Malaysian Journal of Social Sciences and Humanities (MJSSH) (e-ISSN : 2504-8562)
2022, Volume 7, Issue 11, e001873
DOI: https://doi.org/10.47405/mjssh.v7i11.1873

Transmission of Tuberculosis and Reproduction Number Using Lyapunov Function of SIR Model

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KEYWORDS:
Nonlinear System Dynamic
Basic Reproduction Number
SIR Model

CITATION:
Mohd Rahimie Md Noor et al. (2022). Transmission of Tuberculosis and

ABSTRACT

This paper studies the mechanism of transmission of Tuberculosis (TB) caused by the mycobacterium tuberculosis bacteria. TB is an airborne disease that endangering human population globally. Mathematical modelling of tuberculosis was developed using the Susceptible-Infected-Recovered (SIR) model in this analysis. The model generated by the four-dimensional, nonlinear dynamic system is reduced to three dimensions, with some assumptions. Then, the model will be analyzed by creating a mathematical theorem that will prove the existence of a TB event, the disease-free equilibrium phase, and the TB endemic disease stage. By using the Lyapunov function method, the three theorems can be proved. The

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Reproduction Number Using Lyapunov Function of SIR Model. *Malaysian Journal of Social Sciences and Humanities (MJSSH), 7*(11), e001873. https://doi.org/10.47405/mjssh.v7i11.1873

basic reproduction number R0 also can be obtained from the model. If the basic reproduction number R0 ≤ 1, then the disease-free equilibrium is global asymptotically stable and if R0 > 1, then the endemic equilibrium is asymptotically stable globally. Carrying out a simulation using data in a selected region, the result of the model successfully describes and forecast the number of TB cases and it may also be used for assessing the TB disease status.

Contribution/Originality: This study contributes derivation of formula and estimation of R0 values. The method that used in this paper SIR modelling but combine with Lyapunov function. SIR model is logical analysis consist of Susceptible, Infected, and Recovery. This method very helpful for predicting the data of TB disease.

1. Introduction

Tuberculosis (TB) is an airborne disease that mainly affects the human lungs and occurring in all countries in the world. In 2017, 62% of new TB cases were reported in Southeast Asia and West Pacific and 25% of new cases in African region. In 30 countries with highest tuberculosis prevalence, 87% of new cases of tuberculosis were reported in 2017. Two thirds of world's TB new cases contributed by eight countries: India, China, Indonesia, the Philippines, Pakistan, Nigeria, Bangladesh and South Africa. In Malaysia number of TB cases decreased 1.3% from 2018 (25,837 cases) compared to 2017 (26,168 cases). Based on the official data released by Malaysian Health Director General Datuk Dr Noor Hisham Abdullah, Selangor reported the highest TB cases in 2018 (5071 cases), followed by Sabah (5008 cases) (BERNAMA.com, 2019).

Müller (2016) presented that Mycobacterium tuberculosis is a bacterium that causes tuberculosis in humans. This bacteria was first discovered by German microbiologist, Robert Koch in 1882, identified as tubercle bacillus. After few years of studies, he found that these tubercle bacilli, named Mycobacterium also causing leprosy infection in human. The tubercle bacillus that cause tuberculosis is then called Mycobacterium tuberculosis.

As stated by Centers for Disease Control and Prevention (CDC) (2016), TB is an airborne disease than can spread when infected person cough or sneeze. It is less commonly spread by human touch or body fluids exposure. Once infected, these bacteria will replicate inside the lungs and potentially spread through blood circulation to other parts of human body such as liver, bone, heart and brain. TB infection in the lungs is more infectious compared to TB in other parts of human body.

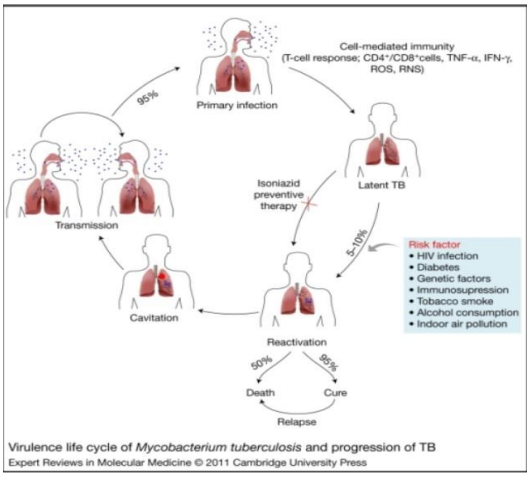
Figure 1 shows virulence life cycle of Mycobacterium tuberculosis and progression of TB. TB of the lung can be classified into Active TB and Latent TB infection. In Active TB, patient will develop symptoms and signs of infection supported by positive findings on clinical test related to tuberculosis. Meanwhile in Latent TB, patients usually are asymptomatic despite having a positive finding on laboratory tuberculin skin/blood testing.

