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Analysis of the Stability of Anti-Tuberculosis Drug Administration in Cases of Tuberculosis in Children Using the SIR Model

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A B S T R A C T

The SIR model is a commonly used mathematical model to analyze the spread of disease. One example of a disease that can be studied using this model is tuberculosis (TBC). TBC is a contagious disease that is transmitted through the air. The study aims to examine the SIR model with administration anti-tuberculosis medicine. The result obtained when $R_0 < 1$, he stability of the disease-free equilibrium point is locally asymptotically stable. Conversely, if $R_0 > 1$, then the stability of the disease endemic equilibrium point is locally asymptotically stable. Administration anti-tuberculosis medicine in the model plays a significant role to reduce the spread of the disease when the minimum level of administration anti-tuberculosis medicine.

$n_v > \frac{R_0 - 1}{R_0 \theta}$

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INTRODUCTION

Tuberculosis (TB) is an infectious disease found in all ages including children. TB is a disease caused by the complex organism Mycobacterium tuberculosis, which includes M. africanum, M. bovis, and M. canetti (and others that do not affect humans). This disease is transmitted through infected small respiratory tracts (about 1-5 mm) and is released in the form of droplet nuclei from TB sufferers and inhaled by other individuals and then enters the alveoli through close contact (Thomas, 2017).

Signs and symptoms of TB disease in children include cough, feeling weak and lethargic, weight loss or failure to thrive, fever, and night sweats. Infants, young children, and children with compromised immune systems (eg, children with HIV) are at high risk of developing severe forms of TB such as TB meningitis or miliary TB disease (Sterling et al., 2020).

According to the World Health Organization (WHO, 2023), Indonesia ranks second in the world after India with an estimated number of new TB cases of 1,060,000 cases with deaths reaching 134,000 per year. The gap between TB patients found and treated with TB patients estimated to exist in Indonesia is still above 30% in the last three years. Lampung Province is on a fluctuating graph for the number of TB case detection rates or Case Detection Rate (CDR) and the success rate of treatment or Success Rate (SR) from year to year. In 2023, the proportion of TB cases in children was 67% of all TB cases in Indonesia with 1,060,000 cases. Based on data from the Lampung Provincial Health Office in 2023, the number of new TB cases was 19,618 cases with 3,513 of them being TB cases in children aged 0-14 years. Based on the CDR, Metro Regency is the highest area with 109% of new TB cases and the lowest is in East Lampung Regency with 29% of cases. The higher the CDR, the more TB cases are found early and treated, thus reducing the transmission rate in the community. A low CDR means that there are still many TB cases that have not been found, indicating high TB transmission in the Regency/City (Lampung Provincial Health Office, 2023).

Tuberculosis in children has received special attention from the community and government and has not escaped the attention of scientists because it can threaten human life. Given the importance of further knowledge about tuberculosis in children, it is necessary to apply a mathematical model in the spread of tuberculosis in children. In applying a mathematical model for the spread of tuberculosis, the human population is divided into three parts, namely: the Susceptible subpopulation is a subpopulation that is susceptible to tuberculosis, the Infectious subpopulation is a subpopulation that is infected and transmits tuberculosis, and the Recovered subpopulation is a subpopulation that has recovered.

Research related to mathematical modeling of the spread of TB disease using the SIR model has been widely conducted by Muhammad S.D. et al. (2019) on Risk Factors for Tuberculosis in Children, Leni Darlina (2012) on the Stability of the Equilibrium Point of the SIR Model of Fatal Diseases with Migration, Muhammad Faudzi. et al. (2023) on the SIR Model for the Spread of

Tuberculosis in Jepara Regency, and K. Queen Fredina. et al. (2012) on the SIR Model for the Spread of Tuberculosis Disease.

Based on the research that has been conducted on the SIR model for TB disease, there is motivation to conduct research on the SIR model for TB disease in children by adding the assumption of administering Anti-Tuberculosis Drugs (OAT).

LITERATURE REVIEW

1. Differential Equations

A differential equation is an equation that involves a derivative of an unknown function, or the equation may also involve the function itself and constants. From the derivatives that form in the differential equation will determine the type and classification of the differential equation itself (Prayudi, 2006).

2. Differential Equation System

A system of differential equations is a system containing n differential equations, with n unknown functions, where n is a positive integer greater than or equal to two. The differential equations are consistently related to each other.

The general form of a system of n first order equations has the following form:

$$\begin{aligned} \frac{dx_1}{dt} &= g_1\,(t, x_1, x_2, \ldots, x_n) \\ \frac{dx_2}{dt} &= g_2\,(t, x_1, x_2, \ldots, x_n) \\ &\vdots \\ \frac{dx_n}{dt} &= g_n\,(t, x_1, x_2, \ldots, x_n) \end{aligned} \qquad (2.2.1)$$

With $x_1, x_2, \ldots, x_n$ are independent variables and t is the dependent variable, so that $x_1 = x_1(t), x_2 = x_2(t), \ldots, x_n = x_n(t)$, where $\frac{dx_n}{dt}$ is the derivative of the function x_n with respect to t, and g is a function that depends on the variables $x_1, x_2, \ldots, x_n$ and t (Neuhauser, 2004). With $x_1, x_2, \ldots, x_n$ are independent variables and t is the dependent variable, so that $x_1 = x_1(t), x_2 = x_2(t), \ldots, x_n = x_n(t)$, where $\frac{dx_n}{dt}$ is the derivative of the function x_n with respect to t, and g is a function that depends on the variables $x_1, x_2, \ldots, x_n$ and t (Neuhauser, 2004).

3. Ordinary Differential Equations

An ordinary differential equation is an equation that contains derivatives of a function containing one independent variable. If x is a function of t, then an example of an ordinary differential equation is:

$$\frac{dx}{dt} = t^2 \cos x \qquad (2.3.2)$$

where the equation has an order of one.

The order of a differential equation is the highest derivative of the unknown function (dependent variable) that appears in the differential equation (Campbell & Haberman, 2008).

4. Mathematical Modeling

A model is a simplified representation of a complex reality (usually aimed at understanding the reality) and has the same characteristics as its imitation in solving problems. A model is a general characteristic that represents a group of existing forms or a representation of a problem in a simpler and easier-to-work form. In mathematics, model theory is the science that presents mathematical concepts through the concept of sets or the science of models that support a mathematical system.

Model theory begins with the assumption of the existence of mathematical objects (for example, the existence of all numbers) and then seeks and analyzes the existence of operations, relations, or axioms inherent in each object or in those objects. The mathematical model obtained from a given mathematical problem is then solved with existing rules. The solution obtained needs to be tested to determine whether the solution is valid or invalid. Valid results will answer the mathematical model correctly and are called mathematical solutions. If the solution is invalid or does not meet the mathematical model, then the solution to the problem has not been found, and a re-solving of the mathematical model is needed (Frederick H. Bell, 1978).

5. Model SIR

The SIR model was first introduced by W.O. Kermack and Mc. Kendrick in their paper entitled A Contribution to the Mathematical Theory of Epidemis, which later appeared in the Procedings of the Royal Society of London and became an important role in the development of epidemic mathematics. The summary has been written in full by Murray. In his model, the human population is divided into three groups, namely suspects with the symbol S, infected with the symbol I, and cured or recovered with the symbol R, which are given in the form of s, i and r, respectively.

