

Mathematics Modeling Of Diabetes Mellitus Type $SEIIT_T$ By Considering Treatment and Genetic Factors

Asmaidi^{a,1}, Eka Dodi Suryanto^{b,2}

^a Polytechnic of South Aceh, Merdeka Street, Komplek Reklamasi Pantai, Tapaktuan city, 23751, Indonesia

^b Polytechnic of South Aceh, Merdeka Street, Komplek Reklamasi Pantai, Tapaktuan city, 23751, Indonesia
¹ asmedmat@gmail.com; ² ekadodipoltas@gmail.com

ARTICLE INFO

Article history:

Received

Revised

Accepted

Keywords:

Diabetes mellitus

Mathematical models

Fixed points stability

Treatment

Genetics

ABSTRACT

$SEIIT_T$ stands for Susceptible (S), Exposed (E), Infected population untreated (I) and Infected population treated (I_T). Infected groups consisted in two categories, untreated (I) and with treatment (I_T) by presented to insulin. Susceptible shifted to exposed by gene. Preferred outcomes are mathematical models for diabetes mellitus type $SEIIT_T$, conventional type, determining breakpoint and basic reproduction number, breakpoint analysis, breakpoint stability simulation. The results were mathematical models or diabetes mellitus compartment charts/diagrams. These diagram were both analysed analitically and numerically. The analyses presented two fixed points, with disease and without disease. Each point was analysed by its basic reproduction number, analitically and numerically, at fixed points without disease $R_0 < 1$, while the other $R_0 > 1$. Human population at condition $R_0 < 1$ tent to move from susceptibel from the initial standpoint and becomes stabilized at $s = 0.9999$. Proportion of exposed (e) is diminishing from the starting point and stabilized at $e = 0$. Infected untreated dimished from the initial stage and stabilized at $i = 0$. Infected with treatment (i_T) was increased from initial point, diminished and stabilized at $i_T = 0$. Human behavior when $R_0 > 1$, susceptible (s) increased at the beginning then fluctuated, stabilized finally at $s = 0.54711$. Exposed (e) lower at first then stabilized at $e = 0.05655$. Untreated infected group (i) lower from initial then stabilized when $i = 0.00393$. Treatment group (i_T) initiate an increasing value, then fluctuated and stabilized at $i_T = 0.39241$.

I. Introduction

A. Background

Julia Ulfah et al in 2014 developed a mathematical modeling of type SEIIT diabetes mellitus that considered the treatment factor. $SEIIT_T$ stands for *susceptible* (S), *exposed* (E) and *infected* (I). Infected population was divided into two, ie infected population without treatment (I) and infected population with treatment (I_T). Furthermore, the SEIIT type mathematical model was further developed by involving genetic factors. This assumption is taken from the research of Abrahan and San Rikardus in 2015. In his research population susceptible move into population exposed due to the influence of genetic factors.

In the mathematical model of diabetes mellitus type $SEIIT_T$ developed will be determined fixed point and basic reproduction number. Furthermore, stability analysis of fixed points based on basic reproduction number obtained and simulation of fixed point stability. In addition, a simulation of the effect of treatment and genetic factors on people with diabetes mellitus. It is expected that mathematical modeling of diabetes mellitus disease can describe the behavior of the population, so the precautions and control of the disease can be done optimally.

B. Research Objectives

This research aims to,

- 1) How to create a mathematical model of diabetes mellitus type SEIIT taking into account the treatment and genetic factors?
- 2) How to determine the fixed point and basic reproduction number of SEIIT type mathematical modeling by considering treatment and genetic factors?
- 3) How to analyze the stability of a fixed point mathematical modeling taking into account the type SEIIT care and genetic factors?
- 4) How to simulate the stability of a fixed point mathematical modeling taking into account the type SEIIT care and genetic factors?

II. Literature Review

A. Linear-age

For a nonlinear differential equations system, the Taylor expansion runs around the fixed point, as sample given:

$$\dot{\bar{x}} = J\bar{x} + \varphi(\bar{x}), \quad (1)$$

by J is Jacobi matrix,

$$J = \frac{\partial f(x)}{\partial x} \Big|_{x=\bar{x}} = \begin{bmatrix} \frac{\partial f_1}{\partial x_1} & \frac{\partial f_1}{\partial x_2} & \dots & \frac{\partial f_1}{\partial x_n} \\ \frac{\partial f_2}{\partial x_1} & \frac{\partial f_2}{\partial x_2} & \dots & \frac{\partial f_2}{\partial x_n} \\ \vdots & \vdots & \ddots & \vdots \\ \frac{\partial f_n}{\partial x_1} & \frac{\partial f_n}{\partial x_2} & \dots & \frac{\partial f_n}{\partial x_n} \end{bmatrix} \quad (2)$$

and $\varphi(x)$ is high-tiered where $\lim_{x \rightarrow 0} \varphi(x) = 0$.

