

Analysis And Simulation Of SII Model For Diabetes Mellitus

Syafuruddin Side, Muh. Isbar Pratama, M. Kasim Aidid, Wahidah Sanusi

Abstract: In this paper, we construct the SII model for Diabetes Mellitus. New Lyapunov function was developed for analysis of the SII model on Diabetes Mellitus. Lyapunov function was used to prove as a result, disease-free basic reproductive number compilation and endemic diabetes mellitus compilation base replacement number. The model simulation results predict the number of Diabetes Mellitus cases, so that the government can increase and prevent the increase in the number of Diabetes Mellitus sufferers.

Index Terms: Diabetes Mellitus, Lyapunov Function, Model SII, Model simulation.

1. INTRODUCTION

Urban lifestyle with majority of foods contained a high fat, sugar, and salt leads to various diseases including type 2 Diabetes Mellitus (DM). It is interesting to observe that the increasing number of restaurants is followed by the increasing number of type 2 Diabetes Mellitus patients. Diabetes Mellitus is non-infectious disease, environmental factors and climate changes as well as other lifestyles such as lack of physical exercise are also some of the factors of type 2 DM. In addition, DM can also be caused by genetic factors [1]. Mathematical modeling for infectious and non-infectious diseases such as dengue fever, tuberculosis, and hepatitis has been widely studied by many mathematics researchers [2,3,4,5,6,7,8], including the modeling for the DM [9,10,11,12,13,14]. The DM modelling studies work on different models and approaches. [9] employed numerical methods which were Euler and finite difference methods. [10] worked on the delay modelling analysis using functional differential equation. [11] analyzed the DM by SEI model with Routh-Hurwitz Criterion. [13] run the analysis by Small-Perturbation with linearizing at an equilibrium point. Therefore, in the beginning, this paper discuss the modelling of the DM by using SII model, furthermore, we analyzed the existence and the status of DM whether diseases-free or endemic by employing Lyapunov function. Lastly, we simulate the endemic status of the DM with MAPLE software. Hence, this mathematical model offers the solutions to control and to monitor the DM since it provides a simulation of model that can predict the number of DM case then the disease can be prevented and treated beforehand.

2 MATERIAL AND METHOD

This Mathematical modeling of SII for DM is a theoretical study. The SII model for the DM is analyzed by Lyapunov function by [5,8] in order to prove theorems of the existence and the DM status whether disease-free or endemic. The model simulation used MAPLE software to predict the number endemic cases of DM.

- S. Side, M.I. Pratama, W. Sanusi, Department of Mathematics, Universitas Negeri Makassar, Indonesia 90222
 - M. K. Aidid, Department of Statistics, Universitas Negeri Makassar, Indonesia 90222
- Email: syafuruddin@unm.ac.id

3 RESULT

3.1 SII model formulation

The population scheme for the stages of DM patients using

the SII model is presented in Figure 1.

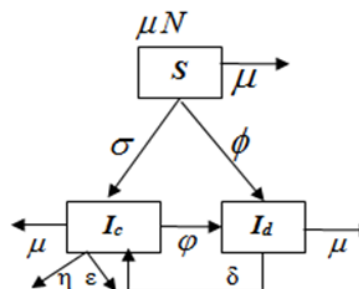


Fig. 1. Population Scheme of SII Model for DM

Figure 1 reformulated into 3-D non-linear differential equations as in the system (1).

$$\begin{cases} \frac{dS}{dt} = \mu N - (\sigma + \phi + \mu)S \\ \frac{dI_d}{dt} = \phi S + \phi I_c - (\mu + \delta)I_d \\ \frac{dI_c}{dt} = \sigma S + \delta I_d - (\mu + \phi + \varepsilon + \eta)I_c \end{cases} \quad (1)$$

with $(N(t) = S(t) + I_d(t) + I_c(t))$

The definition of variables and parameters in the model used for DM disease presented in Table 1.