Initially, in Latent TB, the bacteria will remain dormant in patient's body for a certain duration. When the bacteria become active, patient will develop symptoms of tuberculosis and have the ability to spread the infection to other person. Based on Side

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(2015), SIR model will be applied to compute the probability of susceptible, infected human and infected human by virus from an infected human of tuberculosis disease in South Sulawesi. SIR model of TB transmission is formed by dividing the human population into three sub-populations which are Suspected, Infected, and Recovered (SIR).

Figure 1: Transmission of tuberculosis diseases



2. Theoretical Background

According to the World Health Organization (WHO) (2019), globally, the incidence of tuberculosis is dropping by around 2% per year. It has to progress to an average fall of 4-5 percent to reach the end of the TB strategy's 2020 targets. Since 2000 and 2017, an unprecedented 54 million lives have been saved by TB diagnosis and treatment. One of the health goals of sustainable development objectives is to stop the TB outbreak by 2030.

Sakamoto et al. (2019) reported that the Sustainable Development Goals (SDGs) goal on TB will not be feasible, despite significant progress over the past decades, at the existing rate of progress. The annual rate of decline in TB incidence is actually about 1–2%, while the figure would have to be 4–5% by 2020 and over 10% by 2025 to achieve the goal of stopping the outbreak by 2030. In addition, new challenges are increasing, including a rise in multidrug resistant tuberculosis (MDR-TB), a large number of missed cases (6.4 million reported cases accounted for 64 percent of the total 10.0 million new cases in 2017), and global migration, which will place a significant financial and political pressure on TB regulation.

Thru this study, the mathematical analysis describes and predict the number of tuberculosis cases in one region. SIR model will be applied for tuberculosis to achieve further understanding of the progression disease especially the changes of number of susceptible, infected and recovered in the population. The limitation of theoretical model is less realistic and not suitable for local situation bring the author to investigate the tuberculosis disease using the SIR model. This will help the responsible party to identify adequate measures to put in place to prevent an outbreak of the disease in small proportion.

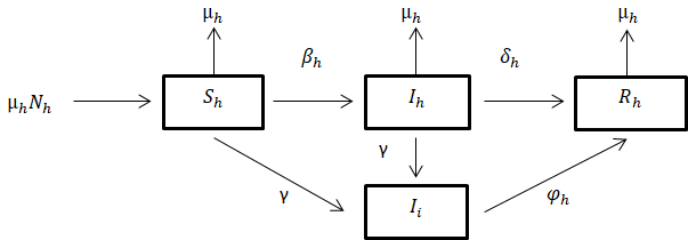
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3. Methodology

3.1. SIR Model

The SIR model classified TB infection into 2 groups, which are Active TB and Latent TB. SIR model based on Figure 2, shows the relations between different compartments. From the whole human population (N_h), susceptible group (S_h)are identified. People in susceptible group who are infected with TB will be divided into 2 infected groups, named infected human group 1 (I_h) and infected human group 2 (I_i). (I_h) represents people who has been infected with TB, either Active TB or Latent TB. These infected group may the spread TB to infected human group 2 (I_i). These 2 infected groups will be observed in certain period of time until they are fully recovered. Infected people who recovered from TB is labelled as (R_h). SIR model also implements the use of probability rate to connect the relationships between groups using parameters as per Figure 2.

Figure 2: SIR Model



3.2. Method

Compartment such as S, I, and R are usually used to represent epidemiological classes. The compartmental model derived from a system of differential equation. The models generated by four-dimensional nonlinear dynamical system are reduced to three dimensional system to solve the transmission of TB disease. The numerical and qualitative analysis are solved to determine the stability state of disease free equilibrium (DFE) and endemic equilibrium (EE). This process involves the use of linear algebra and first order linear differential equation method. After that, to determine the stability of SIR model, we need to find the reproduction number, R0. If R_0<1, the disease is eliminated and for R_0>1, the disease will spread. The data obtained from this study will be analyzed using two mathematical software, MATLAB and ODESOLVE.

