Mathematics Modeling of Diabetes Mellitus Type $SEII_T$ by Considering Treatment and Genetics Factors

Mathematics Modeling of Diabetes Mellitus Type $SEII_T$ by Considering Treatment and Genetics Factors

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Abstract $SEII_T$ stands for susceptible (S), exposed (E), infected population without treatment (I) and infected population with treatment (I_T). For infected population is grouped into infected without treatment and infected with treatment by insulin injection. Susceptible group migrate to exposed by genetics factors. The aims of this study are such as composing mathematics models for diabetes mellitus tipe $SEII_T$, composing mathematics models for diabetes mellitus, determining fixed point and basic reproduction number, stability analysis for fixed point, and fixed point stability. The result of the study is mathematical modeling or compartment diagram for diabetes mellitus. Compartment diagram was analyzed analytically and numerically. Analyses result gained two fixed points that are, fixed point without disease and fixed point with disease. Each fixed point was analyzed based on basic reproduction number in order to obtained data analyzed both analytically and numerically which the fixed point without disease was stabilized when $R_0 < 1$, while its counterpart stabilized at $R_0 > 1$. Human behavior at $R_0 < 1$ is when susceptible population proportion (s) was increased from initial value then stabilized about $s = 0.9999$. For exposed (e) was diminished in the beginning then rested around $e = 0$. For infected without treatment(i)was lowered first, then stabilized around $i = 0$. For infected population with treatment (i_T) were increased from the beginning then lowered and stabilzed at around $i_T = 0$. Human behavior at $R_0 > 1$ shown as the susceptible (s) population increased from initial point to fluctuated and then rested around $s = 0.54711$. Exposed (e)group lowered at first, then stopped around $e = 0.05655$. Infected population without treatment (i) diminished at first then rested at around $i = 0.00393$. Infected population with treatment (i_T) went up first then fluctuated and finally rested at around $i_T = 0.39241$.

1.Introduction

1.1 Background

Ulfah develop mathematical models for diabetes mellitus disease type $SEII_T$ which considering treatment factors. $SEII_T$ stands for susceptible (S), exposed (E) and infected (I) [1, 3-4]. Infected population is divided into two groups; infected population without treatment (I) and infected population with treatment (I_T). Next, mathematical model type $SEII_T$ was developed by considering genetics factors. This assumption was obtained from studies conducted by [2, 5]. In their study, susceptible population shifted to exposed population engineered by genetic factors.

1.2 Problem Formulations

How the effect of infective contact rate to the spread of diabetes mellitus type $SEII_T$ by considering treatment and genetic factors in population? This study aims to see the effect of changes in the rate of infective contact to population behavior in mathematical modeling of disease spread of diabetes mellitus type $SEII_T$ by considering treatment and genetic factors.

2. Methods

2.1 Mathematical Modelling Type $SEII_T$

Mathematical modeling for diabetes mellitus desease in this research is designed as figure 1 below:

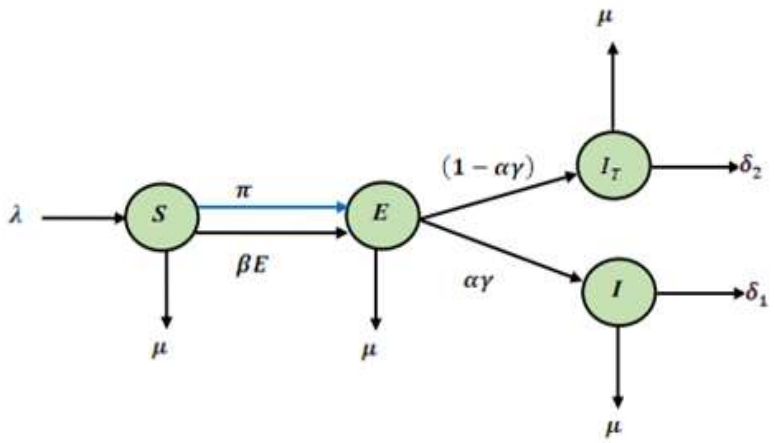


Figure 1. Mathematical Model Type $SEII_T$ with treatment factors and genetics factors

2.2 Research Conduct

The stages of the research are as follows;

i. Firstly is the modeling stage.
ii. Secondly, fixed point determination stage.
iii. Thirdly, the stage of determining the basic reproduction number.
iv. Fourthly, the fixed point stability analysis phase.
v. Next is the simulation phase of fixed point stability.
vi. The simulation phase of the effect of contact rate infective for the spread of disease in the population.

2.3 Data and Resources

Data in this research is secondary which gained from references in the form of journals and literatures.

3. Result and Discussion

3.1 Differential Equation

Differential equation for compartment diagram as follows;

$$\frac{dS}{dt} = \lambda - (\pi + \mu + \beta E)S$$

$$\frac{dE}{dt} = (\pi + \beta E)S - (\mu + 1)E$$

$$\frac{dI}{dt} = \alpha\gamma E - (\mu + \delta_1)I \tag{1}$$
$$\frac{dI_T}{dt} = (1-\alpha\gamma)E - (\mu + \delta_2)I_T$$
$$N = S + E + I + I_T$$

by *N* is total population. To solve equation (1), the simplification is done by making the proportion of each population to the total population.