B. Fixed-point and Stability

1) Fixed-point

Point \bar{x} is fixed when $f(\bar{x}) = 0$ [2].

2) Fixed-point Stability

The trait of fixed-point stability are:

a) Stabilized, when

- Each real eigenvalue is negative: $\lambda_i < 0$ for each i , or
- Complex eigenvalues of parts $\text{Re}(\lambda_i) < 0$ for each i .

b) Unstable, when

- There is at least one positive real eigen value: $\lambda_i > 0$.
- There is at least one complex eigenvalue with $\text{Re}(\lambda_i) > 0$, [2].

C. Routh-Hurwitz Requisition

Given the characteristic equation:

$$\lambda^k + a_1\lambda^{k-1} + a_2\lambda^{k-2} + \dots + a_k = 0 \quad (3)$$

by,

$$H_1 = [a_1], H_2 = \begin{bmatrix} a_1 & 1 \\ a_2 & a_1 \end{bmatrix}, H_3 = \begin{bmatrix} a_1 & 1 & 0 \\ a_2 & a_1 & a_1 \\ a_3 & a_2 & a_2 \end{bmatrix}, \dots$$

$$H_j = \begin{bmatrix} a_1 & 1 & 0 & 0 & \dots & 0 \\ a_2 & a_2 & a_1 & 1 & \dots & 0 \\ a_3 & a_4 & a_3 & a_2 & \dots & 0 \\ \vdots & \vdots & \vdots & \vdots & \ddots & \vdots \\ a_{2j-1} & a_{2j-2} & a_{2j-3} & a_{2j-4} & \dots & a_k \end{bmatrix}, \dots$$

$$H_k = \begin{bmatrix} a_1 & 1 & 0 & \dots & 0 \\ a_2 & a_2 & a_1 & \dots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \dots & \dots & a_k \end{bmatrix}$$

Terms of each element (l,m) on matrix H_j are:

$$h_{lm} = \begin{cases} a_{2l-m}, & \text{untuk } 0 < 2l - m < k \\ 1, & \text{untuk } 2l = m \\ 0, & \text{untuk } 2l < m \text{ atau } 2l > k + m \end{cases} \tag{4}$$

Fixed-point \bar{x} is stable if and only if $\det H_j > 0$, for each $j = 1, 2, \dots, k$. by Routh-Hurwitz Requisition for $k = 2, 3$, dan 4 , that:

$k = 2: a_1 > 0, a_2 > 0$
 $k = 3: a_1 > 0, a_2 > 0, a_1 a_2 > a_3$
 $k = 4: a_1 > 0, a_2 > 0, a_4 > 0, a_1 a_2 a_3 > a_3^2 + a_1^2 a_4$. [2]

D. Basic Reproduction Numbers (\mathcal{R}_0)

The basic reproduction number is the expected value of the many vulnerable populations that become infected during the infection [5]. Possible conditions for \mathcal{R}_0 are:

- a) If $\mathcal{R}_0 < 1$, then the average individual infected will infect less than one new individual, so the disease will not spread.
- b) If $\mathcal{R}_0 > 1$, then the average individual infected will infect more than one new individual, so the disease will spread.

The reproduction number is determined by using the next generation matrix G . The next generation matrix G has two parts; F and V^{-1} defined:

$$G = FV^{-1} \tag{5}$$

with

$$F = \frac{\partial F_i}{\partial x_j}(x_0) \text{ dan } V = \frac{\partial V_i}{\partial x_j}(x_0), [3].$$

where F is a new infection rate matrix, while V is the individual shift-rate matrix which are evaluated at a fixed point (x_0) . To [3], \mathcal{R}_0 is the dominant eigen value of the matrix $G = FV^{-1}$.

III. Research Methods

A. Mathematical Modeling Tipe SEI_T

The researchers developed a mathematical model of type SEI_T diabetes mellitus by considering treatment factors [6] and genetic factors [1].

The assumptions used in the modeling are,

- 1) The birth rate is only in the susceptible population.
- 2) There is a natural mortality rate in each population.
- 3) There mortality rate for diseases both in the infected population are receiving treatment or not.
- 4) All parameters are positive.