TABLE 1

. DEFINITION OF VARIABLE/PARAMETER

| Variable/Parameter | Definition |
|--------------------|--|
| N | Number of human population |
| S | Number of Suspected population |
| I_c | Number of DM patients that cause complications with other diseases |
| I_d | Number of DM patients |
| μ | The rate of birth/death population |
| σ | Probably of changing from S to I_c |
| ϕ | Probably of changing from S to I_d |
| φ | Probably of changing from I_c to I_d |
| δ | Probably of changing from I_d to I_c |
| η | The rate of I_c death |
| ε | The rate of I_c disabilities |

3.2 Existence of SII model for DM disease

The DM disease exists if all variables and parameters of the

model are non-negative. It is shown in the system (1), octant non-negative is positive invariant. The existence of the DM disease is provided by Theorem 1.

Theorem 1.

Let is a solution of system (1) with an initial condition and a compact set

$$D = \{(S, I_d, I_c) \in R_+^3, L \leq N\} \tag{2}$$

for a model in system (1), D is a positive invariant set covering all solutions in R_+^3 .

Proof:

An elegant constructed Lyapunov function

$$L(t) = S + I_d + I_c \tag{3}$$

Differentiating equation (3), we obtain

$$\begin{aligned} L'(t) &= \dot{S} + \dot{I}_d + \dot{I}_c \\ &= (\mu N - (\sigma + \phi + \mu)S) + (\phi S + \phi I_c - (\mu + \delta)I_d) + (\sigma S + \delta I_d - (\mu + \phi + \varepsilon + \eta)I_c) \\ &= \mu N - \sigma S - \phi S - \mu S + \phi S + \phi I_c - \mu I_d - \delta I_d + \sigma S + \delta I_d - \mu I_c - \phi I_c - \varepsilon I_c - \eta I_c \\ &= \mu N - \mu(S + I_d + I_c) - (\varepsilon + \eta)I_c \\ &= \mu N - \mu(L) - (\varepsilon + \eta)I_c \end{aligned}$$

Since $L \geq N$ then

$$\frac{dL}{dt} = \mu N - \mu(S + I_d + I_c) - (\varepsilon + \eta)I_c \leq 0 \tag{4}$$

with $L(0)$ is an initial condition of $L(t)$ then $t \rightarrow \infty, 0 \leq L(t) \leq N$. Thus, concluded that D is a positive invariant set covering all solutions in . The theorem 1 has been proven. Theorem 1 guarantees the existence of the DM disease in an area that was originally not found the DM patients then changed after the suspected DM, $S(t) > 0$, DM patients, $I_d(t) > 0$, and DM patients that cause complications with other diseases, $I_c(t) > 0$. This theorem also indicates that it needs a further investigation on the step of the DM spread in order to identify the DM status whether disease-free or endemic in an area by using SII model.

3.3 Global Stability Analysis

SII Model for Diabetes Mellitus on system (1) is a system of 3D non-linear ordinary differential equation. The model can be simplified by assuming the fractions:

$$x(t) = \frac{S}{N}, y(t) = \frac{I_d}{N}, z(t) = \frac{I_c}{N}$$

Based on the assumption, the SII model for DM simplified as the system (5).

$$\begin{cases} \frac{dx}{dt} = \mu - (\sigma + \phi + \mu)x \\ \frac{dy}{dt} = \phi x + \phi z - (\mu + \delta)y \\ \frac{dz}{dt} = \sigma x + \delta y - (\mu + \phi + \varepsilon + \eta)z \end{cases} \tag{5}$$

System (5) is a mathematical model for DM as a system of 3D non-linear differential equation. SII Model then simplified in Jacobian Matrix to get the eigen value λ .

$$0 = |A - \lambda I|$$

$$0 = \begin{vmatrix} -(\sigma + \phi + \mu + \lambda) & 0 & 0 \\ \phi & -(\mu + \delta + \lambda) & \phi \\ \sigma & \delta & -(\mu + \phi + \varepsilon + \eta + \lambda) \end{vmatrix} \tag{6}$$