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

Hence, equation (1) can be written as follow and from that can get the equation (2):

$$\frac{ds}{dt} = \frac{\lambda}{N}(1-s) - (\pi + \beta eN - \delta_1 i - \delta_2 i_T)s$$
$$\frac{de}{dt} = (\pi + \beta eN)s - \left(1 + \frac{\lambda}{N} - \delta_1 i - \delta_2 i_T\right)e$$
$$\frac{di}{dt} = \alpha\gamma e - \left(\delta_1 + \frac{\lambda}{N} - \delta_1 i - \delta_2 i_T\right)i \tag{2}$$
$$\frac{di_T}{dt} = (1-\alpha\gamma)e - \left(\delta_2 + \frac{\lambda}{N} - \delta_1 i - \delta_2 i_T\right)i_T$$

with $s + e + i + i_T = 1$. The parameters contained in $SEII_T$ type mathematical modeling can be seen in table 1.

Table 1. Parameter in mathematical modeling Type $SEII_T$.

Parameter	Annotation	Units
λ	Birth rate	time^{-1}
μ	Mortal rate by nature	time^{-1}
δ_1	Mortal rate by disease towards population infected without treatment	time^{-1}
δ_2	Mortal rate by disease towards infected with treatment	time^{-1}
π	Population shift rate from susceptible to exposed by gene factors	time^{-1}
β	Population shift rate from susceptible to exposed by infective contacts inter-population	time^{-1}
α	Population shift rate from exposed to infected without treatment	time^{-1}

3.2 Fixed Point

3.2.1 Fixed Point without disease

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

3.2.2 Fixed Point with disease

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

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

$$e^* = -\frac{\pi Ns}{N(N1s\beta+\delta_1 i+\delta_2 i_T-1)-\lambda}$$

$$i_1^* = \frac{\mathrm{N}(\delta_1-\delta_2 i_T)+\lambda-\sqrt{(\delta_1 N-\delta_2 N i_T+\lambda)^2-4\alpha\gamma\delta_1 \mathrm{eN}^2}}{2\delta_1 \mathrm{N}}$$

$$i_{T1}^* = \frac{-\delta_1 Ni+\delta_2 N+\lambda-\sqrt{4(\alpha\gamma-1)\delta_2 N^2 e+(-\delta_1 Ni+\delta_2 N+\lambda)^2}}{2\delta_2 \mathrm{N}}$$

3.3 Basic Reproduction Number Equation (3) is determine the basic of reproduction number:

$$\begin{aligned}\frac{de}{dt} &= (\pi+\beta eN)s-\left(1+\frac{\lambda}{N}-\delta_1 i-\delta_2 i_T\right)e\\ \frac{di}{dt} &= \alpha\gamma e-\left(\delta_1+\frac{\lambda}{N}-\delta_1 i-\delta_2 i_T\right)i\\ \frac{di_T}{dt} &= (1-\alpha\gamma)e-\left(\delta_2+\frac{\lambda}{N}-\delta_1 i-\delta_2 i_T\right)i_T\end{aligned} \tag{3}$$

Basic reproduction number gained by following equation (4)

$$R_0 = \frac{\beta\lambda^{\ 2}}{(\lambda+N)(\lambda+\pi\mathrm{N})} \tag{4}$$

3.4 Population shift rate from susceptible to exposed by infective contacts inter-population simulation Population shift rate from susceptible to exposed by infective contacts inter-population simulation ($\boldsymbol{\beta}$) is done to show the dynamics of disease in its population. Besides, it will show the trend of diminishing value due to the shift of susceptible to exposed by infective contact that lower the score of basic reproduction number R_0. There are four values ($\boldsymbol{\beta}$) taken from interval [0.0903: 0.0003] with this step $\mathbf{3 \times 10^{-2}}$, while other parameter fixed as shown in table 2.

Table 2. Parameter value for model $R_0 > 1$.

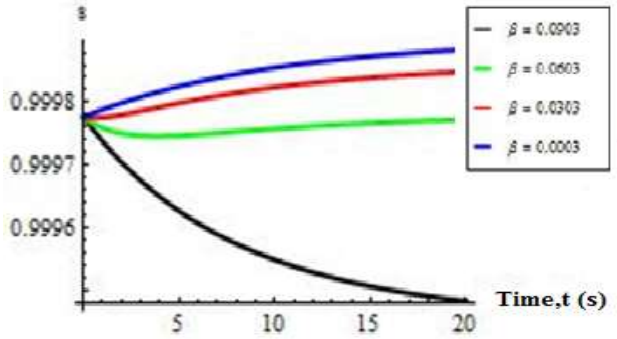
Parameter	Value	Sources
λ	2.000	[5]
μ	0.132	-
δ_1	0.139	-
δ_2	0.134	-
β	0.900	-
α	0.004	[5]
γ	1.000	[5]

R_0 value at the population shift rate susceptible to exposed by genetics factor becomes lower as shown in table 3.

