHF transmission are:

$\lambda_1=-0.0236$, $\lambda_2=-0.0236$, $\lambda_3=-0.026$, $\lambda_4=-4.9155$ and $\lambda_5=-4.2887$

The values λ obtained are real and negative, so based on Table 1, then this type of stability at this equilibrium point is asymptotic stable. While the basic reproduction number for dengue fever disease is , this means that someone who is infected with DHF will transmit to 31 other people or the stage of DHF is endemic case.

3.4.1. Simulation Results of SIRI Model for DHF in Endemic Case

The simulation results of the SIRI model of DHF transmission for endemic cases were obtained by MAPLE software with the initial values and parameters as in Table 3. The *x*-axis and *y*-axis coordinates represent the time (month) and number of cases for each variables S_h (t , I) $_h$ (t , R) $_h$ (t , S) $_v$ (t ,) and I_v (t .)

Based on Figure 3, it can be concluded that the number of infected cases will increase for the next months because the stage of this cases is endemic (basic reproduction number, $R_0 > 1$). It accordance to the SIRI model for DHF transmission in endemic cases that dengue disease will continue to develop in the population and causing outbreaks.

3.5. Simulation of SIRI Model for Dengue Fever Transmission in Makassar

The SIRI model simulation using Maple with initial and parameter values based on the assumptions is presented in Table 4. To determine equilibrium point, with the substitution of parameter values for endemic cases in Table 4, system equation (2) is equal to zero, and then the following system (12) is obtained:

□0.0046□0.2925$I\ S_{v\ h}$ □0.0046S_h 0□ □□0.2925$I\ S_{v\ h}$
□0.000042$I\ R_{v\,h}$ □0.33433I_h □ 0
□□0.32833I_h □□0.0046 □0.000042I_v□R_h □ 0
(12)
□□0.00323□0.0156$I\ S_{h\,v}$ □0.00323S_v 0□ □□0.0156$I\ S_h$
$_v$ □0.00323I_v 0□

The system (12) provides equlibrium points for SIRI dengue fever transmission in Makassar city, South Sulawesi, Indonesia are:

TABLE 3. Initial values and parameters of SIRI model for endemic case of DHF

N_h
S_h
I_h
R_h
N_v
S_v
I_v

Parameter	**Values $R_0 \le 1$**		**Variable**	
Initial value β_h	0.0052	(0)	2500	μ_h
0.0236 (0)	1300 b 150	(0)	800	α_h
0.037 (0)	400 γ_h 0.156	(0)	1000	μ_v
0.026 (0)	700 β_v 0.451	(0)	300	

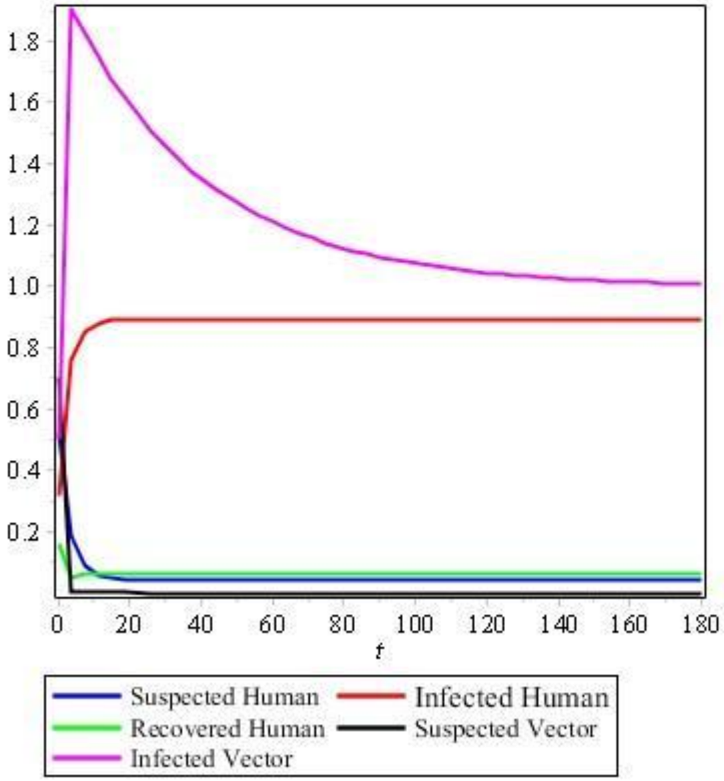

FIGURE 3. Prediction of suspected, infeted, recovered number for endemiccase of DHF.