Mathematical modeling of diabetes mellitus disease discussed in this study is illustrated as Figure 1 below:

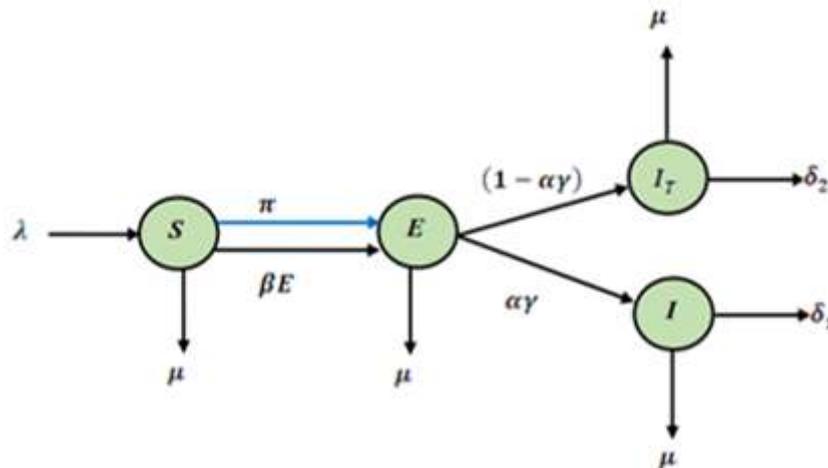


Figure 1. Mathematical Modeling of Type $SEII_T$ with Treatment and Genetic Factors

B. Research conduct

The research was done as follow:

1) Modelling

Treatment and genetic parameters were obtained from the study [6] and the study [1]. From both models, a mathematical model for the spread of diabetes mellitus type $SEII_T$ was developed.

2) Fixed Point Determination Stage

Fixed point without disease and fixed point of disease is obtained by making the rate equation changes each population to time laps equals to zero. For fixed point case without disease, population proportion *infected* and *exposed* has zero value.

3) Determination of Basic Reproduction Numbers

The next generation matrix G is used to determine the value of the basic reproduction number.

4) Analysis of Fixed Points Stability

The stability of the fixed point is done by aligning the *exposed* and *infected* populations, then obtained the matrix *Jacobi*. The fixed point is substituted into the matrix *Jacobi* to find the *eigen* value. The eigenvalues were analyzed using *Routh-Hurwitz requisition*.

5) Fixed Point Stability Simulation

The simulation was analyzed and described to obtain the dynamics of population behavior in the model and to see the effect of treatment and genetic factors on people with diabetes mellitus.

C. Data and Data Sources

The data used are secondary data sourced from references such as journals and books related to the mathematical modeling of diabetes mellitus disease.

D. Notasi

λ	=	Birth rate
μ	=	Mortality rate by nature
δ_1	=	Mortality rate by illness to <i>infected</i> untreated population
δ_2	=	Mortality rate by illness to <i>infected</i> treated population
π	=	Population-shift rate <i>susceptible</i> to <i>exposed</i> by genetical factor
β	=	Population-shift rate <i>susceptible</i> to <i>exposed</i> by invective contact among population
α	=	Population-shift rate <i>exposed</i> to <i>infected</i> untreated

IV. Results and Discussion

A. Differential Equations System

Based on the compartment diagram in Figure 1 we get a system of differential equations,

$$\begin{aligned}\frac{dS}{dt} &= \lambda - (\pi + \mu + \beta E)S \\ \frac{dE}{dt} &= (\pi + \beta E)S - (\mu + 1)E \\ \frac{dI}{dt} &= \alpha \gamma E - (\mu + \delta_1)I \\ \frac{dI_T}{dt} &= (1 - \alpha \gamma)E - (\mu + \delta_2)I_T \\ N &= S + E + I + I_T\end{aligned}\quad (6)$$

with N is total population.

B. Model Transformation

Total population (N) are deferred against time (t),

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dI_T}{dt} \quad (7)$$

Then the system of differential equations (6) is substituted into the equation (7), so obtained

$$\frac{dN}{dt} = \lambda - \mu N - \delta_1 I - \delta_2 I_T \quad (8)$$

To simplify the solution of equation (6) a simplification is made by making the proportion of each population to the total population

$$s = \frac{S}{N}; \quad e = \frac{E}{N}; \quad i = \frac{I}{N}; \quad i_T = \frac{I_T}{N}$$

Proportion for *susceptible* (s), *exposed* (e), *infected untreated* (i) dan *infected treated* (i_T) are deferred against time (t) so,

$$\begin{aligned}\frac{ds}{dt} &= \frac{1}{N} \frac{dS}{dt} - \frac{s}{N} \frac{dN}{dt} \\ \frac{de}{dt} &= \frac{1}{N} \frac{dE}{dt} - \frac{e}{N} \frac{dN}{dt} \\ \frac{di}{dt} &= \frac{1}{N} \frac{dI}{dt} - \frac{i}{N} \frac{dN}{dt} \\ \frac{di_T}{dt} &= \frac{1}{N} \frac{dI_T}{dt} - \frac{i_T}{N} \frac{dN}{dt}\end{aligned}\quad (9)$$