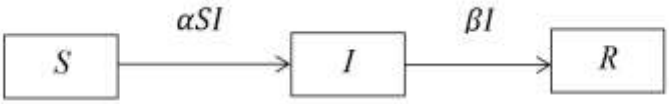
The total number of all the groups is

$$n = s + i + r \qquad (2.5.3)$$

S or susceptible in SIR modeling is an individual who is not infected but this group can be infected with the disease. Therefore, this group also has the possibility of becoming infected to become I or infected. I or infected is an individual who can spread the disease to individuals who can spread the disease called the disease period. After experiencing the disease period, this individual then moves and becomes an individual who is cured or recovered. R or recovered is an individual who has recovered or is immune to life.

The SIR model is generally written in the form of an ordinary differential equation, which is one part of the deterministic model (not random selection, this is due to the similarity of the initial conditions given to obtain the output), with continuous time (as opposed to discrete time). So it can be assumed that the change in infected and susceptible individuals occurs at a rate proportional to the population size. The rate of change of newly infected individuals is defined as αsi - βi, where α is the transmissivity value while β is the healing rate

value. Infected individuals are assumed to be able to recover with a constant probability over time, which then changes constantly with the per capita healing rate denoted as β and the whole is symbolized as βi. With this assumption, the SIR model formulation can be formulated as shown in the following figure:



Gambar 2.1 Skema Pembentukan Model SIR Sederhana

So the differential equation obtained in the explanation is as follows:

$$\begin{aligned} \frac{ds}{dt} &= -\alpha si \\ \frac{di}{dt} &= \alpha si - \beta i \\ \frac{dr}{dt} &= \beta i \end{aligned} \qquad (2.5.4)$$

This equation describes the transition of each individual from S to I and then to R. By adding these three equations, it can be easily shown that the total population is constant (Iswanto, 2012).

6. Balance Point

An equilibrium point is a condition where a system remains unchanged over time. If the dynamics of the system are described by differential equations, the equilibrium point can be identified by setting the first derivative to zero.

For example, suppose a differential equation is given in the following form:

$$\begin{aligned} \frac{dx}{dt} &= f(x,y) \\ \frac{dy}{dt} &= g(x,y) \end{aligned} \qquad (2.6.5)$$

A point (x_0 ,y_0) is considered as an equilibrium point of the system of equations above, if it satisfies the conditions $f(x_0,y_0) = 0$ and $g(x_0,y_0) = 0$. Since the derivative of a constant is always equal to zero, then the pair of functions $x(t) = x_0$ and $y(t) = y_0$ is an equilibrium solution of the system (2.6.5) (Campbell & Haberman, 2008).

Theorem 2.1 (Olsder et al., 2008):

1. The equilibrium point of a system of differential equations is considered stable, if all real parts of the eigenvalues of the Jacobian matrix are negative.
2. The equilibrium point of a system of differential equations is considered unstable, if at least one eigenvalue of the Jacobian matrix is positive.

7. System Stability

To obtain the stability of a system, an easier method is given by investigating the effect of small changes in the initial conditions. If the point (x*,y*) is an equilibrium point, then the effect of small changes in the equilibrium point is investigated.

If point (x,y) is a point around the equilibrium point, then mathematically point x,y is denoted as

$$(x, y) = (x^* + \Delta x, y^* + \Delta y) \tag{2.7.6}$$

The function approximation f_1 (x,y) and f_2 (x,y) can be determined using the Taylor series expansion as follows.

$$f_{1,2}(x, y) \approx f_{1,2}(x^*, y^*) + \frac{\partial f_{1,2}(x^*, y^*)}{\partial x}(x - x^*) + \frac{\partial f_{1,2}(x^*, y^*)}{\partial y}(y + y^*) \tag{2.7.7}$$

Because (x* ,y*) is an equilibrium point then f_1,2 (x* ,y*) - 0. Therefore, the system dx/dt = f_1 (x,y) and dy/dt = f_2 (x,y) can be approximated as a linear system.

$$\begin{aligned} \frac{dx}{dt} &= \frac{\partial f_1(x^*, y^*)}{\partial x}\Delta x + \frac{\partial f_1(x^*, y^*)}{\partial y}\Delta y \\ \frac{dx}{dt} &= \frac{\partial f_2(x^*, y^*)}{\partial x}\Delta x + \frac{\partial f_2(x^*, y^*)}{\partial y}\Delta y \end{aligned} \tag{2.7.8}$$

The linear system above can be presented in matrix form.

$$\begin{aligned} \begin{pmatrix} \frac{dx}{dt} \\ \frac{dy}{dt} \end{pmatrix} &= \begin{pmatrix} \frac{\partial f_1(x^*, y^*)}{\partial x} & \frac{\partial f_1(x^*, y^*)}{\partial y} \\ \frac{\partial f_2(x^*, y^*)}{\partial x} & \frac{\partial f_2(x^*, y^*)}{\partial y} \end{pmatrix} \begin{pmatrix} \Delta x \\ \Delta y \end{pmatrix} \\ &= J(x) \begin{pmatrix} \Delta x \\ \Delta y \end{pmatrix} \end{aligned} \tag{2.7.9}$$

The matrix J(x) in the system above is a Jacobian matrix (Khamsi, 2004).

8. Jobian Matrix

Given $g = (g_1, \ldots, g_n)$ on the system (2.2.1) above with $g_i \epsilon c^1(E), i = 1, 2, \ldots, n.$

Matrix:

$$\begin{bmatrix} \frac{\partial g_1}{\partial x_1}(x) & \cdots & \frac{\partial g_1}{n}(x) \\ \vdots & \ddots & \vdots \\ \frac{\partial g_n}{\partial x_1}(x) & \cdots & \frac{\partial g_n}{n}(x) \end{bmatrix} \tag{2.8.10}$$

called the Jacobian matrix g at the point x.

Next, the solution will be carried out using the linearization method. The following is the definition of the linearization method.

Definition 2.2 (Meiss, 2007)

System $\dot{x} = J(g(x))$ called system linearization (2.2.1) in (x). After the linearization process is carried out on system (2.2.1), then the stability behavior around the point *equilibrium* can be determined. The stability of the equilibrium point in system (2.2.1) can be determined based on the eigenvalues of the Jacobian matrix in the linearization method. The eigenvalues can be determined through the characteristic equation of the Jacobian matrix at the point x.

9. Analysis of Equilibrium Point Stability

The stability of linear systems and the linearization of nonlinear systems is known as the stability of equilibrium points. The stability at an equilibrium point can be defined by evaluating the sign of the real part of the Jacobian matrix around the equilibrium point.

Definition 2.3:

If J is an n x n matrix, then a nonzero vector x is called a characteristic vector of J if it satisfies:

$$Jx = \lambda x \tag{2.9.11}$$

Scalar λ which meets the characteristic equation $det(Jx = \lambda x) = 0$ are called the eigenvalues of the matrix J, and the vector x is considered to be the characteristic vector corresponding to λ.