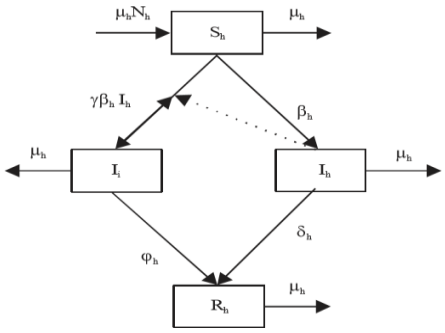
3.2.1. Finding The Positivity of Solutions for Presence of Tuberculosis Disease Applying the SIR Model

Figure 3 below shows the compartmental model of SIR which consist of susceptible S_h, infected I_h, and recovered R_h individuals. $\gamma\beta_h I_h S_h$ and $\beta_h S_h$ are the incidence rate of when susceptible, S_h becomes infected with TB. I_i and I_h are people who had TB infection. The diagram represents the transmission of the tuberculosis. Assume that the population size *N* holds a relation :

$$N(t) = S_h(t) + I_h(t) + I_i(t) + R(t) \quad (1)$$

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Figure 3: Compartmental model of SIR



The Table 1 below describe in detail the four compartments of the model and the various parameters used in SIR model for each of the compartment.

Table 1: Definition of compartment and parameters of the model

Variables/ paramates	Definition
S_h	The number of suspectible humans
I_h	The number of infected humans 1
I_i	The number of infected humans 2
R_h	The number of recovered humans
N_h	Total population
μ_h	The rate of birth/death of human population
β_h	The rate of suspected to infected human
γ	The rate of suspected and infected 1 to infected 2
δ_h	The rate of infected 1 to recovered human
ϕ_h	The rate of infected 2 to recovered human

The differential equations of (2)-(5) represent every compartment per unit time according to theorem in Side et al. (2016):

$$\frac{dS_h}{dt} = \mu_h N_h - \beta_h S_h - \gamma\beta_h I_h S_h - \mu_h S_h \quad (2)$$

$$\frac{dI_h}{dt} = \beta_h S_h - (\mu_h + \delta_h) I_h \quad (3)$$

$$\frac{dI_i}{dt} = \gamma\beta_h I_h S_h - (\mu_h + \varphi_h) I_i \quad (4)$$

$$\frac{dR_h}{dt} = \delta_h I_h + \varphi_h I_i - \mu_h R_h \quad (5)$$

D is positively invariant set that covers all settlement in R^4 . With the initial state (S_{0h}, I_{0h}, I_{0i} ,R_{0h}) let the ($S_h > 0$, $I_h > 0$, $I_i > 0$, $R_h > 0$) be the completion of equation (2)-(5) and compact set as in equation :

$$D = (S_h(t), I_h(t), I_i(t), R_h(t) \in R^4, L \leq N_h) \quad (6)$$

With the condition, $\frac{dN}{dt} = 0$ and $N_h = S_h + I_h + I_i + R_h$ are also constant.

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3.2.2. Analysis of global stability of disease-free equilibrium(DFE) and endemic equilibrium(EE) for SIR model using lyapunov function

Step 1: To analyze the Reproduction Number, R_0

Solve the SIR model until the reproduction number R_0 found, based on the global asymptotic stability of the system.

$$R_0 = \mu_h \alpha \eta \text{ for } \alpha = \mu_h + \delta_h \; and \; \eta = \mu_h + \phi_h \quad (7)$$

There is always a disease-free equilibrium (DFE) point for equation (2)-(5) where $P^* = S_h^*, I_h^*, I_{ih}^*, R_h^*) = (N_h^*, 0,0,0)$. This point is the point where the disease will disappear.

Step 2: Applying Lyapunov function in Disease free Equilibrium

Let the candidate Lyapunov function be
$$V(t) = (S_h - S_h^* ln S_h) + I_h + I_i + R_h \quad (8)$$

Then, differentiate equation (8)

$$V'(t) = S_h' \left(1 - \frac{S_h^*}{S_h}\right) + I_h' + I_i' + R_h' \quad (9)$$

Compute equation (2) – (5) into (9):
$$V'(t) = \mu_h N_h \; - \; \beta_h S_h \; - \; \gamma \beta_h I_h S_h \; - \; \mu_h S_h \left(1 - \frac{S_h^*}{S_h}\right) + \beta_h S_h \; - \; (\mu_h + \delta_h) I_h + \gamma \beta_h S_h I_h - (\mu_h + \varphi_h) I_i + \delta_h I_h + \varphi_h I_i \; - \; \mu_h R_h \; (10)$$