Further, the system of equations (6) and equation (8) is substituted into the system of equation (9), so that system equation (9) can be rewritten as.

$$\begin{aligned}\frac{ds}{dt} &= \frac{\lambda}{N} (1 - s) - (\pi + \beta e N - \delta_1 i - \delta_2 i_T) s \\ \frac{de}{dt} &= (\pi + \beta e N) s - \left(1 + \frac{\lambda}{N} - \delta_1 i - \delta_2 i_T\right) e \\ \frac{di}{dt} &= \alpha \gamma e - \left(\delta_1 + \frac{\lambda}{N} - \delta_1 i - \delta_2 i_T\right) i \\ \frac{di_T}{dt} &= (1 - \alpha \gamma) e - \left(\delta_2 + \frac{\lambda}{N} - \delta_1 i - \delta_2 i_T\right) i_T\end{aligned}\quad (10)$$

with,

$$s + e + i + i_T = 1$$

The system of differential equations (10) will be used for a) determining fixed points and basic reproduction numbers, b) analyzing the stability of fixed points, c) simulating fixed point stability so as to obtain a description of population behavior.

C. Fixed-points

1) Fixed-point without disease

This point is gained as $\frac{ds}{dt} = 0$, $\frac{de}{dt} = 0$, $\frac{di}{dt} = 0$, and $\frac{di_T}{dt} = 0$ that accommodate $e = 0$, $i = 0$, and $i_T = 0$.

$$T_0 = (s, e, i, i_T) \text{ with } s = \frac{\lambda}{\lambda + \pi N}; \quad e = 0; \quad i = 0; \quad i_T = 0.$$

2) Fixed-point with disease

This point is obtained at $\frac{ds}{dt} = 0$, $\frac{de}{dt} = 0$, $\frac{di}{dt} = 0$, and $\frac{di_T}{dt} = 0$ that accommodate $e \neq 0$, $i \neq 0$, and $i_T \neq 0$.

$$T_1 = (s^*, e^*, i^*, i_T^*)$$

$$s^* = \frac{\lambda}{\lambda + N(\beta e N - \delta_1 i - \delta_2 i_T + \pi)}$$

$$e^* = -\frac{N(N\beta + \delta_1 i + \delta_2 i_T - 1) - \lambda}{N(N\beta + \delta_1 i + \delta_2 i_T - 1) - \lambda}$$

$$i^* = \frac{N(\delta_1 - \delta_2 i_T) + \lambda - \sqrt{(\delta_1 N - \delta_2 N i_T + \lambda)^2 - 4\alpha\gamma\delta_1 e N^2}}{2\delta_1 N}$$

$$i_T^* = \frac{-\delta_1 N i + \delta_2 N + \lambda - \sqrt{4(\alpha\gamma - 1)\delta_2 N^2 e + (-\delta_1 N i + \delta_2 N + \lambda)^2}}{2\delta_2 N}$$

The next step is to determine the basic reproduction number (\mathcal{R}_0). Basic reproduction numbers are needed to analyze the stability of fixed points.

D. Basic Reproduction Number

To determine the basic reproduction number, these equations are provided:

$$\begin{aligned} \frac{de}{dt} &= (\pi + \beta e N) s - \left(1 + \frac{\lambda}{N} - \delta_1 i - \delta_2 i_T\right) e \\ \frac{di}{dt} &= \alpha\gamma e - \left(\delta_1 + \frac{\lambda}{N} - \delta_1 i - \delta_2 i_T\right) i \\ \frac{di_T}{dt} &= (1 - \alpha\gamma) e - \left(\delta_2 + \frac{\lambda}{N} - \delta_1 i - \delta_2 i_T\right) i_T \end{aligned} \quad (11)$$

The new disease matrix is denoted by F_i , while the individual displacement matrix by V_i .

$$F_i = \begin{pmatrix} (\delta_1 i + \delta_2 i_T) e + (\pi + \beta N e) s \\ \alpha\gamma e + (\delta_1 i + \delta_2 i_T) i \\ (\delta_1 i + \delta_2 i_T) i_T + e \end{pmatrix} \quad (12)$$

And

$$V_i = \begin{pmatrix} \left(\frac{\lambda}{N} + 1\right) e \\ \left(\frac{\lambda}{N} + \delta_1\right) i \\ \left(\frac{\lambda}{N} + \delta_2\right) i_T + \alpha\gamma e \end{pmatrix} \quad (13)$$

The new disease rate matrix is denoted by F and the individual displacement rate matrix by V by aligning equation (12) and (13) around fixed point without disease T_0 so,

$$F = \begin{pmatrix} \frac{\beta \lambda N}{\lambda + \pi N} & 0 & 0 \\ \alpha \gamma & 0 & 0 \\ 1 & 0 & 0 \end{pmatrix} \tag{14}$$