The Jacobian matrix equation can be written as follows:

$$J = \frac{\partial f(x)}{\partial x} \begin{bmatrix} \frac{\partial f_1}{\partial x_1} & \frac{\partial f_1}{\partial x_2} & \cdots & \frac{\partial f_1}{\partial x_n} \\ \frac{\partial f_2}{\partial x_1} & \frac{\partial f_2}{\partial x_2} & \cdots & \frac{\partial f_2}{\partial x_n} \\ \vdots & \vdots & \ddots & \vdots \\ \frac{\partial f_3}{\partial x_1} & \frac{\partial f_3}{\partial x_2} & \cdots & \frac{\partial f_3}{\partial x_n} \end{bmatrix} \tag{2.9.12}$$

To get the matrix value J which is sized which is sized $n \times n$, then we can repeat Equation (2.9.11) or its equivalent. $(\lambda I - J)x = 0$. If the matrix $J\begin{bmatrix} a & b \\ c & d \end{bmatrix}$ and $I\begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix}$, then it can be written as $\begin{bmatrix} \lambda - a & -b \\ -c & \lambda - d \end{bmatrix}$ or $\lambda^2 - \lambda(a + d) + (ad - bc) = 0$ (Derouich & Boutayeb, 2008).

In general, the stability characteristics of an equilibrium point have the following properties:

1. **Stable**
   a. All real eigenvalues are negative. $(\lambda i < 0$ for all $i)$
   b. Each real number component of the complex eigenvalue is less than or equal to zero. $(R_e(\lambda_i) \leq 0$ for all $i)$
2. **Unstable**
   a. There are positive real eigenvalues $(\lambda i > 0$ for all $i)$
   b. Each real number component of the complex eigenvalue is less than or equal to zero. $(R_e(\lambda_i) > 0$ for all $i)$(Tu, 1994).

10. Routh-Hurwitz Criteria

The Routh-Hurwitz Stability Criterion provides an assessment of the stability of a system without calculating its fundamentals. This method uses a polynomial characteristic equation to measure the stability of the system. If the

polynomial equation is the characteristic equation of the system, this standard can be applied to evaluate the stability of the system (A'maludin et al., 2016).

The procedure in applying the Routh-Hurwitz criteria is as follows:

1. The n^{th} order polynomial equation can be written:

$$det(\lambda I - A) = a_n\lambda^n + a_{n1}\lambda^{n-1} + \ldots + a_1\lambda + a_0 \qquad (2.10.13)$$

2. A zero or negative coefficient indicates that there are one or more imaginary roots or positive real parts, indicating that the system is unstable.
3. If all coefficients have positive values, it can form a matrix called the Routh-Hurwitz array as shown below:

$$\begin{bmatrix} \lambda^n & a_n & a_{n2} & a_{n4} & \cdots \\ \lambda^{n1} & a_{n1} & a_{n3} & a_{n5} & \cdots \\ \lambda^{n2} & b_1 & b_2 & b_3 & \cdots \\ \vdots & c_1 & c_2 & c_3 & \cdots \\ \lambda^0 & \vdots & \vdots & \vdots & \end{bmatrix} \qquad (2.10.14)$$

Coefficient $b_1, b_2, \ldots, b_k$ and $c_1, c_2, \ldots, c_k$ can be calculated using the following formulas:

$$b_1 = -\frac{1}{a_{n1}}\begin{vmatrix} a_n & a_{n2} \\ a_{n1} & a_{n3} \end{vmatrix}, b_2 = -\frac{1}{a_{n3}}\begin{vmatrix} a_{n2} & a_{n4} \\ a_{n3} & a_{n5} \end{vmatrix}, \ldots \qquad (2.10.15)$$

$$c_1 = -\frac{1}{b_1}\begin{vmatrix} a_{n1} & a_{n3} \\ b_1 & b_2 \end{vmatrix}, c_2 = \frac{1}{b_2}\begin{vmatrix} a_{n3} & a_{n5} \\ b_2 & b_3 \end{vmatrix}, \ldots \qquad (2.10.16)$$

4. The number of unstable roots can be identified by looking at the number of sign changes in the first column of the matrix. (2.10.14).
5. When all elements in the first column of the matrix (2.10.14) have positive values, and the coefficients of the characteristic equation have positive values, then the system is considered stable. After the second column reaches zero, iteration is given.

11. Numerical Methods

Numerical Method is a technique used to formulate mathematical problems so that they can be solved by ordinary arithmetic or calculation operations (add, subtract, multiply and divide). Numerical methods are also called alternatives to analytical methods, which are methods for solving mathematical problems with standard or common algebraic formulas. It is called so because mathematical problems are often difficult to solve or even cannot be solved analytically. So it can be said that the mathematical problem does not have an analytical solution. So as an alternative, the mathematical problem is solved by numerical methods.

The difference between analytical methods and numerical methods is that analytical methods can only be used to solve simple problems and produce actual solutions or true solutions. The solution produced from numerical solutions is an approximate solution or approach that approaches the exact

solution or true solution. The results of the solution obtained from numerical methods and analytical methods have differences, where the difference is called an error (Triatmodjo, 2002).

METHODOLOGY

This research was conducted using a library research method or literature study using sources that can be in the form of books, research journals, theses, theses, or the internet. The steps taken in this study are as follows:

1. Establish assumptions and define the parameters used.
2. Developing a SIR model for TB disease in children by including assumptions about the administration of Anti-Tuberculosis Drugs.
3. Determining the equilibrium point of the SIR model for TB disease in children.
4. Identifying the value of (R_0) using the Jacobian matrix.
5. Conduct stability analysis using the Routh-Hurwitz criteria.
6. Determine the minimum number of individuals given Anti-Tuberculosis drugs.
7. Provide an example of a numerical simulation to see how TB disease in children can spread by considering the administration of Anti-Tuberculosis Drugs.

RESULTS AND DISCUSSION

1. Mathematical Modelling

The SIR model of TB disease in children by considering the factor of giving Anti-Tuberculosis Drugs (OAT) can be derived by using certain assumptions or limitations. As the assumptions used in the disease spread model are.

a. The human population is divided into 3 groups, namely Susceptible (S) are healthy individuals who are at risk of infection, Infected (I) are individuals who are susceptible to infection with a disease, and Recovered (R) are individuals infected with a disease who have recovered.
b. Birth and death factors are taken into account with the number of births and the number of deaths per unit of time assumed to be different.
c. Birth is considered to occur in class S, but the newborn individual is healthy but susceptible to TB disease.
d. TB disease has the potential to cause fatal death in sufferers.
e. OAT is given only to individuals in class S, the success rate of giving OAT is 85% which means that individuals who have received OAT can move to class I.
f. Individuals who have recovered are assumed to be able to be reinfected with TB, but can also form antibodies..

