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Numerical Solution of Drug Addiction Mathematical Model Using Adams Moulton Method

Nurul Ismi Maulida[1]*, Syafruddin Side[2], Rahmat Syam[3]

[1,2,3]Departement of Mathematics Postgraduate Program, Makassar State University
Bonto Langkasa St, Banta-Bantaeng, Makassar City, 90222, South Sulawesi, Indonesia

***E-mail Correspondence Author:** *isminurul460@gmail.com*

Abstract

Rug abuse is one of the major social issues in Indonesia, particularly in South Sulawesi. This study aims to develop a mathematical model that represents the dynamics of drug addiction in the population and to solve the model numerically using the Adams-Moulton method. The model applied is the SIIHR compartment model, which segments the population into five groups: susceptible (S), light addict (IR), heavy addict (IB), in rehabilitation (H), and recovered (R). The analysis results indicate that the basic reproduction number R_0 is less than 1, suggesting that drug addiction in the population can be managed. Numerical simulations are conducted using the fifth-order Runge-Kutta method for initial values, followed by the Adams-Bashforth-Moulton method as the numerical solution technique. The model demonstrates stability at the drug-free equilibrium point and consistency between the outcomes of mathematical and numerical analysis.

Keywords: *Adams-moulton, basic reproduction, drug addiction, mathematical model, numerical solution.*

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1. INTRODUCTION

Mathematical models translate mathematical concepts into solutions for real-world problems that often arise. In 1927, Kermack and McKendrick developed the SIR model, which plays a crucial role in the field of epidemic mathematics by dividing individuals into three categories: Susceptible (S), Infected (I), and Recovered (R) [1]. Now, this SIR model has evolved into other models that are suitable for real-world cases or problems [2]. Mathematical models are formed based on assumptions that have been made; many problems arising from various fields can be made into mathematical models, such as the spread of a disease [3]. Mathematical models are one of the tools that can help facilitate problem-solving in real life [4]. The example is the application to determine the numerical solution of mathematical models on the problem of drug addiction in a certain area, which is known by several models including Susceptible Infected (SI), Susceptible Infected Susceptible (SIS), Susceptible Infected Recovered (SIR), Susceptible Exposed Infected Recovered (SEIR) and Susceptible Exposed Infected Recovered Susceptible (SEIRS). Mathematical models consist of variables, parameters, and functions that express the relationship between variables and parameters. [5]. Many problems can arise from various fields of science, one of which is in the health sector, namely the problem of drug addiction. According to the National Narcotics Agency (BNN), the prevalence of drug abuse in Indonesia tends to increase, with the productive age group as the most vulnerable victims. In South Sulawesi Province, data shows that the rate of drug abuse continues to rise, including among adolescents and young adults, triggering concerns about its impact on future generations [6].

The problem of drug addiction has complex characteristics and involves dynamics between individuals in a population [7]. Therefore, quantitative approaches such as mathematical models are very relevant to understanding and analyzing the pattern of spread. Mathematical models in the field of epidemiology, such as the SIR (Susceptible-Infected-Recovered) model [8], is effective in modeling the spread of infectious diseases and can be adapted for non-epidemiological cases, such as drug addiction, with certain modifications [2]. SIIHR model [9] It was developed to reflect the dynamics of drug addiction by considering several stages of an individual's condition, namely, vulnerable individuals, light users, heavy users, in rehabilitation, and recovered. This approach allows for a more comprehensive analysis of the transition process between states, as well as the role of rehabilitation in reducing addiction rates.

The system of nonlinear differential equations formed from the model is generally difficult to solve analytically [10]. Therefore, numerical methods are required. [11] Which is capable of providing high-fidelity approximation solutions. One of the excellent numerical methods for this kind of system is the Adams-Moulton method. [12], which is part of the predictor-corrector multi-step method. This method is not only stable but also has a good level of accuracy in solving ordinary differential equations (ODEs), especially in the long term. This study aims to develop and analyze a mathematical model of drug addiction using the SIIHR model approach and solve the model system numerically using the Adams-Moulton method [13]. Through this approach, a better understanding of the dynamics of the spread of drug addiction and the effectiveness of rehabilitation interventions in South Sulawesi Province is expected.

2. METHODOLOGY

The type of research used is theoretical and applied research. [14], which can be used to solve problems by first compiling concepts as needed. The type of data used in this research is secondary data. The author collected data on drug addiction in 2023 at the National Narcotics Agency of South Sulawesi Province, and collected various references from previous researchers related to this research [15]. The technique used in this research is a literature review. In this technique, researchers read research-related articles to obtain relevant simulation parameters. The literature review was used as part of the data collection technique component.