And

$$V^{-1} = \begin{pmatrix} \frac{\delta_1 \delta_2 + \frac{\delta_1 \lambda}{N} + \frac{\delta_2 \lambda}{N} + \frac{\lambda^2}{N^2}}{(\delta_2 + \frac{\lambda}{N})(\delta_1 + \frac{\lambda}{N} + \frac{\delta_2 \lambda}{N} + \frac{\lambda^2}{N^2})} & 0 & 0 \\ 0 & \frac{\delta_2 + \frac{\lambda}{N} + \frac{\lambda \delta_2}{N} + \frac{\lambda^2}{N^2}}{(\delta_2 + \frac{\lambda}{N})(\delta_1 + \frac{\lambda}{N} + \frac{\lambda \delta_1}{N} + \frac{\lambda^2}{N^2})} & 0 \\ \frac{-\alpha \gamma \delta_1 - \frac{\alpha \gamma \lambda}{N}}{(\delta_2 + \frac{\lambda}{N})(\delta_1 + \frac{\lambda}{N} + \frac{\lambda \delta_1}{N} + \frac{\lambda^2}{N^2})} & 0 & \frac{1}{\delta_2 + \frac{\lambda}{N}} \end{pmatrix} \tag{15}$$

Based on the next generation matrix G in equation (5) obtained matrix,

$$G = \begin{pmatrix} \frac{\beta \lambda N (\delta_1 \delta_2 + \frac{\lambda \delta_1}{N} + \frac{\lambda \delta_2}{N} + \frac{\lambda^2}{N^2})}{(\delta_2 + \frac{\lambda}{N})(\delta_1 + \frac{\lambda}{N} + \frac{\lambda \delta_1}{N} + \frac{\lambda^2}{N^2})(\lambda + \pi N)} & 0 & 0 \\ 0 & 0 & 0 \\ \frac{-\alpha \gamma \delta_1 - \frac{\alpha \gamma \lambda}{N}}{(\delta_2 + \frac{\lambda}{N})(\delta_1 + \frac{\lambda}{N} + \frac{\lambda \delta_1}{N} + \frac{\lambda^2}{N^2})} & 0 & 0 \end{pmatrix} \tag{16}$$

The dominant eigenvalue of the G matrix is called the basic reproduction number. The basic reproduction number obtained is,

$$\mathcal{R}_0 = \frac{\beta \lambda N^2}{(\lambda + N)(\lambda + \pi N)} \tag{17}$$

E. Stability Analysis of Fixed Points

1) Stability Analysis of Fixed Points without disease

Stability analysis of fixed point without disease is done by aligning equation (10) that is,

$$J = \begin{pmatrix} \frac{\partial f_1}{\partial s} & \frac{\partial f_1}{\partial e} & \frac{\partial f_1}{\partial i} & \frac{\partial f_1}{\partial r} \\ \frac{\partial f_2}{\partial s} & \frac{\partial f_2}{\partial e} & \frac{\partial f_2}{\partial i} & \frac{\partial f_2}{\partial r} \\ \frac{\partial f_3}{\partial s} & \frac{\partial f_3}{\partial e} & \frac{\partial f_3}{\partial i} & \frac{\partial f_3}{\partial r} \\ \frac{\partial f_4}{\partial s} & \frac{\partial f_4}{\partial e} & \frac{\partial f_4}{\partial i} & \frac{\partial f_4}{\partial r} \end{pmatrix} \tag{18}$$

gained *Jacobi matrix* (J), then the fixed point without disease (T_0) substituted into *Jacobi matrix*,

$$J_{T_0} = \begin{pmatrix} -\frac{\lambda+\pi N}{N} & -\frac{S\lambda N}{\lambda+\pi N} & \frac{\lambda\varepsilon_1}{\lambda+\pi N} & \frac{\lambda\varepsilon_2}{\lambda+\pi N} \\ \pi & \frac{S\lambda N}{\lambda+\pi N} - \frac{\lambda}{N} - 1 & 0 & 0 \\ 0 & \alpha\gamma & -\frac{\lambda+\varepsilon_1 N}{N} & 0 \\ 0 & 1 - \alpha\gamma & 0 & -\frac{\lambda+\varepsilon_2 N}{N} \end{pmatrix} \quad (19)$$