Simplify (10),
$$V'(t) = \mu_h N_h \left(1 - \frac{S_h^*}{S_h}\right) + \mu_h S_h^* \left(\frac{S_h}{S_h^*}\right) + \; \beta_h S_h^* \; - \; \mu_h I_h \; - \; \mu_h I_i \; - \; \mu_h R_h \quad (11)$$

Based on [13], the state of endemic equilibrium is the situation in which the disease cannot be eradicated but persist within the population. To obtain the Endemic equilibrium (EE), the system (2)-(5) has an equilibrium point $P^{**} = (S_h^{**}, I_h^{**}, I_i^{**}) \in D$ and satisfied $S_h^{**} > 0, I_h^{**} > 0, I_i^{**} > 0$. To satisfied the condition:

$$S_h^{**} = \frac{-(\mu_h \beta_h)\alpha + \sqrt{(\beta_h^2 + \mu_h^2)\alpha^2 + 2\mu_h \beta_h \alpha(\alpha + \gamma \beta_h)}}{2\gamma \beta_h^2}$$
$$I_h^{**} = \frac{\beta_h \left(-(\mu_h \beta_h)\alpha + \sqrt{(\beta_h^2 + \mu_h^2)\alpha^2 + 2\mu_h \beta_h \alpha(\alpha + \gamma \beta_h)}\right)}{2\gamma \beta_h^2}$$
$$I_i^{**} = \frac{\mu_h + \left((\mu_h \beta_h)^2 \alpha - (\mu_h \beta_h)\sqrt{(\beta_h^2 + \mu_h^2)\alpha^2 + 2\mu_h \beta_h \alpha(\alpha + \gamma \beta_h)}\right)}{2\gamma \eta \beta_h^2} \quad (12)$$

If $R_0 > 1$ then the positive equilibrium state of the system are endemic and asymptotic global stage is stable on D, with assumption the rate of infected 1 and infected 2 is equal to 0 and susceptible is equal to susceptible at equilibrium point P^{**},

$$\frac{dI_h}{dt} = \beta_h S_h \; - \; (\mu_h \delta_h) I_h = 0 \; and \; (\mu_h + \delta_h) = \frac{\beta_h S_h}{I_h^{**}} \quad (13)$$

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$$\frac{dI_i}{dt} = \gamma\beta_h S_h I_h - (\mu_h+\varphi_h)I_i = 0 \; and \; (\mu_h + \varphi_h) = \frac{\gamma\beta_h S_h I_h}{I_i^{**}} \quad (14)$$

$$S_h^{**} = S_h \quad (15)$$

Step 3: Applying Lyapunov function in Endemic Equilibrium

By using Lyapunov function, let

$$V(t) = (S_h - S_h^{**} lnS_h) + (I_h - ln\, I_n) + (I_i - I_i^{**} ln\, l_i) \quad (16)$$

Then, derive the equation (16)

$$V'(t) = S_h'\left(1 - \frac{S_h^{**}}{S_h}\right) + I_h'\left(1 - \frac{I_h^{**}}{I_h}\right) + I_i'\left(1 - \frac{I_i^{**}}{I_i}\right) \quad (17)$$

Substitute equation (2) - (4) into equation (17)

$$V'(t) = (\mu_h N_h - \beta_h S_h - \gamma\beta_h I_h S_h - \mu_h S_h)\left(1 - \frac{S_h^{**}}{S_h}\right) + (\beta_h S_h - (\mu_h + \delta_h)I_h)\left(1 - \frac{I_h^{**}}{I_h}\right) + (\gamma\beta_h S_h I_h - (\mu_h + \varphi_h)I_i)\left(1 - \frac{I_i^{**}}{I_i}\right) \quad (18)$$

Simplify (18),

$$V'(t) = \mu_h N_h\left(1 - \frac{S_h^{**}}{S_h}\right) - \mu_h S_h\left(1 - \frac{S_h^{**}}{S_h}\right) + \beta_h S_h\left(-\left(1 - \frac{S_h^{**}}{S_h}\right) + \left(1 - \frac{I_h^{**}}{I_h}\right)\right) + \gamma\beta_h S_h I_h\left(-\left(1 - \frac{S_h^{**}}{S_h}\right) + \left(1 - \frac{I_i^{**}}{I_i}\right)\right) - (\mu_h + \delta_h)I_h\left(1 - \frac{I_h^{**}}{I_h}\right) - (\mu_h + \varphi_h)I_i\left(1 - \frac{I_i^{**}}{I_I}\right) \quad (19)$$