2. SIR Model with Anti-Tuberculosis Drug Administration

Based on the assumptions that have been applied, a SIR model diagram can be designed for TB disease in children with OAT administration as shown in the following image:

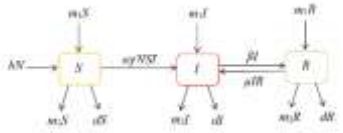


Figure 1. SIR Compartment Diagram for TB Disease in Children with OAT Administration

Based on the assumptions that have been made, the model parameters can be defined as follows:

N : total population

b : birth rate

d : death rate

α : rate of infection

β : Individuals who have received OAT recover from the disease

m_1 : rate of receiving OAT administration

m_2 : rates did not receive OAT administration

γ : total individuals who did not receive and had received OAT but were infected

μ : re-infection rate (relapse)

with $\gamma = 1 - \theta n$

θ = efficacy (ability to achieve goals) of administering OAT

n = number of individuals who have been given OAT

From the compartment diagram in the image above, the SIR model of the differential equation system is obtained as follows:

$$\frac{dS}{dt} = bN + m_1 S - m_2 S - dS - \alpha\gamma NSI \tag{4.2.1}$$

$$\frac{dI}{dt} = \alpha\gamma NSI + \mu IR + m_1 I - m_2 I - dI - \beta I \tag{4.2.2}$$

$$\frac{dR}{dt} = \beta I + m_1 R - m_2 R - dR - \mu IR \tag{4.2.3}$$

with

$$S(0) > 0, I(0) > 0, R(0) \geq 0$$
$$b, d, \alpha, \beta, m_1, m_2\gamma, \mu > 0$$

Thus, the total population can be expressed as follows:

$$N(t) = S(t) + I(t) + R(t)$$

and the total population rate is obtained as follows:

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} \tag{4.2.4}$$

Based on equation (4.2.4), a model transformation will be carried out by comparing each class to the total population rate to obtain:

$$s = \frac{S}{N};\ i = \frac{I}{N};\ r = \frac{R}{N} \tag{4.2.5}$$

Based on equation (4.2.4) and equation (4.2.5), the transformation of the total population rate is as follows:

$$\begin{aligned}
\frac{dN}{dt} &= \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} \\
\frac{dN}{dt} &= bn + m_1 S - m_2 S - dS - \alpha\gamma NSI + \alpha\gamma NSI + \mu IR + m_1 I + m_2 I \\
&\quad - dI - \beta I + \beta I + m_1 R - m_2 R - dR - \mu IR \\
\frac{dN}{dt} &= bN + m_1 I + m_2 R - dS - dI - dR - m_2 S - m_2 I - m_2 R - \alpha\gamma NSI \\
&\quad + \alpha\gamma - \beta I + \beta I + \mu IR - \mu IR \\
\frac{dN}{dt} &= bN + (S + I + R)m_1 - (S + I + R)d - (S + I + R)m_2 \\
\frac{dN}{dt} &= bN + m_1 N - dN - m_2 N
\end{aligned} \tag{4.2.6}$$

After obtaining equation (4.2.6), transform equation (4.2.1) by substituting equation (4.2.5) and equation (4.2.6) into equation (4.2.1), resulting in the following equation:

$$\begin{aligned}
\frac{dS}{dt} &= bN + m_1 S - m_2 S - dS - \alpha\gamma NSI \\
\frac{d(sN)}{dt} &= bN + m_1(sN) - m_2(sN) - d(sN) - \alpha\gamma(sN))(iN) \\
N\frac{ds}{dt} + s\frac{dN}{dt} &= bN + m_1 sN - m_2 sN - dsN - \alpha\gamma NsNiN \\
N\frac{ds}{dt} + s(bN + m_1 N - dN - m_2 N) &= bN + m_1 sN - m_2 sN \\
&\quad - dsN - \alpha\gamma NsNiN \\
N\frac{ds}{dt} bsN + m_1 sN - dsN - m_2 sN &= bN + m_1 sN - m_2 sN \\
&\quad - dsN - \alpha\gamma NsNiN \\
N\frac{ds}{dt} &= bN - bsN + m_1 sN + m_1 sN - m_1 sN - m_2 sN + m_2 sN \\
&\quad - dsN + dsN - \alpha\gamma NsNiN \\
N\frac{ds}{dt} &= (1 - s)bN - \alpha\gamma NsNiN \\
\frac{ds}{dt} &= (1 - s)b - \alpha\gamma si
\end{aligned}$$

Transform equation (4.2.2) by substituting equation (4.2.5) and equation (4.2.6) into equation (4.2.2) to obtain the following:

$$\frac{dI}{dt} = \alpha\gamma NSI + \mu IR + m_1 I - m_2 I - dI - \beta I$$
$$\frac{d(iN)}{dt} = \alpha\gamma N(sN)(iN) + \mu(iN)(rN) + m_1(iN) - d(iN) - \beta(iN)$$
$$N\frac{di}{dt} + i\frac{dN}{dt} = \alpha\gamma NsNiN + \mu iNrN + m_1 iN - m_2 iN - diN - \beta iN$$
$$N\frac{di}{dt} + i(bN + m_2 N - dN - m_2 N) = \alpha\gamma NsNiN + \mu iNrN + m_1 iN - m_2 iN - diN - \beta iN$$
$$N\frac{di}{dt} + biN + m_1 iN - diN - m_2 iN = \alpha\gamma NsNiN + \mu iNrN + m_1 iN - m_2 iN - diN - \beta iN$$
$$N\frac{di}{dt} = \alpha\gamma NsNiN + \mu iNrN - biN + m_1 iN - m_1 iN - m_2 iN + m_2 iN - diN - \beta iN$$
$$N\frac{di}{dt} = \alpha\gamma NsNiN + \mu iNrN - biN$$
$$\frac{di}{dt} = \alpha\gamma si + \mu ir - bi$$

Transform equation (4.2.3) by substituting equation (4.2.5) and equation (4.2.6) into equation (4.2.3) to obtain the following:

$$\frac{dR}{dt} = \beta I + m_1 R - m_2 R - dR - \mu IR$$
$$\frac{d(rN)}{dt} = \beta(iN) + m_1(rN) - m_2(rN) - d(rN) - \mu(iN)(rN)$$
$$N\frac{dr}{dt} + r\frac{dN}{dt} = \beta iN + m_1 rN - m_2 rN - drN - \mu iNrN$$
$$N\frac{dr}{dt} + r(bN + m_1 N - dN - m_2 N) = \beta iN + m_1 rN - m_2 rN - drN - \mu iNrN$$
$$N\frac{dr}{dt} + brN + m_1 rN - drN - m_2 rN = \beta iN + m_1 rN - m_2 rN - drN - \mu iNrN$$
$$N\frac{dr}{dt} = \beta iN + m_1 rN - m_1 rN - m_2 rN - drN + drN - \mu iNrN - brN$$
$$N\frac{dr}{dt} = \beta iN - \mu iNrN - brN$$
$$\frac{dr}{dt} = \beta i - \mu ir - br$$

After obtaining the transformed equation, the following system of equations is obtained:

$$\frac{ds}{dt} = (1-s)b - \alpha\gamma si \qquad (4.2.7)$$
$$\frac{di}{dt} = \alpha\gamma si + \mu ir - bi \qquad (4.2.8)$$
$$\frac{dr}{dt} = \beta i - \mu ir - br \qquad (4.2.9)$$