Eigen value of SII model for DM as follows:

$$\lambda_1 = -(\sigma + \phi + \mu) \tag{7}$$

$$\begin{aligned} \lambda_2 &= \\ &= -\mu - \frac{1}{2}(\delta + \phi + \varepsilon + \eta) + \\ &= \frac{1}{2}\sqrt{\delta^2 + 2\delta(\phi - \varepsilon - \eta) + \phi^2 + 2\phi(\varepsilon + \eta) + \varepsilon^2 + 2\varepsilon\eta + \eta^2} \tag{8} \\ \lambda_2 &= \end{aligned}$$

$$-\mu - \frac{1}{2}(\delta + \phi + \varepsilon + \eta) - \frac{1}{2}\sqrt{\delta^2 + 2\delta(\phi - \varepsilon - \eta) + \phi^2 + 2\phi(\varepsilon + \eta) + \varepsilon^2 + 2\varepsilon\eta + \eta^2} \tag{9}$$

Basic reproduction number (R_0) in system (5) is obtained by Diekmann and Heesterbeek Method (2000).

$$R_0 = \frac{\delta\phi}{(\mu + \delta)(\mu + \phi + \varepsilon + \eta)} \tag{10}$$

3.4 Global stability of equilibrium of model SII for disease-free

System (1) has equilibrium of disease-free ($S^*, I_d^*, I_c^* = (N, 0, 0)$) which means that the disease will disappear. Theorem 2 explain the global stability of equilibrium condition of disease-free for system (1).

Theorem 2.

If $R_0 \leq 1$ then the equilibrium of disease-free P^* of model SII is a global stage where the stable asymptotic at D.

Proof.

Suppose that a proposed Lyapunov function

$$W(t) = (S - S^* \ln S) + I_d + I_c \tag{11}$$

Differentiating equation (11) by time obtains equation (12)

$$W'(t) = \dot{S} \left(1 - \frac{S^*}{S}\right) + \dot{I}_d + \dot{I}_c = (\mu N - \sigma S - \phi S - \mu S) \left(1 - \frac{S^*}{S}\right) + (\phi S + \phi I_c - \mu I_d - \delta I_d) + (\sigma S + \delta I_d - \mu I_c - \phi I_c - \varepsilon I_c - \eta I_c)$$

$$\begin{aligned} &= \mu N \left(1 - \frac{S^*}{S}\right) - \sigma S \left(1 - \frac{S^*}{S}\right) - \phi S \left(1 - \frac{S^*}{S}\right) - \mu S \left(1 - \frac{S^*}{S}\right) + \phi S + \phi I_c - \mu I_d - \delta I_d + \sigma S + \delta I_d - \mu I_c - \phi I_c - \varepsilon I_c - \eta I_c \\ &= \mu N \left(1 - \frac{S^*}{S}\right) - \sigma S + \sigma S^* - \phi S + \phi S^* + \mu S^* \left(1 - \frac{S}{S^*}\right) + \phi S - \mu I_d + \sigma S - \mu I_c - \varepsilon I_c - \eta I_c \\ &= \mu N \left(1 - \frac{S^*}{S}\right) + \mu S^* \left(1 - \frac{S}{S^*}\right) + (\sigma + \phi)S^* - \mu I_d - (\mu + \varepsilon + \eta)I_c \end{aligned} \tag{12}$$

In free-disease cases $\sigma \rightarrow 0, \phi \rightarrow 0$ and $S^* = N$, then the equation (12) can be simplified:

$$\begin{aligned} W(t) &= \mu N \left(1 - \frac{S^*}{S}\right) + \mu N \left(1 - \frac{S}{S^*}\right) - \mu I_d - (\mu + \varepsilon + \eta)I_c \\ &= \mu N \left(2 - \frac{S^*}{S} - \frac{S}{S^*}\right) - \mu I_d - (\mu + \varepsilon + \eta)I_c \\ &= -\mu N \frac{(S - S^*)^2}{SS^*} - \mu I_d - (\mu + \varepsilon + \eta)I_c \end{aligned} \tag{13}$$

Equation (13) shows that $W(t) \leq 0$. By using advanced Lyapunov function rule [5], the finite set for all solutions is in the largest invariant set with $S = S^*$, is a singleton set $\{S^*, I_d^*, I_c^*\}$. It means that the equilibrium of disease-free is a global stage with has stable asymptotic at D. Theorem 2 has been proven.

Global stability of disease-free theorem of model SII explains one stage that DM case exists, described in theorem 1. However, it does not describe whether it can influence from one person to another. Theorem 2 states that if $R_0 \leq 1$ then one person who is DM patient will not influence to others. It means that the DM can be controlled and it is not worrisome.