For the formation of the SIIHR model, the assumptions as a solution to drug addiction with rehabilitation are as follows [5]:

a. The birth rate is equal to the death rate.
b. Every group of individuals has an equal chance of becoming a drug addict.
c. Individuals aged 15-64 years old are vulnerable (S).
d. There is a group of mildly addicted individuals who permanently recover after IR rehabilitation.
e. There is a group of severely addicted individuals who recover and are prone to re-addiction after rehabilitation (IB).
f. Group of individuals undergoing rehabilitation (H).
g. Group of individuals recovering from drug addiction (R).

Based on the assumptions that have been determined, a compartment model is built as shown below:

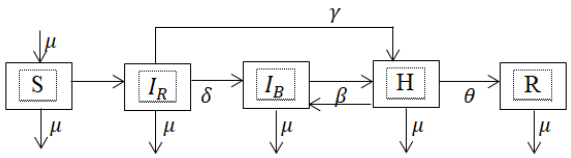

Figure 1. Compartment Diagram of the SIIHR Model

Description :

μ: Natural birth and death rate.
ϱ: Contact rate (infection rate)/Movement of vulnerable population to the light drug addict population.
ε: Rate of movement of light drug addict population to heavy drug addict population.
β: Rate of movement of the heavy drug addict population to the rehabilitated population.
δ: Displacement rate of rehabilitated population back to heavy drug addicts.
γ: Displacement rate of light drug addicts into the rehabilitated population.
θ: The rate at which the rehabilitated population moves into the recovered population.

The research procedures applied to achieve the objectives in this study are as follows:

1. Identify the problem by studying mathematical models that describe the dynamics of drug addiction and determine the variables that affect the drug addiction problem.
2. Develop a suitable mathematical model to describe the dynamics of drug addiction, and the model may take the form of a system of differential equations.
3. Attempt to solve the mathematical model analytically if possible and provide theoretical insights into the behavior of the solution.
4. Numerical solution using numerical methods such as the Adams-Moulton method.

5. Implementing the Adams-Moulton method : Discretize the mathematical model to fit the Adams-Moulton method, write a computational algorithm to obtain the Adams-Moulton method, and Implement the algorithm in a suitable programming language.
6. Analysis of results, which include: Analyze the numerical solution obtained from the Adams-Moulton method, evaluate the stability, accuracy, and convergence of the method and comparing the results with analytical solutions, if available.
7. Interpretation and discussion: Interpret the results of numerical solutions in the context of drug addiction problems in South Sulawesi, Examine the implications of the numerical solution for understanding the dynamics of drug addiction in South Sulawesi, and discuss the limitations of the model and method, as well as suggestions for further research.

For the numerical solution of the system of differential equations formed cannot be solved analytically, so a multistep numerical approach is used, namely the Adams Moulton method, which is part of the predictor-corrector method. The choice of this method is based on its stability and high accuracy in solving ODE (Ordinary Differential Equations) systems efficiently, especially in mapping population dynamics over long time intervals. The completion step is done as follows:

1. Initialization of the initial solution is performed using the fifth-order Runge-Kutta method, which provides a high-precision initial value to start the multistep scheme.
2. The Adams Basforth scheme is used as a predictor to estimate the solution value at the next time step.
3. The predicted values are then corrected by the Adams Moulton method, which integrates the ODE function with an implicit formula, thus improving the precision of the results.

The general form of the formula used is :

$$y_n + 1 = y_n + h\sum_{j=0}^{k} a_j f(t_n + 1 - j, y_n + 1 - j) \quad (1)$$

where a_j is the method coefficient, h is the time step, and f is the ODE system function of the SIIHR model.

3. RESULTS AND DISCUSSION

The SIIHR mathematical model on the problem of drug addiction in South Sulawesi is written in the following equation:

$$\frac{\delta S}{\delta t} = \mu - (\mu + \rho I_R)S \quad (2)$$

$$\frac{\delta I_R}{\delta t} = \rho S I_R - (\mu + \gamma + \varepsilon)I_R \quad (3)$$

$$\frac{\delta I_B}{\delta t} = \varepsilon I_R + \delta H - (\mu + \beta)I_\beta \quad (4)$$

$$\frac{\delta H}{\delta t} = \beta I_B + \gamma I_R - (\delta + \mu + \theta)H \quad (5)$$

$$\frac{\delta R}{\delta t} = \theta H - \mu R \quad (6)$$

Based on the population change diagram in **Figure (1)**, population S, which is a group of vulnerable individuals, increases with the birth rate (μ), because the birth rate and natural death rate are assumed to be the same, population S also decreases with the natural death rate (μ). Then, it also decreases due to contact (ρI_R) between the lightly infected population by the vulnerable population, which results in population S becoming infected/lightly drug addicted. Therefore, the equation model of vulnerable

population change can be written in **Equation (2)**. Thus, as the population of S moves to I_R, it can be interpreted that the population of light drug addicts (I_R) experience a population increase due to the contact rate ρI_R between the population of light drug addicts by the vulnerable population (S), then experiences a population reduction due to the natural mortality rate (μ). In addition, the population of light drug addicts (ε) can migrate to the population of heavy drug addicts (I_B). Furthermore, the population (I_R) also experiences a reduction due to the population rate of light drug addicts to the rehabilitated population (γ), which makes the lightly infected population move to the rehabilitated population (H). So that the equation model of mild drug addict population change can be written in **Equation (3)**.