3. Balance Point

The equilibrium points of equations (4.2.7), (4.2.8) and (4.2.9) can be defined by comparing the first derivatives which are equal to zero, namely $\frac{ds}{dt} = 0, \frac{dr}{dt} = 0$. Two equilibrium points will be identified, namely the disease-free equilibrium point and the disease-endemic equilibrium point.

a. Disease-Free Balance Point

At the disease-free equilibrium point, the condition indicates that there is no disease in the population. Therefore, the value of i = 0. Thus, no one can transmit TB. From equation (4.2.7) substitute i = 0, obtained:

$$(1 - s)b - \alpha\gamma si = 0$$

Can $i = 0$, so that it is obtained:

$$\begin{aligned} (1 - s)b &= 0 \\ b - bs &= 0 \\ bs &= b \\ s &= \frac{b}{b} \\ s &= 1 \end{aligned} \qquad (4.3.10)$$

$$\beta i - \mu ir - br = 0$$

Next, substitute $i = 0$ to the equation (4.2.9) obtained: Because $i = 0$, so:

$$\begin{aligned} -br &= 0 \\ r &= 0 \end{aligned} \qquad (4.3.11)$$

Thus, the disease-free equilibrium point for TBC in children can be stated as follows.:

$$(s, i, r) = (1, 0, 0) \qquad (4.3.12)$$

b. Endemic Disease Balance Point

At the endemic equilibrium point of the disease, this condition indicates that a person is sick. This indicates that there is a possibility that a person can transmit TB to others, so $i * > 0$.

From equation (4.2.8) we obtain:

$$\begin{aligned}
\alpha\gamma s^* i^* + \mu i^* r^* - b^* &= 0 \\
i^*(\alpha\gamma s^* + \mu r^* - b) &= 0 \\
\alpha\gamma s^* + \mu r^* - b &= 0 \\
\alpha\gamma s^* &= b - \mu r \\
s^* &= \frac{b - \mu r^*}{\alpha\gamma} \qquad (4.3.13)
\end{aligned}$$

Next, change the value of s ∗ from equation (4.3.13) into equation (4.2.7), resulting in:

$$\begin{aligned}
\left(1 - \frac{b - \mu r^*}{\alpha\gamma}\right) b - \alpha\gamma \left(\frac{b - \mu r^*}{\alpha\gamma}\right) i^* &= 0 \\
b - b\left(\frac{b - \mu r^*}{\alpha\gamma}\right) - (b - \mu r^*) i^* &= 0 \\
-(b\mu - r^*) i^* &= -\left(b - b\left(\frac{b - \mu r^*}{\alpha\gamma}\right)\right) \\
i^* &= \frac{b - b\left(\frac{b - \mu r^*}{\alpha\gamma}\right)}{b - \mu r^*} \qquad (4.3.14)
\end{aligned}$$

Next, change the value of s ∗ from equation (4.3.13) into equation (4.2.7), resulting in:

$$\beta\left(\frac{b - b\left(\frac{b - \mu r^*}{\alpha\gamma}\right)}{b - \mu r}\right) - \mu\left(\frac{b - b\left(\frac{b - \mu r^*}{\alpha\gamma}\right)}{b - \mu r^*}\right) r^* - b r^* = 0$$

To simplify the equation, let's assume:

$$x = b - \mu r^*$$

So that

$$\beta\left(\frac{b - b\left(\frac{x}{\alpha\gamma}\right)}{x}\right) - \mu\left(\frac{b - b\left(\frac{x}{\alpha\gamma}\right)}{x}\right) r^* - b r^* = 0$$

$$\beta\left(b - b\left(\frac{x}{\alpha\gamma}\right)\right) - \mu\left(b - b\left(\frac{x}{\alpha\gamma}\right)\right) r^* - b r^* x = 0$$

$$\beta b - \beta b\left(\frac{x}{\alpha\gamma}\right) - \mu b r^* + \mu b r^*\left(\frac{x}{\alpha\gamma}\right) - b r^* x = 0$$

$$\begin{aligned}
\alpha\gamma\beta b - \beta b x - \alpha\gamma\mu b r^* + \mu b r^* x - \alpha\gamma b r^* x &= 0 \\
\alpha\gamma\beta b - \beta b(b - \mu r^*) - \alpha\gamma\mu b r^* + \mu b r^*(b - \mu r^*) - \alpha\gamma b r^*(b - \mu r^*) &= 0 \\
\alpha\gamma\beta b - \beta b^2 + \beta b\mu r^* - \alpha\gamma\mu b r^* + \mu b^2 r^* - \mu b r^{*2} - \alpha\gamma b^2 r^* + \alpha\gamma b\mu r^{*2} &= 0 \\
\alpha\gamma\beta b - \beta b^2 - r^*(\beta b\mu - \alpha\gamma\mu b + \mu b^2) - r^{*2}(\mu b + \alpha\gamma b\mu) &= 0 \\
\beta b(\alpha\gamma - b) + r^*(\beta b\mu + \mu b^2 + \alpha\gamma b^2 - \alpha\gamma\mu b) - r^{*2}(\mu b + \alpha\gamma b\mu) &= 0 \\
r^{*2}(\mu b + \alpha\gamma b\mu) &= -r^*(\beta b\mu + \mu b^2 + \alpha\gamma\mu b) - \beta b(\alpha\gamma - b) \\
r^* &= -\frac{r^*(\beta b\mu + \mu b^2 - \alpha\gamma b^2 - \alpha\gamma\mu b) - \beta b(\alpha\gamma - b)}{r^*(\mu b + \alpha\gamma b\mu)}
\end{aligned}$$

(4.3.15)

Based on equations (4.3.13), (4.3.14) and (4.3.15), the endemic equilibrium point for TB disease in children is obtained:

$$(s^*, i^*, r^*) = \begin{pmatrix} \frac{b-\mu r^*}{\alpha\gamma}, \\ \frac{b-b\left(\frac{b-\mu r^*}{\alpha\gamma}\right)}{b-\mu r}, \\ -\frac{r^*(\beta b\mu+\mu b^2)-\alpha\gamma b)-\beta b(\alpha\gamma-b))}{r^*(\mu b+\alpha\gamma b\mu)} \end{pmatrix} \quad (4.3.16)$$

4. Basic Reproduction Number

To obtain the R_0 value of equations (4.2.7), (4.2.8) and (4.2.9), the steps that can be taken involve the use of the Jacobian matrix. In a disease-free state, it is assumed that $I = 0$, so that S = 1, $I = 0$, R = 0. The Jacobian matrix is obtained by partial derivatives of the system of equations with respect to S, I and R as follows

$$J = \begin{bmatrix} \frac{\partial(\frac{dS}{dt})}{\partial S} & \frac{\partial(\frac{dS}{dt})}{\partial I} & \frac{\partial(\frac{dS}{dt})}{\partial R} \\ \frac{\partial(\frac{dI}{dt})}{\partial S} & \frac{\partial(\frac{dI}{dt})}{\partial I} & \frac{\partial(\frac{dI}{dt})}{\partial R} \\ \frac{\partial(\frac{dR}{dt})}{\partial S} & \frac{\partial(\frac{dR}{dt})}{\partial I} & \frac{\partial(\frac{dR}{dt})}{\partial R} \end{bmatrix}$$