3.5 Global stability of equilibrium of endemic SII model

SII Model at system (1) has an equilibrium point $P^* = (S^{**}, I_d^{**}, I_c^{**}) \in D$ called an endemic equilibrium point and satisfies $S^{**} > 0, I_d^{**} > 0, I_c^{**} > 0$ with:

$$S^{**} = \frac{\mu}{\sigma + \phi + \mu} \tag{14}$$

$$I_d^{**} = \frac{\mu(\sigma\phi + \phi\mu + \phi\phi + \phi\varepsilon + \phi\eta)}{(\sigma + \phi + \mu)(\mu(\mu + \delta + \phi + \varepsilon + \eta) + \delta\varepsilon + \delta\eta)} \tag{15}$$

$$I_c^{**} = \frac{\mu(\sigma\mu + \sigma\delta + \phi\delta)}{(\sigma + \phi + \mu)(\mu(\mu + \delta + \phi + \varepsilon + \eta) + \delta\varepsilon + \delta\eta)} \tag{16}$$

Theorem 3 provides the endemic equilibrium global of system (1)

Theorem 3

If $R_0 > 1$, then equilibrium of the disease is in the positive endemic stage, system (1) exists, and the global stage with stable asymptotic at D.

Proof.

Let condition:

$$\begin{cases} \mu N \geq (\mu + \phi + \sigma)S \\ \phi S \geq (\mu + \delta)I_d \\ \sigma S \geq (\mu + \varepsilon + \eta + \varphi)I_c \end{cases} \quad (17)$$

Let a proposed Lyapunov function is

$$V(t) = (S - S^{**} \ln S) + (I_d - I_d^{**} \ln I_d) + (I_c - I_c^{**} \ln I_c) \quad (18)$$

Differentiating equation (18) by the time obtains equation (19).

$$\begin{aligned} \dot{V}(t) &= (\mu N - \sigma S - \phi S - \mu S) \left(1 - \frac{S^{**}}{S}\right) + (\phi S + \varphi I_c - \mu I_d - \delta I_d) \left(1 - \frac{I_d^{**}}{I_d}\right) + (\sigma S + \delta I_d - \mu I_c - \varphi I_c - \eta I_c) \left(1 - \frac{I_c^{**}}{I_c}\right) \\ &= (\mu + \phi + \sigma)S^{**} + (\mu + \delta)I_d^{**} + (\mu + \varepsilon + \eta + \varphi)I_c^{**} - \mu N \left(\frac{S^{**}}{S}\right) - \phi I_c \left(\frac{I_d^{**}}{I_d}\right) - \phi S \left(\frac{I_d^{**}}{I_d}\right) - \delta I_d \left(\frac{I_c^{**}}{I_c}\right) - \sigma S \left(\frac{I_c^{**}}{I_c}\right) - \mu I_d - \mu I_c - \mu S + \mu N - \eta I_c - \varepsilon I_c \\ &= (\mu N - \mu(S + I_d + I_c)) + ((\mu + \phi + \sigma)S - \mu N) \left(\frac{S^{**}}{S}\right) + ((\mu + \delta)I_d - \phi S) \left(\frac{I_d^{**}}{I_d}\right) + ((\mu + \varepsilon + \eta + \varphi)I_c - \sigma S) \left(\frac{I_c^{**}}{I_c}\right) - \phi I_c \left(\frac{I_d^{**}}{I_d}\right) - \delta I_d \left(\frac{I_c^{**}}{I_c}\right) - \mu I_d - \mu I_c - \eta I_c - \varepsilon I_c \end{aligned} \quad (19)$$

Substituting the value in condition (17) to equation (19) gets:

$$\begin{aligned} \dot{V}(t) &= ((\mu + \phi + \sigma)S - \mu N) \left(\frac{S^{**}}{S}\right) + ((\mu + \delta)I_d - \phi S) \left(\frac{I_d^{**}}{I_d}\right) + ((\mu + \varepsilon + \eta + \varphi)I_c - \sigma S) \left(\frac{I_c^{**}}{I_c}\right) - \phi I_c \left(\frac{I_d^{**}}{I_d}\right) - \delta I_d \left(\frac{I_c^{**}}{I_c}\right) - \mu I_d - \mu I_c - \eta I_c - \varepsilon I_c \leq 0 \end{aligned} \quad (20)$$