To simplify solving equation (19) assume,

$$\begin{aligned} A_{11} &= -\frac{\lambda+\pi N}{N}, & A_{12} &= -\frac{S\lambda N}{\lambda+\pi N}, & A_{13} &= \frac{\lambda\varepsilon_1}{\lambda+\pi N}, & A_{14} &= \frac{\lambda\varepsilon_2}{\lambda+\pi N}, & A_{21} &= \pi, & A_{22} &= \frac{S\lambda N}{\lambda+\pi N} - \frac{\lambda}{N} - 1, & A_{23} &= 0, \\ A_{24} &= 0, & A_{31} &= 0, & A_{32} &= \alpha\gamma, & A_{33} &= -\frac{\lambda+\varepsilon_1 N}{N}, & A_{34} &= 0, & A_{41} &= 0, & A_{42} &= 1 - \alpha\gamma, & A_{43} &= 0, \\ A_{44} &= -\frac{\lambda+\varepsilon_2 N}{N} \end{aligned}$$

So,

$$J_{T_0} = \begin{pmatrix} A_{11} & A_{12} & A_{13} & A_{14} \\ A_{21} & A_{22} & A_{23} & A_{24} \\ A_{31} & A_{32} & A_{33} & A_{34} \\ A_{41} & A_{42} & A_{43} & A_{44} \end{pmatrix} \quad (20)$$

The next stage determined the eigenvalues to obtain a *nontrivial* solution,

$$\begin{vmatrix} A_{11} - \xi & A_{12} & A_{13} & A_{14} \\ A_{21} & A_{22} - \xi & A_{23} & A_{24} \\ A_{31} & A_{32} & A_{33} - \xi & A_{34} \\ A_{41} & A_{42} & A_{43} & A_{44} - \xi \end{vmatrix} = 0 \quad (21)$$

Where ξ is eigen value from matrix J_{T_0} . Based on the analysis, the eigen value equation is as follows,

$$\lambda^4 + \alpha_1 \lambda^3 + \alpha_2 \lambda^2 + \alpha_3 \lambda + \alpha_4 = 0 \quad (22)$$

where,

$$\begin{aligned} \alpha_1 &= -(A_{11} + A_{22} + A_{33} + A_{44}) \\ \alpha_2 &= ((A_{11} + A_{22})(A_{33} + A_{44}) + A_{11}A_{22} + A_{33}A_{44} - A_{12}A_{21}) \\ \alpha_3 &= (A_{33}A_{44}(A_{11} + A_{22}) + A_{11}A_{22}(A_{33} + A_{44}) - (A_{12}A_{33} - A_{13}A_{32} + A_{12}A_{44} - A_{14}A_{42})A_{21}) \\ \alpha_4 &= (A_{11}A_{22}A_{33}A_{44} + (A_{14}A_{42}A_{33} + A_{44}A_{13}A_{32} - A_{44}A_{12}A_{33})A_{21}) \end{aligned}$$

Based on *Routh-Hurwitz Requisition* to Eigen value equation scale-4, the equilibrium point T_0 is asymptotically stable at,

$$\alpha_1 > 0, \alpha_2 > 0, \alpha_3 > 0, \alpha_4 > 0 \text{ dan } \alpha_1\alpha_2\alpha_3 > \alpha_3^2 + \alpha_1^2\alpha_4.$$

2) Endemic Fixed-point Stability Analysis

Endemic Fixed-point Stability Analysis as well as stability analysis for fixed point without disease. Fixed-point with disease (T_1) was substituted into *Jacobi matrix* then assume,

$$\begin{aligned}
 B_{11} &= \delta_1 i^* + \delta_2 i_T^* - \beta N e^* - \frac{\lambda}{N} - \pi, \quad B_{12} = -\beta N s^*, \quad B_{13} = \delta_1 s^*, \quad B_{14} = \delta_2 s^* \quad B_{21} = \pi + \beta N e^*, \\
 B_{22} &= \beta N s^* + \delta_1 i^* + \delta_2 i_T^* - \frac{\lambda}{N} - 1, \quad B_{23} = \delta_1 e^*, \quad B_{24} = \delta_2 e^* \quad B_{31} = 0, \quad B_{32} = \alpha \gamma, \\
 B_{33} &= (2i^* - 1)\delta_1 + \delta_2 i_T^* - \frac{\lambda}{N}, \quad B_{34} = \delta_2 i^*, \quad B_{41} = 0, \quad B_{42} = 1 - \alpha \gamma, \quad B_{43} = \delta_1 i_T^*, \\
 B_{44} &= \delta_1 i^* + (2i_T^* - 1)\delta_2 - \frac{\lambda}{N}
 \end{aligned}$$

So,

$$J_{T_1} = \begin{pmatrix} B_{11} & B_{12} & B_{13} & B_{14} \\ B_{21} & B_{22} & B_{23} & B_{24} \\ B_{31} & B_{32} & B_{33} & B_{34} \\ B_{41} & B_{42} & B_{43} & B_{44} \end{pmatrix} \tag{23}$$

then the eigenvalue is determined to obtain a *nontrivial* solution

$$\begin{vmatrix} B_{11} - \xi & B_{12} & B_{13} & B_{14} \\ B_{21} & B_{22} - \xi & B_{23} & B_{24} \\ B_{31} & B_{32} & B_{33} - \xi & B_{34} \\ B_{41} & B_{42} & B_{43} & B_{44} - \xi \end{vmatrix} = 0 \tag{24}$$