Analysis of graph

Step 1: To transform the four-dimensional nonlinear dynamical system into three dimensions. As stated by [14], in order to analyse the graph, instead of solving the ordinary differential equation system in (2)- (5) with known population N, the transformation of are applied to the system where *x, y, z* and *u* stand for fractions the number of individuals in classes S_h, I_h, I_i and R_h with population N_h.

$$x(t) = \frac{S_h}{N_h}, y(t) = \frac{I_h}{N_h}, z(t) = \frac{I_i}{N_h}, u(t) = \frac{R_h}{N_h} \quad (20)$$

Then, the transformations in (20) are substitute into equations (2) - (5) to get a simple system without population N_h. In order to find steady-state solution for we have to solve the following system of equation

$$\frac{dx}{dt} = \mu_h - \beta_h\frac{S_h}{N_h} - \gamma\beta_h\frac{S_h}{N_h}\frac{I_h}{N_h} - \mu_h\frac{S_h}{N_h} \quad (21)$$

$$\frac{dy}{dt} = \beta_h\frac{S_h}{N_h} - (\mu_h + \delta_h)\frac{I_h}{N_h} \quad (22)$$

$$\frac{dz}{dt} = \gamma\beta_h\frac{S_h}{N_h}\frac{I_h}{N_h} - (\mu_h + \varphi_h)\frac{I_i}{N_h} \quad (23)$$

$$\frac{du}{dt} = \delta_h\frac{I_h}{N_h} + \varphi_h\frac{I_i}{N_h} - \mu_h\frac{R_h}{N_h} \quad (24)$$

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Then,

$$\frac{dx}{dt} = \mu_h - \beta_h x - \gamma\beta_h xy - \mu_h x \quad (25)$$

$$\frac{dy}{dt} = \beta_h x - (\mu_h + \delta_h)y \quad (26)$$

$$\frac{dz}{dt} = \gamma\beta_h xy - (\mu_h + \varphi_h)z \quad (27)$$

$$\frac{du}{dt} = \delta_h y + \varphi_h z - \mu_h u \quad (28)$$

which is equivalent to the system of equation (2)-(5). Table 2 shows the data and parameter values are obtained from the transmission dynamic of tuberculosis disease in South Sulawesi, Indonesia. The data will be substituted into equation (2)-(5) to produce graph for every compartment against time.

Step 2: Identify the parameters value

Table 2: The initial condition and parameter values

	Simulation			
Initial parameter / condition	**1**	**2**	**3**	**4**
x(0)	0.998934	0.998934	0.997586	0.997586
y(0)	0.000953	0.000953	0.002069	0.002069
z(0)	0.000112	0.000112	0.000345	0.000345
μ_h	0.000046	0.015	0.00015	0.05
β_h	0.326666	0.325	0.21250	0.12
γ	0.123111	0.125	0.02005	0.13
δ_h	0.041230	0.055	0.20005	0.02
φ_h	0.003700	0.165	0.15000	0.15

3.3. Implementation

3.3.1. Positivity solution of SIR Model

Consider the Lyapunov function,
$S_h(t) + I_h(t) + I_i(t) + R_h(t) = L(t)$ or $S_h'(t) + I_h'(t) + I_i'(t) + R_h'(t) = L'(t)$ (29)

at any time, t ≥ 0. Therefore, as stated by [14] by substitution of the ordinary differential equation system in (2)-(5) into the relationship of (29),

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$$\frac{dS_h}{dt} + \frac{dI_h}{dt} + \frac{dI_i}{dt} + \frac{dR_h}{dt} = \frac{dL}{dt}$$
(30)

$$\mu_h N_h - \beta_h S_h - \gamma\beta_h I_h S_h - \mu_h S_h + \beta_h S_h - (\mu_h + \delta_h)I_h + \gamma\beta_h I_h S_h - (\mu_h + \varphi_h)I_i + \delta_h I_h + \varphi_h I_i - \mu_h R_h = \frac{dL}{dt}$$ (31)

The equation (31) is simplified and the Lyapunov function is determined by the ordinary differential equation:

$$\frac{dL}{dt} = \mu_h N_h - \mu_h L(t) \quad (32)$$

$$\frac{dL}{dt} = -\mu_h[L - N_h]$$
(33)

$$dL = -\mu_h[L - N_h]dt \quad (34)$$

Considering that (34), the population N is counted by using separation of variables.
$$ln(L - N) = -\mu_h t + c \quad (35)$$

As a result of solving (35) over an exponentiation, the population N is specified as:
$$L(t) = N_h + Ce^{-\mu_h(t)} \; where \; C = e^c \quad (36)$$

At t = 0 , $L(0) = C$
(37)
Hence, the solution of the linear differential equation then becomes:

$$L(t) = N_h + L(0)e^{-\mu_h(t)}$$
(38)
Therefore, it is proven that (38) is positively invariant with time-varying.