The change in the population of heavy drug addicts (I_B) experienced an increase in individuals due to the population rate of light drug addicts to heavy drug addicts (ε) so that the population of light drug addicts moved to the population of heavy drug addicts (I_B) so that it experienced a reduction due to the population rate of heavy drug addicts to the rehabilitated population (γ) which made the lightly infected population move to the rehabilitated population (H). So that the equation model for the change in the population of light drug addicts can be written in **Equation (4)**. As for the change in the rehabilitated population (H), the increase in individuals is due to the population rate of heavy drug addicts who rehabilitate (γ), so that the population of heavy drug addicts who rehabilitate (H). The H population also decreases due to the natural mortality rate (μ). Rehabilitation is carried out because it is an effort to recover from drug addiction, therefore, the population (H) decreases due to the rate of recovery (θ) due to rehabilitation towards the population. So that the equation model for changes in the rehabilitation population can be written in **Equation (5).** The change in the recovered population increases due to the natural recovery rate of the population of drug addicts (θ) and the recovery rate of the population who have undergone rehabilitation (γ). Then, experienced a reduction in population due to the natural death rate (μ) among those who recovered from drug addiction. So that the equation model of the recovered population change can be written in **Equation (6)**.

The model used in this study will be solved using the parameter values in **Table 1**.

Table 1. Parameter Values

Symbol	Parameters	Value
μ	Natural birth and death rates	0.5
ρ	Contact rate (infection rate) / Movement of susceptible population to light addicts	0.0009
ε	Population transfer rate of light addicts to heavy addicts	0.05
β	Laju perpindahan pecandu berat ke populasi yang direhabilitasi	0.5
δ	Displacement rate of the rehabilitated population back to heavy addicts	0.07
γ	Movement rate of light addicts in the rehabilitated population	0.035
θ	Displacement rate of the rehabilitated population to the cured population	0.8

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1. Equilibrium point

In **Equations (2)** to **(6)**, it is a system of linear tidal differential equations that describes the SIIHR model of drug addiction. **Equations (2)** to **(6)** have equilibrium points. To linearize the equations, **Equations (2)** to **(6)** are written as:

$$\mu - (\mu + \rho I_R)S = 0 \quad (7)$$

$$\rho S I_R - (\mu + \gamma + \varepsilon)I_R = 0 \quad (8)$$

$$\varepsilon I_R + \delta H - (\mu + \beta)I_\beta = 0 \quad (9)$$

$$\beta I_B + \gamma I_R - (\delta + \mu + \theta)H = 0 \quad (10)$$

$$\theta H - \mu R = 0 \quad (11)$$

a. Drug Addiction Free Equilibrium Point

The drug addiction-free equilibrium point is a state where no population has mild or severe drug addiction, so the value of I_R=I_B≠0. The equilibrium point S is obtained from **Equation (7)**, namely:

$$\mu - (\mu + \rho I_R)S = 0, \qquad S = \frac{\mu}{\mu} = 1$$

To obtain the equilibrium point H, **Equation (9)**:

$$\varepsilon I_R + \delta H - (\mu + \beta)I_\beta = 0, \qquad \varepsilon(0) + \delta H - (\mu + \beta)0 = 0$$

So that: $H = 0$

To obtain the equilibrium point R, substitute the value of H into **Equation (11)**:

$$\theta H - \alpha R = 0, \qquad \theta 0 - \alpha R = 0, \qquad R = 0$$

Thus, the drug addiction-free equilibrium point obtained from **Equations (2)-(6)** is :

$$E_1(S, I, I, H, R) = (1, 0, 0, 0, 0) \quad (12)$$

b. Endemic Equilibrium Point

The endemic equilibrium point is the state when the population is addicted to drugs, so that it is at the drug-free equilibrium point, at the endemic equilibrium point. $I_R = I_B \neq 0$ So that :

$$\mu - (\mu + \rho I_R)S = 0, \qquad S = \frac{\mu}{I_R\rho + \mu}$$

Next is to determine the equilibrium point I_R:

$$\rho S I_R - (\mu + \gamma + \varepsilon)I_R = 0$$

$$\rho\left(\frac{\mu}{I_R\rho + \mu}\right)I_R - (\mu + \gamma + \varepsilon)I_R = 0$$

$$\frac{\rho\mu I_R}{I_R\rho + \mu} - (\mu + \gamma + \varepsilon)I_R$$

$$\frac{(\rho\mu I_R - ((\mu + \gamma + \varepsilon)I_R)(I_R\rho + \mu))}{I_R\rho + \mu} = 0$$

so the I_R The Value obtained is: $I_R = 0$

And since the endemic equilibrium point $I_R = I_B \neq 0$ The value of I_R That satisfies:

$$I_R = -\frac{\mu(\gamma + \varepsilon + \mu - \rho)}{\rho(\mu + \gamma + \varepsilon)}$$