Equation (20) shows that $\dot{V}(t) \leq 0$ for all $S(t), I_d(t), I_c(t) \in D$ and $\dot{V}(t) = 0$, and satisfies for $S = S^*, I_d = I_d^*, I_c = I_c^*$. The equilibrium of system (5) includes in

$$L = \{(S(t), I_d(t), I_c(t)), S = S^*, I_d = I_d^*, \text{ and } I_c = I_c^*\}.$$

Furthermore, by the stability of asymptotic theorem [8], a positive endemic equilibrium P^* is in the global stage with stable asymptotic at D. Theorem 3 has been proven.

Global Stability Theorem of SII model on this stage states that if one person DM patient with $R_0 > 1$ then, the person will affect more than one person. It shows that the DM disease in this stage is endemic since it cannot be controlled and it is dangerous for people around the area.

3.6 SII model simulation for Diabetes Mellitus

In simulating the model, we used MAPLE software. The initial values $S(0), I_d(0),$ and $I_c(0)$ and the parameters of the model based on assumption R_0 , obtained from equation (10)

$$R_0 = \frac{\delta \phi}{(\mu + \delta)(\mu + \varphi + \varepsilon + \eta)}.$$

The value of equilibrium points of SII model is determined by substituting the parameter values for simulation 1 of an endemic case in Table 2 on system (1) which equal zero. We obtain the following system (21):

$$\begin{cases} 0.315 - 0.642S = 0 \\ 0.323S + 0.224I_c - 1.076I_d = 0 \\ 0.004S + 0.761I_d - 0.776I_c = 0 \end{cases} \quad (21)$$

System (21) provides equilibrium points of endemic SII model:

$$(S, I_d, I_c) = (0.4907, 0.1857, 0.1847)$$

These equilibrium points reveal that the number of suspected human are 4907 people, DM patients are 1857 people, the number of DM patients that cause complications with other diseases are 1847 out of 10,000. The Eigen values based on equations (7), (8) and (9) with parameter values on Table 2 for SII model of the DM are:

$$\lambda_1 = -0.642, \lambda_2 = -0.258, \lambda_3 = -0.148$$

The values λ are real and negative. Based on [2], this stability equilibrium is called asymptotic stability. In addition, the basic reproduction number for free-disease DM case is $R_0 = 0.2042$. It indicates that one person wouldn't affect for another person. Similar with simulation 1, the values of equilibrium points, eigen values, and R_0 value for simulation 2 and 3 based on parameter in Table 1 are shown in Table 3. All Eigen values in simulation 2 and 3 also are real and negative, then it is also called asymptotic stability. The value R_0 in simulation 2 and 3 are $R_0 < 1$, it means, state that one person wouldn't affect for another person

TABLE 2.

INITIAL VALUES AND PARAMETERS OF SII MODEL

| Parameter | Value (Simulation 1) | Value (Simulation 2) | Value (Simulation 3) | Variable | Initial value |
|---------------|----------------------|----------------------|----------------------|----------|---------------|
| μ | 0.315 | 0.615 | 0.515 | $N(0)$ | 5000 |
| σ | 0.004 | 0.602 | 0.304 | $S(0)$ | 3500 |
| ϕ | 0.323 | 0.253 | 0.453 | $I_c(0)$ | 1000 |
| φ | 0.224 | 0.324 | 0.124 | $I_d(0)$ | 500 |
| δ | 0.761 | 0.261 | 0.861 | | |
| ε | 0.032 | 0.232 | 0.432 | | |
| η | 0.205 | 0.105 | 0.105 | | |

TABLE 3.