TABLE 4. Initial and parameter values of SIRI model for dengue fever in Makassar

Variable	Initial value	Source
N_h (0)	1663479	[17]
S_h (0)	1663212	[17]
I_h (0)	135	[17]
R_h (0)	132	[17]
N_v (0)	1000	[16]
S_v (0)	350	[16]
I_v (0)	56	[16]

Parameter	Values $R_0 \leq 1$	Source
β_h	0.20124	KKRI [16]
μh	0.0046	KKRI [16]
b		Assumption
α_h	0.000045	KKRI [16]
γ_h	0.3288	KKRI [16]
μ_v	0.00323	KKRI [16]
β_v	0.0001	KKRI [16]

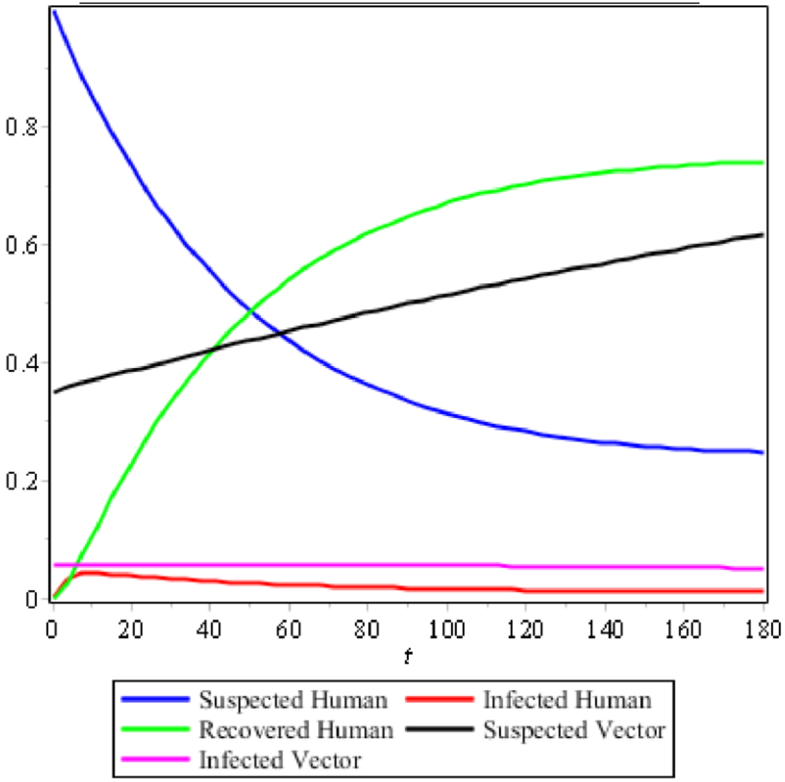

FIGURE 4. Prediction of suspected, infeted, recovered number for DHF in Makassar.

$(S\,I\,R_h, {}_h, {}_h, S_v, I_v)$=(0.4209;0.0046;0.5745;0.1116;0.9784)

These equilibrium points shown that the number of suspected human populations is 420,900 people, infected with dengue is 46,000 people and the number of recovered is 574,500 people out of the total 1,000,000 human population.

Eigen values with parameter values in Table 3 for the SIRI model of DHF transmission are:

$$\lambda_1=-0.0046, \lambda_2=-0.0046, \lambda_3=-0.00323, \lambda_4=-0.587 \text{ and } \lambda_5=-0.0019$$

The values $_\lambda$ obtained are real and negative, so based on Table 1, then this type of stability at this equilibrium point is asymptotic stable. While the basic reproduction number for dengue fever found $R_0 = 0.0272 < 1$, this means that infected individuals cannot transmit to other individuals in Makassar city that cause the disease to disappear from the population or the stage of DHF in Makassar city, South Sulawesi Indonesia is free disease case.

3.5.1. Simulation Results of SIRI Model for Dengue Fever Transmission in Makassar

The simulation results of the SIRI model of DHF transmission in Makassar city were obtained by Maple software with the initial values and parameters as in Table 4 shown in Figure 4. The x-axis and y-axis coordinates represent the time (month) and number of cases for each variables be concluded that DHF number cases for infected populations will continue to decline $S\,t\,I_h(\,)$, $_h$ $(t\;R\;t\;S\;t)$, $_h(\,)$, $_v(\,)$, and $I_v(t)$. Based on Figure 4, it can and the disease will disappear in the 14th month, this is caused by the value of $R_0 < 1$, which means that infected individuals cannot transmit the disease to other individuals in Makassar city that cause the disease to disappear from the population or the stage of DHF in Makassar city is free disease case.

4. Conclusion

The SIRI model for dengue fever transmission have been found, which is a modification of SIR model; analysis of the SIRI model is shown that the equation system in the model is asymptotic stable which means that dengue transmission still continues at a certain time in Makassar city, Indonesia. Whereas, the SIRI simulation model uses Maple, giving an illustration of the number of dengue patients in the following month, both for disease-free and endemic cases. In Makassar City, the prediction of dengue fever will reach its peak in the 14th month, but Makassar City is not endemic for DHF, however early anticipation needs to be done because the cycle of DHF sufferers in Makassar city, Indonesia is very fast from the three-years cycle become fourteen months.

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