3.3.2. Solving global asymptotic stability of the system based using Lyapunov function

Based on the parameter values in Table 2, the epidemic conditions also known as basic reproduction number, R_0 for simulation 1 and 3 was calculated and shows in Table 3. The value of R_0 for simulation which is lower than unity, 1. The value obtained implies that there will not be epidemic for the tuberculosis virus in the population.

Table 3: R_0 values for simulation 1 and 3

Simulation 1	**Simulation 3**
$R_0 = 0.00000000718385$	$R_0 = 0.000004509$

Disease-free equilibrium (DFE)

According to disease-free equilibrium $P^* = (S_h^*, I_h^*, I_i^*, R_h^*) = (N_h, 0, 0, 0)$. Because of $I_h = 0$ and $S^* = N_h$, then $\beta_h = 0$.

$$\mu_h N_h - \beta_h S_h - \mu_h S_h = 0$$
$$\mu_h N_h = \mu_h S_h$$

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$$S_h^* = N_h \quad (39)$$

substitute $\beta_h = 0$ and $S^* = N_h$ in equation (12)

$$V'(t) = \mu_h N_h \left(1 - \frac{N_h}{S_h}\right) + \mu_h N_h \left(1 - \frac{S_h}{N_h}\right) - \mu_h I_h - \mu_h I_i - \mu_h R_h \quad (40)$$

simplify the equation (40) to obtained

$$V'(t) = -\mu_h N_h \left(\frac{(N_h - S_h)^2}{S_h N_h}\right) - \mu_h I_h - \mu_h I_i - \mu_h R_h \quad (41)$$

based on the parameter values in Table 2 and Table 3, the DFE for simulation 1 is calculated, where $V'(t) = -0.0004383$.

Endemic Equilibrium (EE)

According to Endemic equilibrium point $P^{**} = (S_h^{**}, I_h^{**}, I_i^{**})$, substitutes the assumption in equation (14)-(16) into equation (20) and simplify the equation

$$V'(t) = \mu_h N_h \left(1 - \frac{S_h^{**}}{S_h}\right) - \mu_h S_h \left(1 - \frac{S_h^{**}}{S_h}\right) + \beta_h S_h \left(-\left(1 - \frac{S_h^{**}}{S_h}\right) + \left(1 - \frac{I_h^{**}}{I_h}\right)\right) +$$
$$\gamma \beta_h S_h I_h \left(-\left(1 - \frac{S_h^{**}}{S_h}\right) + \left(1 - \frac{I_i^{**}}{I_i}\right)\right) - \left(\frac{\beta_h S_h}{I_h^{**}}\right) I_h \left(1 - \frac{I_h^{**}}{I_h}\right) - \left(\frac{\gamma \beta_h S_h I_h}{I_i^{**}}\right) I_i \left(1 - \frac{I_i^{**}}{I_i}\right) \quad (42)$$

$$V'(t) = -\beta_h S_h \left(\frac{(I_h^{**} - I_h)^2}{I_h^{**} I_h}\right) - \gamma \beta_h S_h I_h \left(\frac{(I_i^{**} - I_i)^2}{I_i^{**} I_i}\right)$$
(43)

Based on Table 2 and Table 3 also, the endemic equilibrium for simulation 1 is calculated where $V'(t) = -376.2707306$.

3.4. Graphing the data

By substitution of transformation in (20) into (1) gives

$$x + y + z + u = 1 \text{ or } x' + y' + z' + u' = 0 \quad (44)$$

Equation (44) is substitute into transformed system in (25) – (28) in order to eliminate u and yield to the simplified subsystem:

$$\frac{dx}{dt} = \mu_h - \beta_h x - \gamma \beta_h xy - \mu_h x \quad (45)$$

$$\frac{dy}{dt} = \beta_h x - (\mu_h + \delta_h) y \quad (46)$$

$$\frac{dz}{dt} = \gamma \beta_h xy - (\mu_h + \varphi_h) z$$
(47)

$$\frac{du}{dt} = \delta_h y + \varphi_h z - \mu_h (1 - x - y - z) \quad (49)$$

According to an assumption in SIR model where the number of birth is same as the number of death denoted by μ_h, the transformed subsystems in (45) - (49) can be written as follows:

$$\frac{dx}{dt} = \mu_h - \beta_h x - \gamma \beta_h xy - \mu_h x$$
$$\frac{dy}{dt} = \beta_h x - \alpha y$$
$$\frac{dz}{dt} = \gamma \beta_h xy - \eta z \quad (50)$$