THE VALUES OF EQUIBRIUM POINTS, EIGEN VALUES AND R_0

| | S^* | I_d^* | I_c^* | λ_1 | λ_2 | λ_3 | R_0 |
|----------------|--------|---------|---------|-------------|-------------|-------------|--------|
| Simulation n 1 | 0.4907 | 0.1857 | 0.1847 | - | - | - | 0.2042 |
| | 7 | 7 | 7 | 0.642 | 0.258 | 1.4 | 2 |
| | | | | 2 | 8 | 8 | |
| Simulation n 2 | 0.4184 | 0.2022 | 0.2215 | -1.47 | - | - | 0.075 |
| | 4 | 8 | 5 | | 0.65 | 1.6 | 7 |
| | | | | | 8 | 8 | |
| Simulation n 3 | 0.4049 | 0.1522 | 0.2165 | - | - | - | 0.066 |
| | 9 | 8 | 5 | 1.27 | 0.65 | 2.1 | 0 |
| | | | | 2 | 8 | 8 | |

According to the eigen values in Table 3, all the eigen values are real negative, that means, stability of the SII model for DM is asymptotic stable represent in Figure 2 until Figure 4.

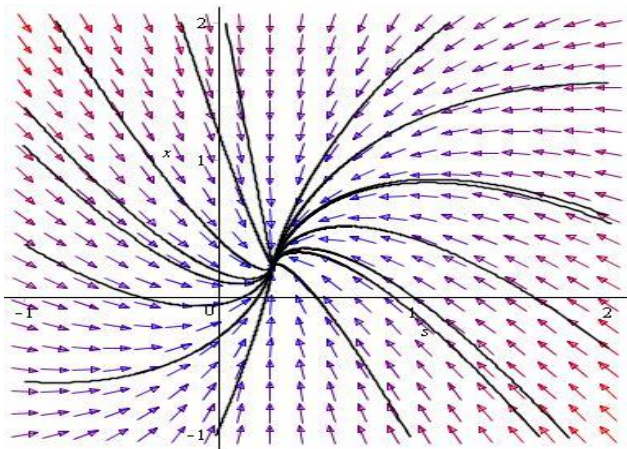


Fig. 2. SII model Stability DM of simulation 1

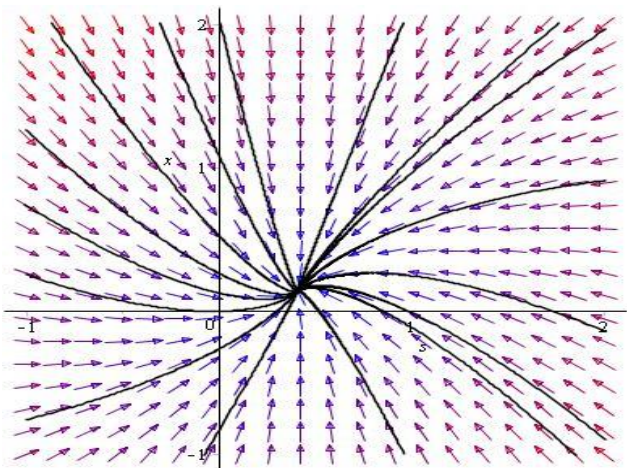


Fig. 3. SII model Stability DM of simulation 2

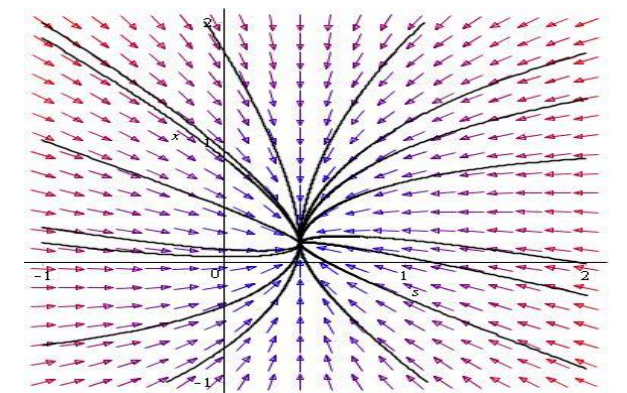


Fig. 4. SII model Stability DM of simulation 3

Simulation results of SII model for the DM disease with MAPLE using initial and parameters values data in Table 1 are shown in Figure 5 until Figure 7. The x-axis and y-axis represent the time (in month) and each variables $S(t)$, $I_d(t)$, and $I_c(t)$