So, substitute $I = 0, S = 0$ and $R = 0$ by taking partial derivatives of $\frac{dI}{dt}$, submatrix for compartments is obtained I.

$$F = \begin{bmatrix} \frac{\partial(\alpha\gamma SI)}{\partial I} & 0 \\ 0 & -(\mu_i + b) \end{bmatrix} \quad (4.4.17)$$

Next, substituting the disease-free equilibrium point value (4.3.12) into the equation above, we obtain R_0 which has the form:

$$R_0 = \frac{\alpha\gamma}{b+\mu_i} \quad (4.4.18)$$

5. Stability Point Analysis at Equilibrium Point

After determining the equilibrium point of the model, the next step is to analyze the stability of each point, namely the disease-free equilibrium point and the disease-endemic equilibrium point. The linearization process is carried out on equations (4.2.7), (4.2.8) and (4.2.9). Suppose:

$$f(s,i,r) = \frac{ds}{dt} = (1-s)b - \alpha\gamma si \quad (4.5.19)$$

$$g(s,i,r) = \frac{di}{dt} = \alpha\gamma si + \mu ir - bi \quad (4.5.20)$$

$$h(s,i,r) = \frac{dr}{dt} = \beta i - \mu ir - br \quad (4.5.21)$$

By linearizing equations (4.5.19), (4.5.20) and (4.5.21) we obtain:

$$\frac{\partial f}{\partial s} = \frac{(1-s)b - \alpha\gamma si}{ds} = -b - \alpha\gamma i$$
$$\frac{\partial f}{\partial i} = \frac{(1-s)b - \alpha\gamma si}{di} = -\alpha\gamma s$$
$$\frac{\partial f}{\partial r} = \frac{(1-s)b - \alpha\gamma si}{dr} = 0$$
$$\frac{\partial g}{\partial s} = \frac{\alpha\gamma si + \mu ir - bi}{ds} = \alpha\gamma i$$
$$\frac{\partial g}{\partial i} = \frac{\alpha\gamma si + \mu ir - bi}{di} = \alpha\gamma s + \mu r - b$$
$$\frac{\partial g}{\partial r} = \frac{\alpha\gamma si + \mu ir - bi}{dr} = \mu i$$
$$\frac{\partial h}{\partial s} = \frac{\beta i - \mu ir - br}{ds} = 0$$
$$\frac{\partial h}{\partial i} = \frac{\beta i - \mu ir - br}{di} = \beta - \mu r$$
$$\frac{\partial h}{\partial r} = \frac{\beta i - \mu ir - br}{dr} = -\mu i - b$$

The result of the linearization carried out is the elements of the Jacobian matrix *J*, which will form the matrix *J* as follows:

$$J = \begin{bmatrix} \frac{\partial f}{\partial s} & \frac{\partial f}{\partial i} & \frac{\partial f}{\partial r} \\ \frac{\partial g}{\partial s} & \frac{\partial g}{\partial i} & \frac{\partial g}{\partial r} \\ \frac{\partial h}{\partial s} & \frac{\partial h}{\partial i} & \frac{\partial h}{\partial r} \end{bmatrix}$$

So we can obtain the Jacobian matrix from the system of equations (4.2.7), (4.2.8) and (4.2.9) which has the form:

$$J = \begin{bmatrix} -b - \alpha\gamma i & -\alpha\gamma s & 0 \\ \alpha\gamma i & \alpha\gamma + \mu r - b & \mu i \\ 0 & \beta - \mu r & -\mu i - b \end{bmatrix} \quad (4.5.22)$$

a. Stability of Disease-Free Balance Point

It will be proven that the disease-free equilibrium point: (*s,i,r*) = (1,0,0) is locally asymptotically stable.

By substituting the disease-free equilibrium point values in equation (4.3.12) into the Jacobian matrix (4.5.22), we obtain:

$$J = \begin{bmatrix} -b & -\alpha\gamma & 0 \\ 0 & \alpha\gamma - b & 0 \\ 0 & \beta & -b \end{bmatrix} \quad (4.5.23)$$

Next, to obtain the eigenvalues of the matrix (4.5.23), a nontrivial solution is required that satisfies:

$$det|\lambda I - J| = 0$$

Where λ is the eigenvalue. The characteristic equation for the Jacobian matrix (4.5.23) analyzed by substituting the disease-free equilibrium points can be expressed as follows:

$$det|\lambda I - J| = 0$$

$$det\left[\lambda\begin{bmatrix}1&0&0\\0&1&0\\0&0&1\end{bmatrix}-\begin{bmatrix}-b&\alpha\gamma&0\\0&\alpha\gamma-b&0\\0&\beta&-b\end{bmatrix}\right]=0$$

$$det\left[\begin{bmatrix}\lambda&0&0\\0&\lambda&0\\0&0&\lambda\end{bmatrix}-\begin{bmatrix}-b&\alpha\gamma&0\\0&\alpha\gamma-b&0\\0&\beta&-b\end{bmatrix}\right]=0$$

$$det\begin{bmatrix}\lambda+b&\alpha\gamma&0\\0&\lambda-\alpha\gamma+b&0\\0&-\beta&\lambda+b\end{bmatrix}=0 \qquad (4.5.24)$$

Using the Det syntax in Wolfram Mathematica software to find the determinant of the matrix (4.5.24), the result is:

$$(b+\lambda)^2(b-\alpha\gamma+\lambda)=0$$

The eigenvalues obtained $\lambda_1 = -b$ and $\lambda_2 = \alpha\gamma - b$. It can be seen that λ_1 is negative, while λ_2 is not necessarily negative. Therefore, it will be proven that λ_2 is negative.

It is known that the condition for a disease-free equilibrium point is considered stable if $R_0 < 1$. It is known $R_0 = \frac{\alpha\gamma}{b+\mu i}$, then obtained:

$$\frac{\alpha\gamma}{b+\mu i} < 0$$

$$\alpha\gamma < b+\mu i$$

$$\alpha\gamma - b - \mu i < 0$$

Because $\lambda_2 = \alpha\gamma - b - \mu i$, then obtained:

$$\lambda_2 < 0$$

Based on the conditions of the Routh-Hurwitz criterion, it can be said that the disease-free equilibrium point has asymptotic local stability. This is indicated by the eigenvalues which are all the same value, namely negative (without any change in sign).

a. Stability of Endemic Disease Equilibrium Point

It will be proven that the disease-free equilibrium point:

$$(s,i,r) = \begin{pmatrix} \frac{b-\mu r}{\alpha\gamma}, \\ \frac{b-b\left(\frac{b-\mu r}{\alpha\gamma}\right)}{b-\mu r}, \\ -\frac{r(\beta b\mu+\mu b^2-\alpha\gamma b^2)-\beta b(\alpha\gamma-b)}{r(\mu b+\alpha\gamma b\mu)} \end{pmatrix}$$