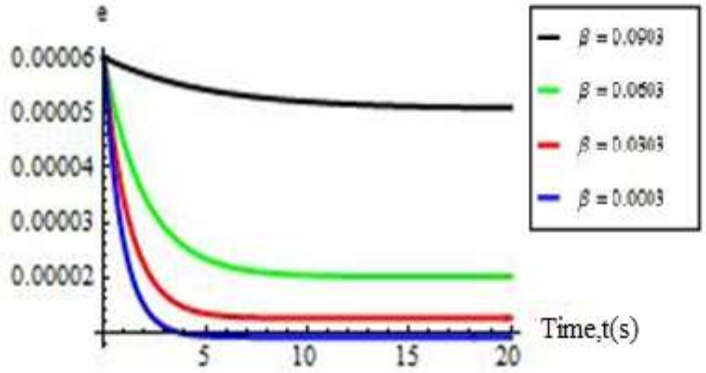
Table 3. R_0 value with parameter (β).

β	Value of R_0
0.9030	0.820
0.0603	0.550
0.0303	0.280
0.0003	0.003

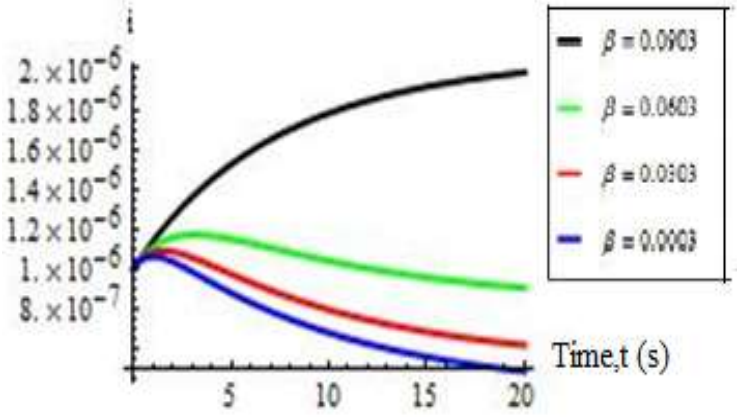
Based on table 3, it can be seen that value of $R_0 < 1$. The diminishing of parameter β causes R_0 lower, so it helps to suppress or to control the disease speed rate in the population. Based on these parameter values, the result of population shifts rate simulation from susceptible to exposed by infective contact as shown in figure 2a-2d.



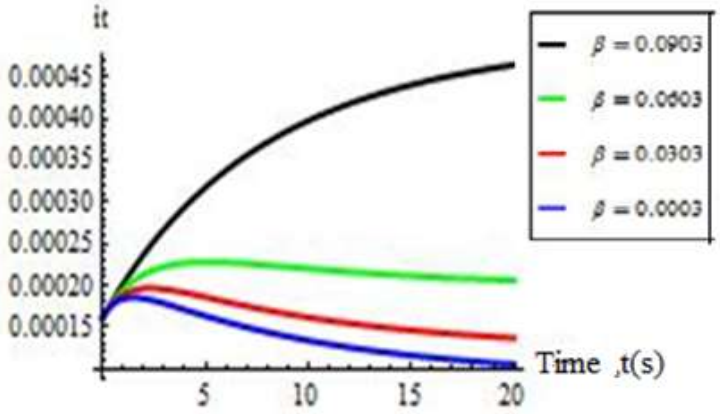
a) Susceptible



b) Exposed



c) Infected population without treatment



d) Infected population with treatment

Figure 2a-2d. Human Population with different coefficient

Figure 2a-2d shows that the shift of human population when parameter value for infective contact (β) is differentiated while other parameter is fixed. Susceptible population with lesser β increase from initial start and at the end of the simulation has the largest population. Exposed population with lesser β lower than at the beginning and at the end of simulation has the lesser population. Infected population without treatment with lesserr β lower at the first place and at the end of simulation has the lesser population. Infected population with treatment with lesser β lower at the beginning and at the end of simulation has the lesser population.

Based on the simulation, it can be concluded that by decreasing infective contact or lowering the communication between susceptible individual and exposed one trend to increase susceptible population and lowering the rest groups. This infective contact rate served as controlling parameter in decreasing the number of disease in population.

4. Conclusion

Based on the analysis and discussions section, as what has be done to mathematical modeling type $SEII_T$, the writers are able to draw some conclusions;

i. Susceptible population with lesser β went up at initial stage and at the end of simulation has the largest population.
ii. Exposed population with lesser β diminished at first and at the end of simulation has smaller population.
iii. Infected population without treatment with lesser β lowered at the beginning and at the end of simulation has lesser population.
iv. Infected population with treatment with lesser β went down from start and at the end of simulation has smaller population.

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