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with positive constants of $\alpha = (\mu_h + \delta_h)$ and $\eta = (\mu_h + \varphi_h)$

4. Result

The article is a full-length original empirical investigation that should present new and significant findings that contribute to the advancement of the research area. Analysis and discussion must be supported with relevant references.

Lyapunov functions, L(t), where t is time approaching infinity, shows that the positivity of the solution for presence of tuberculosis disease is between 0 and N_h. This proves that set D is positive invariant. Even though initially there are no disease carrier of TB in that area, it can change when suspected population , $S_h(t) > 0$, infected with TB, $I_h(t) > 0$, TB infected by people who have a positive TB, $I_i(t) > 0$ and recovered human $R_h(t) > 0$. Positive invariant demonstrates that TB exist in that area and need to be classified whether the spread is endemic, epidemic or pandemic.

From stability analysis, we found that the value of R_0 which is lower than unity or 1. The value of R_0 plays an important role in determining the transmission potential of a disease, in this case tuberculosis especially to the risky group of population (children, elderly, immunocompromised patients).R_0 lower than 1 means that the disease-free equilibrium (DFE) $P^{*,}$ for SIR model is stable asymptotic global stage in D and means that it will have lower infectivity to other individuals. As the R_0 is stable, the spread of tuberculosis virus in a population can be controlled. Lyapunov function in form of V(t) is used to validate the value of R_0. V'(t) obtained from this study is -0.0004383. In conclusion, DFE is proven to be a stable asymptotic global stage.

Endemic equilibrium (EE) shows the number of R_0 lower than 1 means that the positive equilibrium state of the system is non-endemic and asymptotic global stage is not stable in D. So there is no disease transmission among individuals. As the R_0 is stable, the spread of tuberculosis in a population can be controlled and is not at an alarming stage. The value of V'(t) is -376.2707306. This proves that a negative balance P^{**} is not stable in D and the endemic state does not exist in that area. As conclusion, the endemic equilibrium is proven to be not stable in this stage by using Lyapunov function. The value of R_0 and their effect is equal to the result of the V'(t) thus makes the value of R_0 is valid.

4.1. Discussion on the dynamics of susceptible and infected fractions with several set of data and parameter values

The x-curves represents the number of people who are suspected and have not yet been infected by TB. The rapid decline of x-curves indicates that the disease is extremely infectious, with almost every susceptible person being infected by 8 months period. The curve for a less infectious disease will slope more gently to the right. The y-curves is the monthly number of infected people. It is essential as the epidemic-curve for the disease. It also changes rapidly up to a maximum of about 71% people for simulation 1 refer Figure 4 and 68% people for simulation 2 refer Figure 2 at 8 months duration, and then decline more slowly. Increment in infected people stops at 8 months and subsequently starts to decline because at this point, almost all susceptible person has been infected. The slope on the right side of the y-curve reflects the recovery rate and how long it takes for the infected person to be cured.

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Figure 4: Simulation 1

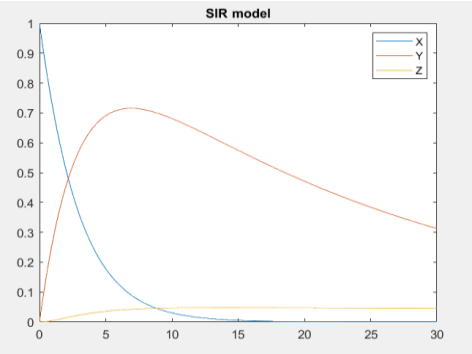
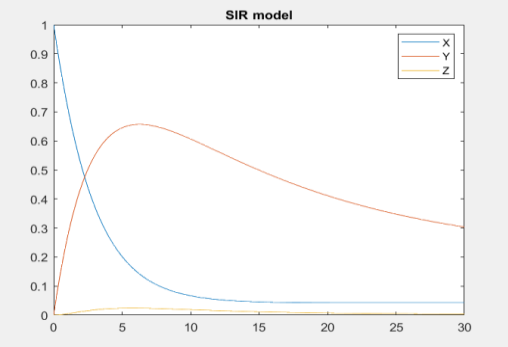


Figure 5: Simulation 2



As the rate of suspected to infected human, β_h increase, higher maximum point of y-curve could be obtained. This is proven by higher value of β_h in simulation 1 (Figure 4) compared to simulation 2 (Figure 5). That also leads to higher maximum point of y-curve in simulation 1(71%) shown in figure 4, compared to simulation 2(68%) shown in Figure 5.