Evidence:
Suppose:

$$x = s = \frac{b-\mu r}{\alpha\gamma}$$

$$y = i = \frac{b-b\left(\frac{b-\mu R}{\alpha\gamma}\right)}{b-\mu r}$$

$$z = r = -\frac{r(\beta b\mu+\mu b^2-\alpha\gamma b^2-\alpha\gamma\mu b)-\beta b(\alpha\gamma-n))}{r(\mu b+\alpha\gamma b\mu)}$$

By substituting the values of x, y, and z into the Jacobian matrix (4.5.22), we obtain:

$$J = \begin{bmatrix} -b-y\alpha\gamma & -x\alpha\gamma & 0 \\ y\alpha\gamma & -b+x\alpha\gamma+z\mu & y\mu \\ 0 & \beta-z\mu & -b-y\mu \end{bmatrix} \quad (4.5.25)$$

Next, to obtain the eigenvalues of the matrix (4.5.25), a nontrivial solution is required that satisfies:

$$det|\lambda I - J| = 0$$

Where λ is the eigenvalue. The characteristic equation for the Jacobian matrix (4.5.25) analyzed by substituting the disease-free equilibrium points can be expressed as follows:

$$det|\lambda I - J| = 0$$

$$det\left[\lambda\begin{bmatrix}1&0&0\\0&1&0\\0&0&1\end{bmatrix} - \begin{bmatrix} -b-y\alpha\gamma & -x\alpha\gamma & 0 \\ y\alpha\gamma & -b+x\alpha\gamma+z\mu & y\mu \\ 0 & \beta-z\mu & -b-y\mu \end{bmatrix}\right] = 0$$

$$det\left[\begin{bmatrix}\lambda&0&0\\0&\lambda&0\\0&0&\lambda\end{bmatrix} - \begin{bmatrix} -b-y\alpha\gamma & -x\alpha\gamma & 0 \\ y\alpha\gamma & -b+x\alpha\gamma+z\mu & y\mu \\ 0 & \beta-z\mu & -b-y\mu \end{bmatrix}\right] = 0$$

$$det\begin{bmatrix} \lambda+b+y\alpha\gamma & x\alpha\gamma & 0 \\ -y\alpha\gamma & \lambda+b-x\alpha\gamma-z\mu & -y\mu \\ 0 & -\beta+z\mu & \lambda+b+y\mu \end{bmatrix} = 0 \quad (4.5.26)$$

Using the Det syntax in Wolfram Mathematica software to find the determinant of the matrix (4.5.26), we obtain:

$$y(b+y\alpha\gamma+\lambda)\mu(-\beta+z\mu)+(b+\lambda+y\mu)(xy\alpha^2\gamma^2+(b+y\alpha\gamma+\lambda)$$
$$(b-x\alpha\gamma+\lambda-z\mu))=0 \quad (4.5.27)$$

Next, the eigenvalues of the determinant (4.5.27) will be searched. By using the Expand syntax in the Wolfarm Mathematica software in describing the results of the determinant (4.5.27) to be directed to the Routh-Hurwitz criterion, the following is obtained:

$$b^3-b^2x\alpha\gamma+b^2y\alpha\gamma+3b^2\lambda-2bx\alpha\gamma\lambda+2by\alpha\gamma\lambda+3b\lambda^2-x\alpha\gamma y\lambda^2+y\alpha\gamma\lambda^2$$
$$+\lambda^3+b^2y\mu-b^2z\mu-by\beta\mu-bxy\alpha\gamma\mu+by^2\alpha\gamma\mu-byz\alpha\gamma\mu-y^2\alpha\beta\gamma\mu$$
$$+2by\lambda\mu-2bz\lambda\mu-y\beta\gamma\mu-xy\alpha\gamma\beta\mu+y^2\alpha\gamma\lambda\mu-yz\alpha\gamma\lambda\mu+y\lambda^2\mu-z\lambda^2\mu=0$$

$$\rightarrow\lambda^3+3b\lambda^3-x\alpha\gamma\lambda^2+y\alpha\gamma\lambda^2+y\lambda^2\mu-z\lambda^2\mu+3b^2\lambda-2bx\alpha\gamma\lambda+2by\alpha\gamma\lambda$$
$$+2by\lambda\mu-2bz\lambda\mu-xy\alpha\gamma\lambda\mu+y^2\alpha\gamma\lambda\mu-yz\alpha\gamma\lambda\mu+b^2y\mu-b^2z-by\beta\mu$$
$$-bxy\alpha\gamma\mu+by^2\alpha\gamma\mu-byz\alpha\gamma\mu-y^2\alpha\beta\gamma\mu+b^3-b^2x\alpha\gamma+b^2y\alpha\gamma=0$$
$$\rightarrow\lambda^3+\lambda^2(3b-x\alpha\gamma+y\alpha\gamma+y\mu-x\mu)+\lambda(3b^2-2bx\alpha\gamma+2by\alpha\gamma+2by\mu$$
$$-2bz\mu-y\beta\mu-xy\alpha\gamma\mu+y^2\alpha\gamma\mu-yz\alpha\gamma\mu)+by(b\mu-\beta\mu-x\alpha\gamma\mu+y\alpha\gamma\mu$$
$$-z\alpha\gamma\mu+b\alpha\gamma)-b^2(z\mu+b-x\alpha\gamma)-y^2\alpha\beta\gamma\mu=0 \quad (4.5.28)$$

Next, analyze equation (4.5.28) using the Routh-Hurwitz criterion, assuming:

$$i=3b-x\alpha\gamma+y\alpha\gamma+y\mu-z\mu$$
$$j=3b^2-2bx\alpha\gamma+2by\alpha\gamma+2by\mu-2bz\mu-y\beta\mu-xy\alpha\gamma\mu+y^2\alpha\gamma\mu-yz\alpha\gamma\mu$$
$$k=by(b\mu-\beta\mu-x\alpha\gamma\mu+y\alpha\gamma\mu-z\alpha\gamma\mu+b\alpha\gamma)-b^2(z\mu+b-x\alpha\gamma)-y^2\alpha\beta\gamma\mu$$

The next step is to form an Array-Routh based on equation (4.5.28), then we obtain:

$$\begin{bmatrix}\lambda^3\\ \lambda^2\\ \lambda^1\\ \lambda\end{bmatrix}=\begin{bmatrix}1 & j\\ i & k\\ \frac{(ij-k)}{i} & 0\\ k & 0\end{bmatrix} \quad (4.5.29)$$

Matrix (4.5.29) satisfies the necessary and sufficient conditions of Theorem 2.1 because each element in the first column of the matrix has a positive sign (no sign change). Therefore, it can be concluded that equation (4.5.28) is asymptotically stable.