Based on the analysis, the eigen value equation is obtained as follows,

$$\begin{aligned}
 \lambda^4 + b_1 \lambda^3 + b_2 \lambda^2 + b_3 \lambda + b_4 &= 0 \tag{25} \\
 b_1 &= -(B_{33} + B_{44} + B_{11} + B_{22}) \\
 b_2 &= (B_{44} B_{11} - B_{12} B_{21} + (B_{44} + B_{11}) B_{22} + B_{33} (B_{44} + B_{11} + B_{22}) - B_{42} B_{24} - B_{23} B_{32} - B_{34} B_{43}) \\
 b_3 &= ((B_{34} B_{43} (B_{11} + B_{22}) - B_{34} B_{42} B_{22}) - B_{44} B_{12} B_{21} + B_{42} B_{14} B_{21} + B_{44} B_{11} B_{22} \\
 &\quad - B_{42} B_{11} B_{24} + B_{33} (B_{44} B_{11} - B_{12} B_{21} + (B_{44} + B_{11}) B_{22} - B_{42} B_{24}) \\
 &\quad + (B_{13} B_{21} - (B_{44} + B_{11}) B_{23} + B_{43} B_{24}) B_{32}) \\
 b_4 &= B_{34} B_{42} B_{11} B_{23} + B_{33} B_{43} B_{12} B_{21} - B_{34} B_{42} B_{12} B_{21} - B_{34} B_{43} B_{11} B_{21} \\
 &\quad - B_{11} B_{21} B_{12} B_{21} + B_{33} B_{42} B_{14} B_{21} + B_{33} B_{44} B_{11} B_{22} - B_{33} B_{42} B_{11} B_{24} \\
 &\quad + B_{44} B_{13} B_{21} B_{22} - B_{43} B_{14} B_{21} B_{22} - B_{44} B_{11} B_{23} B_{22} + B_{43} B_{11} B_{24} B_{22}
 \end{aligned}$$

Based on *Routh-Hurwitz Requisition* to eigen value equation of degree 4, the equilibrium T_1 is stabilized asimtotik at,

$$b_1 > 0, b_2 > 0, b_4 > 0 \text{ dan } b_1 b_2 b_3 > b_3^2 + b_1^2 b_4.$$

F. Human population Behavior

Human behavior when $R_0 \leq 1$ was observed by simulation with $R_0 = 0.0082$, total population $N = 10$ and value of other parameters are based on [4] Table 1.

Table 1. The parameter values on the model at $R_0 \leq 1$

Parameter	Value
λ	1
μ	0.00132
δ_1	0.00139
δ_2	0.00134
π	10^{-5}
β	0.0009
α	0.004
γ	1

1) Human Behavior for $R_0 \leq 1$

The initial value used during the simulation is $s = 0.1$, $e = 0.5$, $i = 0.2$, and $i_T = 0.2$. Population behavior for $\mathcal{R}_0 < 1$ as shown in Figure. 3.

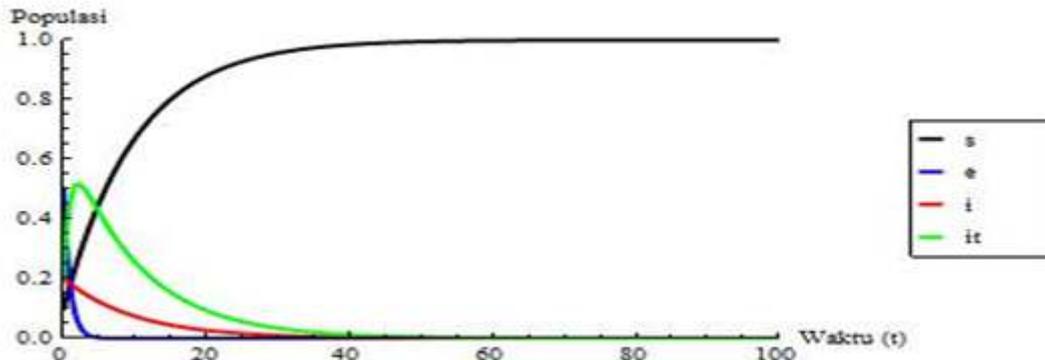


Figure 3. Human Behavior for $\mathcal{R}_0 < 1$

The horizontal axis denotes time (t) in units of days, while the vertical axis represents the population number. The simulation results show that the proportion of the population *susceptible* (s) increase from the initial value, then stabilized around $s = 0.9999$. Proportion of population *exposed* (e) diminished, then stabilized around $e = 0$. Proportion of population *infected* untreated (i) diminished from initial value, then stabilized around $i = 0$. Proportion of population *infected* with treatment (i_T) climb up from beginning, then diminished and stabilized around $i_T = 0$. Based on the simulation it can be noted that the system tend to touch fixed point without disease for the condition $\mathcal{R}_0 < 1$ that is $T_0(s, e, i, i_T) = (0.99999, 0, 0, 0)$.