The x-curves shows that the number of people who are suspected is quickly declining. It also indicates that the disease is very infectious. From Figure 6, y-curve rapidly increases up to a maximum of about 39% people in month 5, and then subsequently falls more slowly. Point on intersection between x-curve and y-curve at about 4.5 months indicates that more people are infected than being in suspected group. In Figure 7, it shows that the total number of infected people increase steadily up to month 13 reaching maximum level of 55% people and then become constant at 33% afterward. The x-curve and y-curve cross at about 7.5 month. The number for susceptible person decline rapidly until 20th month and continues to decrease steadily afterwards. When the rate of suspected to infected human, β_h increases, the faster the maximum point of y-curve could be achieved. For example, in simulation 3 on Figure 6, the value of β_h is higher than in simulation. In result, the maximum point of y -curve in simulation is achieved at month 5 which is faster than the duration of maximum point for simulation 4 (Figure 7) recorded at month 13. When the recovery rate of infected 1, δ_h is higher, the y-curves will decline faster after reaching its maximum point.

Figure 6: Simulation 3

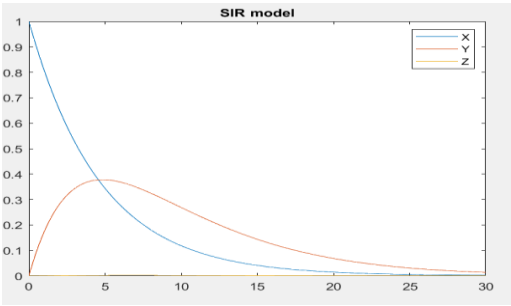
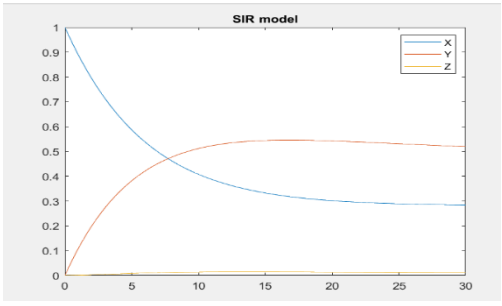


Figure 7: Simulation 4



From the graph, the y-curves is declining faster in simulation 3 (Figure 6) compared to simulation 4 (Figure 7) which almost looks like a constant. Z-curves represents the number of people who had TB transmission from infected person. From the z-curves, we can see that there is only a few people are infected by other people. It does not even reach 5% of the population for all four simulations. This shows that the rate of infection in people who are infected from suspected group is greater than people who are infected

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from another infected person group. It also suggests that the later group will have better recovery compared to the first group.

5. Conclusion

The SIR model has shown success in finding the positivity for presence of tuberculosis and the basic reproduction number, R_0. At any time(t), the tuberculosis disease exists in the Sulawesi region can proved using Lyapunov equation. The value of R_0 is secondary cases that result from single infectious individual in an entirely susceptible population. As in simulation 1, value of R_0 calculated is 0.00000000718385 which means that the model is stable for disease free equilibrium and unstable for endemic equilibrium. Meanwhile, the value of R_0 in simulation 3 is also lower than unity which is 1 despite using different parameters. R_0 value also has weaknesses. However, verification of R_0 using Lyapunov function proves that the theorem is true. Thus, this shows that the SIR model is true as this paper found out that the value of $R_0<1$ which stated that the disease-free equilibrium points of the model is stable and the disease will not be significantly infectious to the other people.

The graph shows that the number of infected people will increase until some point and decline afterwards possibly indicating that the infected people being treated. Otherwise, the number of people infected by people is very low which its peak lower than 5% at the 9^{th} month. This proved that, the endemic condition does not exist in the south Sulawesi region because the rate of infected people by people is very low.

Acknowledgement

Part of this article was extracted from degree thesis submitted to University Technology Mara Cawangan Kelantan.

Funding

This study received no funding.

Conflict of Interests

The authors reported no conflicts of interest for this work and declare that there is no potential conflict of interest with respect to the research, authorship, or publication of this article.

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