6. Minimum Number of Individuals Given Anti-Tuberculosis Drugs

Based on the discussion above, the R_0 for TBC disease in children is:

$$R_0=\frac{\alpha\gamma}{b+\mu i}$$
$$R_0=\frac{\alpha(1-\theta n)}{b+\mu i}$$

With n in the basic reproduction number indicating the number of individuals given OAT. To reduce the spread of disease, a minimum definition of OAT administration is needed so that it does not become endemic. The minimum OAT administration is symbolized as n_v.

$$\begin{aligned} R_0(1-\theta n_v) &< 1 \\ (R_0 - R_0\theta n_v) &< 1 \\ -R_0\theta n_v &< 1 - R_0 \\ R_0\theta n_v &> R_0 - 1 \\ n_v &> \frac{R_0 - 1}{R_0\theta} \end{aligned}$$

7. Example of Numerical Simulation

This simulation aims to test both equilibrium points, the disease-free equilibrium point and the disease-endemic equilibrium point, by assigning arbitrary values to each parameter. The parameter values set in this example are presented in the following table:

Table 1. Estimated Parameter Values

Parameter	Nilai Estimasi Parameter (Tanpa Penyakit)	Nilai Estimasi Parameter (Endemik Penyakit)
N	1000	1000
α	0,1	1
β	0,08	0,25
b	0,5	0,9
μ	0,5	0,5
γ	0,5	0,915

a. Disease-Free Balance Point 1 Disease-Free Balance Point

To test the stability of the disease-free equilibrium, point in equation (4.3.12), the initial conditions will be given as $s_0 = 0,3$; $i_0 = 0,4$; and $r_0 = 0,6$. The disease-free equilibrium point is $(s,i,r) = (1,0,0)$ and $R_0 = 0,1$. The parameters in Table (4.1) are substituted into matrix (4.5.24), resulting in:

$$\begin{bmatrix} \lambda+0,5 & 0,05 & 0 \\ 0 & \lambda+0,45 & 0 \\ 0 & -0,08 & \lambda+0,5 \end{bmatrix} = 0$$

$$\begin{aligned} (\lambda+0,5)\begin{vmatrix} \lambda+0,45 & 0 \\ 0 & \lambda+0,5 \end{vmatrix} - (0)\begin{vmatrix} 0,05 & 0 \\ -0,08 & \lambda+0,5 \end{vmatrix} \\ +(0)\begin{vmatrix} 0,05 & 0 \\ \lambda+0,45 & 0 \end{vmatrix} = 0 \\ \Leftrightarrow (\lambda+0,5)((\lambda+0,45)(\lambda+0,5)-0)-0+0=0 \\ \Leftrightarrow \lambda^3+1,45\lambda^2+0,7\lambda+0,1125=0 \end{aligned}$$

Then we get the characteristic equation

$\lambda^3 + 1,45\lambda\ 2 + 0,7\lambda + 0,1125 = 0$. Using Wolfram Mathematica software to obtain eigenvalues $\lambda_1 = -0,5$; $\lambda_2 = -0,5$; dan $\lambda_3 = -0,45$. Since all eigenvalues are negative, it can be concluded that the disease-free equilibrium is stable.

b. Endemic Disease Balance Point

To test the stability of the equilibrium point for endemic disease in equation (4.3.16), the initial conditions are given as $s_0 = 0,3; i_0 = 0,2$ and $r_0 = 0,05$. The endemic equilibrium point of the disease is:

$$(s_1, i_1, r_1) = \begin{pmatrix} \frac{b-\mu r}{\alpha\gamma}, \\ \frac{b-b\left(\frac{b-\mu r}{\alpha\gamma}\right)}{b-\mu r}, \\ -\frac{r(\beta b\mu+\mu b^2)-\alpha\gamma b)-\beta b(\alpha\gamma-b))}{r(\mu b+\alpha\gamma b\mu)} \end{pmatrix} = (0,437158; 1,26639; 2,84163)$$

and $R_0 = 1,016$. The parameters in Table (4.1) are substituted into the matrix (4.5.24) to produce:

$$\begin{bmatrix} \lambda + 1,042872165 & 0,39999957 & 0 \\ -1,15874685 & \lambda + 0,92081457 & -0,633195 \\ 0 & 1,170815 & \lambda + 0,5698755 \end{bmatrix} = 0$$

$$(\lambda + 1,042872165)\begin{bmatrix} \lambda + 0,92081457 & -0,633195 \\ 1,170815 & \lambda + 0,5698755 \end{bmatrix}$$

$$-(-1,15874685)\begin{bmatrix} 0,39999957 & 0 \\ 1,170815 & \lambda + 0,5698755 \end{bmatrix}$$

$$+(0)\begin{bmatrix} 0,39999957 & 0 \\ \lambda + 0,92081457 & -0,633195 \end{bmatrix} = 0$$

$$\Leftrightarrow (\lambda + 1,042872165)((\lambda + 0,92081457)(\lambda + 0,5698755)$$

$$-(,633195)(1,170815)) - (-1,15874685)$$

$$((0,39999957)(\lambda + 0,5698755)) = 0$$

$$\Leftrightarrow \lambda^3 + 2,99706\lambda^2 + 3,56821\lambda + 1,59584 = 0$$

Then we get the characteristic equation $\lambda^3 + 2,99706\lambda\ 2 + 3,56821\lambda + 1,59584 = 0$. Using Wolfram Mathematica software produces the following eigenvalues:

$\lambda_1 = -1.0428721649999992;$

$\lambda_2 = -0.9770941558694273 - 0.7586350705292351i;$

$\lambda_3 = -0.9770941558694273 + 0.7586350705292351i.$

Since all eigenvalues are negative, it can be concluded that the endemic equilibrium point of the disease is stable.

c. Minimum Number of Anti-Tuberculosis Drugs Given

It is known $R_0 = 1,016$, then the next step is to look for the minimum amount of OAT given or the number of individuals who must be given OAT, namely as follows:

$$n_v > \frac{R_0 - 1}{R_0\theta}$$
$$n_v > \frac{1,016 - 1}{(1,016)(0,85)}$$
$$n_v > 0,0185271$$

Thus it is obtained $n_v > 0,0185271$ This means that the number of individuals who must be given OAT must be greater than $0,0185271$ of the total population so that the disease does not spread. However $n_v > 0,0185271$ it is not yet certain whether it is true $n_v > 0,0185271$ is the minimum number of individuals in this model simulation. Therefore, an examination is carried out based on the value of R_0 with each $n_v > 0,0185271$, The following are the results obtained:

Tabel 2. Value R_0 in Each $n_v > 0,0185271$

Individu yang diberi OAT	Nilai R_0
0,05	1,0638
0,06	1,054
0,07	1,045
0,08	1,035
0,09	1,0261
0,1	1,016
0,2	0,92
0,3	0,827
0,4	0,73
1	0,016

Based on Table (4.2) the minimum number of individuals given OAT is 0.2 because the value of R_0 is less than 1. This means that at the time n_v = 0.2, TB disease is no longer endemic in an area but has not completely disappeared. However, when 100% of individuals are given OAT, TB disease cannot be completely eliminated because this disease can recur and also even though OAT has been given, because the success of giving OAT is not 100%.

The conclusion is that the administration of Anti-Tuberculosis Drugs (OAT) in the model plays a significant role in reducing the spread of the disease if the minimum vaccination rate is reached. $n_v > R_0 - 1\ R_0\theta$, However, because the efficacy of OAT administration is 85%, tuberculosis (TB) in children cannot be completely eliminated because the disease can recur.

FURTHER STUDY

In further research, it is recommended to consider adding other factors to the model to form a more complex model such as medical costs and the obligation to use masks.

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