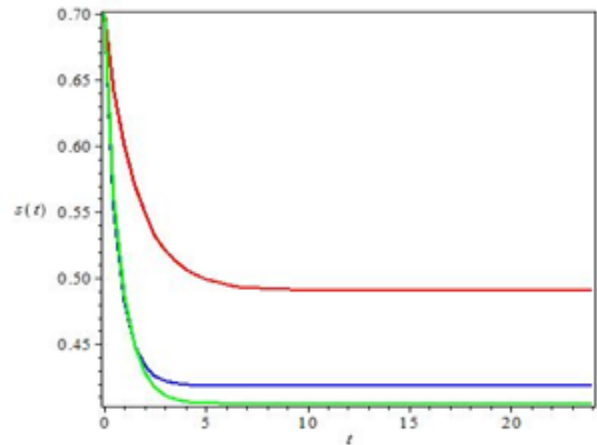


Fig. 5. The number of suspected DM for free disease cases with different R_0

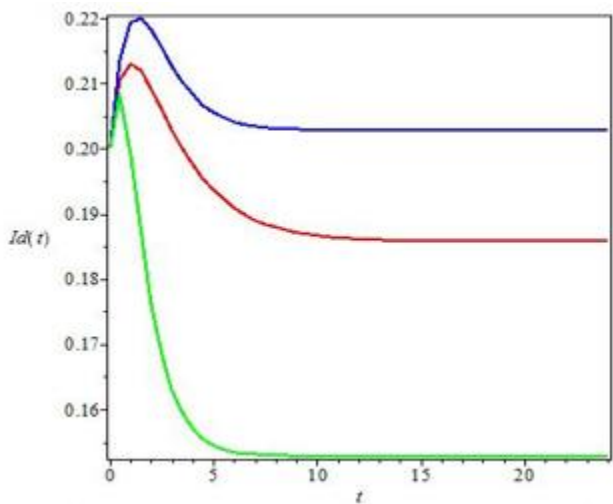


Fig. 6. The number of DM patients for endemic DM free disease cases with different R_0

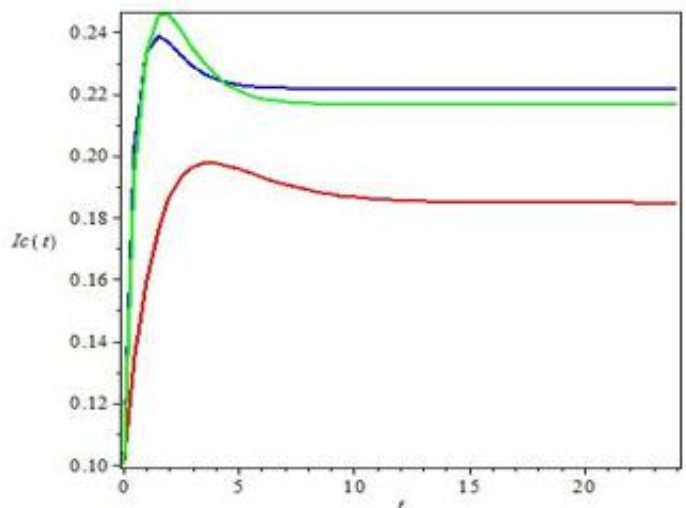


Fig. 7. The number of DM patients that cause complications with other diseases for free disease cases with different R_0

Based on Figure 5, it can be explained that the suspected population graph continues to decrease until it reaches

stability at the equilibrium point for each simulation. Figure 6 and Figure 7 shown that the basic reproduction number, $R_0 < 1$, it indicates, the movement of population status from suspected to DM patients and DM patients that cause complications with other diseases is slower. It can also be found in simulation 1 that the time needed to reach the equilibrium point is 3 months, whereas in simulations 2 and 3 the higher R_0 reaches the balance point faster, 5 and 4 months. Furthermore, the number of cases of DM for DM patients and DM patients that cause complications with other disease populations will peak in a very short time, 4 and 3 months, then continue to decline. The results show that the SII model for free disease DM cases requires very short time to reduce the number of DM patients and the number of DM patients that causes complications with other diseases is faster to reach the peak, then continues to decline. This shows that the number of DM patients can still be overcome.