2) Human Behavior for $\mathcal{R}_0 > 1$

The parameter values used to simulate the behavior of the population at $\mathcal{R}_0 > 1$ with $\mathcal{R}_0 = 1.64$, total population $N = 20$ is shown in Table 1, however, there are some parameter values modified to obtain $\mathcal{R}_0 > 1$. The parameters are as shown in Table 2.

Table 2. Parameter Value at $\mathcal{R}_0 > 1$

Parameter	Value	Source
λ	2	[5]
μ	0.132	Asumsi
δ_1	0.139	Asumsi
δ_2	0.134	Asumsi
ρ	0.9	Asumsi
α	0.004	[5]
γ	1	[5]

The initial value used during the simulation is $s = 0.2$, $e = 0.2$, $i = 0.25$, and $i_T = 0.25$. Population behavior for condition $\mathcal{R}_0 > 1$ as shown in Figure 4.

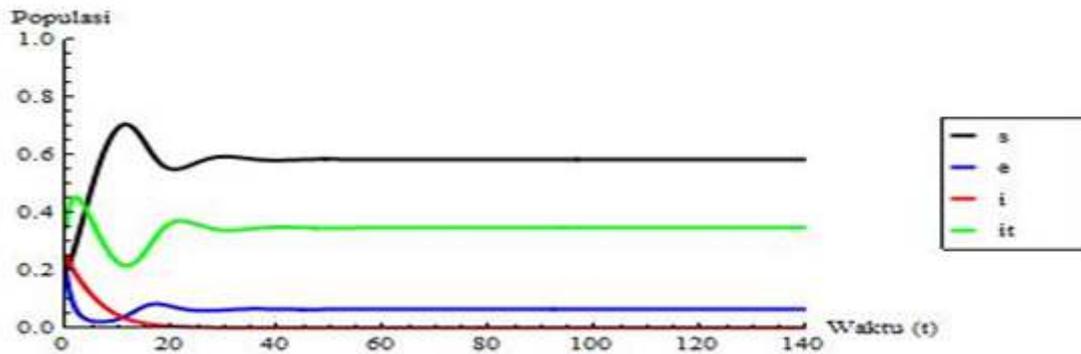


Figure 4. Human Population Behavior at $\mathcal{R}_0 > 1$

Proportion of population *susceptible* (s) increase from the initial value then fluctuate and eventually stabilize around $s = 0.54711$. Proportion of population *exposed* (e) diminished from beginning, then stabilized around $e = 0.05655$. Proportion of population *infected untreated* (i) decreased from initial stage, then stabilized around $i = 0.00393$. Proportion of population *infected with treatment* (i_T) ascend from beginning then fluctuated and rested around $i_T = 0.39241$.

V. Conclusion and Suggestion

A. Conclusion

Based on the analysis and discussion conducted on mathematical modeling type $SEIIT_T$, it can be concluded,

- 1) There are two fixed points obtained, ie fixed point without disease and fixed point endemic.
- 2) Fixed point without stable disease for condition $\mathcal{R}_0 < 1$, while the fixed point for endemic is stable for $\mathcal{R}_0 > 1$.

B. Suggestion

Based on the conclusions that have been described before, it can be given a suggestion that the analysis of mathematical modeling of diabetes mellitus type $SIIIT_T$ disease by considering treatment and genetic factors followed by the rate of human birth is not constant..

References

- [1] Abraham dan San, R. 2015. Analisis Model Matematika Model Penyebaran Penyakit Diabetes Dengan Faktor Genetik. *SAINS*. 15(1)-31-37.
- [2] Edelstein dan Keshet, L. 2005. *Mathematical Models in Biology*. Edisi 7. Random House. New York-USA.
- [3] Jones. 2007. Note on \mathcal{R}_0 . Tesis. Department of Anthropological Sciences Stanford University, California.
- [4] Ulfah, J. Kharis, M. Chotim, M. 2014. Model Matematika Untuk Penyakit Diabetes Mellitus Tanpa Faktor Genetik Dengan Perawatan. *Unnes Journal of Mathematics*. 3(1).
- [5] van den Driessche, Watmough. 2002. Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. *Mathematical Biosciences*. 180(6): 29-48.