4. DISCUSSION

Mathematical model for Diabetes Mellitus performed by [10] used a model with delay differential equation and simulated in real life. In addition, [9] found a DM model using nonlinear equations by dividing the population into non-complicated (C) and with complicated (D). She used finite-difference method to predict the number of complicated DM case and Euler method which cannot predict the number of complicated DM case. Furthermore, [11] developed a DM model using SEI model to predict the number of DM case without genetic factor. This study derived the model of DM using SII model. It also produced a theorem to prove the existence of suspected population and DM patients (Theorem 1). It also found a theorem to describe a status stage which explain that DM patients will not influence to others (Theorem 2). It indicates that the DM disease can be controlled and it is not a worrisome case. Furthermore, another theorem using SII model formulated is the endemic status theorem (Theorem 3). It describe that one DM patients will affect to more than one another person. In this case, the DM is no longer can be controlled and classified as an Extraordinary cases that will harm human population. The simulation result of SII model using MAPLE for free-disease cases provide information and prediction of the number of DM case. So that this model is expected to help improve the strategy of controlling the number of DM cases.

5. CONCLUSION

Mathematical model for DM disease is obtained by employing SII model. The analysis of the model guarantees the existence of the DM case and also the status of DM whether disease-free or endemic. The simulation result of the model on free-disease case giving a prediction of the number of DM patients and DM patients that cause complications with other diseases. Therefore, it can be controlled in order to prevent the DM disease in an area.

REFERENCES

- [1]. Rachmat F S, Indonesia semakin manis. <http://makassar.tribunnews.com>. 2015 [Access 22 January 2017]
- [2]. Boutayeb A and Chetouani A, A critical review of mathematical models and data used in diabetology. *BioMedical Engineering OnLine*. 5:43. (2006)
- [3]. Dontwi I. K, W. Obeng D, E.A Andam & L. Obiri A. A

- mathematical model to predict prevalence and transmission dynamics of TB in amansie west district, Ghana. *British Journal of Mathematics & Computer Science*. Vol 4(3): 402-4025. (2014)
- [4]. Idianto, Bayu & Nilamsari K. Analisis kestabilan local model dinamika penularan tuberculosis satu strain dengan terapi dan efektivitas Chemoprophylaxis. *Buletin Ilmiah Mat. Stat. dan Terapannya*. Vol 02(3), hal 173-182. (2013).
- [5]. Side, S., Sanusi, W., Aidid, M.K., Sidjara, S. Global Stability of SIR and SEIR Model for Tuberculosis Disease Transmission with Lyapunov Function Method. *Asian Journal of Applied Sciences*; Vol 9(3): 87-96. (2016).
- [6]. Side, S., Irwan, Mulbar, U., Sanusi, W., SEIR model simulation for Hepatitis B . *AIP Conference Proceedings*. Vol 1830, 020004. (2017).
- [7]. Side S., A Susceptible-Infected-Recovered Model and Simulation for Transmission of Tuberculosis. *Advanced Science Letters*. Vol 21 (2):137-139. (2015).
- [8]. Syafruddin S. et. al. Lyapunov functions of SIR and SEIR model for transmission of dengue fever disease. *International Journal Simulation & Process Modeling*. Vol 8(2,3):177-184. (2013)
- [9]. Aminah E and Lina A, Model Non Linear Penyakit Diabetes. *Jurnal Matematika Murni dan Terapan*. Vol.5(1):1-11. (2011).
- [10]. Athena M and Iordanis K, Delay differential equation models in diabetes modelling. (2011) [Access, 25 January, 2017]
- [11]. N. Ardiansah dan M. Kharis, Model Matematika Untuk Penyakit Diabetes Tanpa Faktor Genetik. *Jurnal MIPA*. Vol. 35 (1). (2012).
- [12]. S. Javeed, A. Ahmed, M.S. Khan, M. A. Javed, Stability Analysis and Solutions of Dynamical Models for Dengue Punjab University Journal of Mathematics. Vol. 50(2). pp. 45-67. (2018).
- [13]. Yesenia C R, Mathematical Model for Detecting Diabetes. *Proceedings of The National Conference On Undergraduate Research (NCUR)*. (2009).
- [14]. Hailay Weldegiorgis Berhe, et al. Parameter Estimation and Sensitivity Analysis of Dysentery Diarrhea Epidemic Model. *Journal of Applied Mathematics*. Vol (2019). (2019).