Substitute a value of I_R that satisfies :

$$\varepsilon I_R + \delta H - (\mu + \beta)I_B = 0$$

$$\varepsilon\left(-\frac{\mu(\gamma + \varepsilon + \mu - \rho)}{\rho(\mu + \gamma + \varepsilon)}\right) + \delta H - (\mu + \beta)I_B = 0$$

$$(\mu + \beta)I_B = \delta H - \frac{\varepsilon\mu(\gamma + \varepsilon + \mu - \rho)}{\rho(\mu + \gamma + \varepsilon)}$$

$$I_B = \frac{\delta\varepsilon H\rho + \delta\gamma H\rho + \delta H\mu\rho - \varepsilon^2\mu - \varepsilon\gamma\mu - \varepsilon\mu^2 + \varepsilon\mu\rho}{\rho(\mu + \gamma + \varepsilon)(\mu + \beta)}$$

$$I_B = \frac{\delta H\rho(\mu+\gamma+\varepsilon) - \varepsilon\mu(\gamma+\varepsilon+\mu-\rho)}{\rho(\mu+\gamma+\varepsilon)(\mu+\beta)}$$

Substitute I_R and I_B Values into equation H:

$$\beta I_B + \gamma I_R - (\delta+\mu+\theta)H = 0$$

$$\beta\left(\frac{\delta H\rho(\mu+\gamma+\varepsilon) - \varepsilon\mu(\gamma+\varepsilon+\mu-\rho)}{\rho(\mu+\gamma+\varepsilon)(\mu+\beta)}\right) + \gamma\left(-\frac{\mu(\gamma+\varepsilon+\mu-\rho)}{\rho(\mu+\gamma+\varepsilon)}\right) - (\delta+\mu+\theta)H = 0$$

$$\frac{\beta(\delta\varepsilon H\rho + \delta\gamma H\rho + \delta H\mu\rho - \varepsilon^2\mu - \varepsilon\gamma\mu - \varepsilon\mu^2 + \varepsilon\mu\rho)}{\rho(\mu+\gamma+\varepsilon)(\mu+\beta)} + \frac{\gamma\mu(\gamma+\varepsilon+\mu-\rho)}{\rho(\mu+\gamma+\varepsilon)} - (\delta+\mu+\theta)H = 0$$

$$H = \big(\mu(-\beta\varepsilon^2 - \beta\varepsilon\mu + \beta\varepsilon\rho + \beta\gamma^2 + \beta\gamma\mu - \beta\gamma\rho + \varepsilon\gamma\mu + \gamma^2\mu + \gamma\mu^2 - \gamma\mu\rho)\big)/(\rho(\beta\varepsilon\mu + \beta\varepsilon\theta + \beta\gamma\mu + \beta\gamma\theta + \beta\mu^2 + \beta\mu\theta + \delta\varepsilon\mu + \delta\gamma\mu + \delta\mu^2 + \varepsilon\mu^2 + \varepsilon\mu\theta + \gamma\mu^2 + \gamma\mu\theta + \mu^3 + \mu^2\theta))$$

So it can be simplified to :

$$H = \frac{\big(\gamma\mu + \beta(\gamma-\varepsilon)\big)(\gamma+\varepsilon+\mu-\rho)\mu}{(\mu+\gamma+\varepsilon)\rho(\mu^2 + (\beta+\delta+\theta)\mu + \beta\theta)}$$

Then substitute the value of H into the I_B equation:

$$I_B = \frac{\delta\left(\frac{\big(\gamma\mu + \beta(\gamma-\varepsilon)\big)(\gamma+\varepsilon+\mu-\rho)\mu}{(\mu+\gamma+\varepsilon)\rho(\mu^2 + (\beta+\delta+\theta)\mu + \beta\theta)}\right)\rho(\mu+\gamma+\varepsilon) - \varepsilon\mu(\gamma+\varepsilon+\mu-\rho)}{\rho(\mu+\gamma+\varepsilon)(\mu+\beta)}$$

$$I_B = \frac{\delta\varepsilon H\rho + \delta\gamma H\rho + \delta H\mu\rho - \varepsilon^2\mu - \varepsilon\gamma\mu - \varepsilon\mu^2 + \varepsilon\mu\rho}{\rho(\mu+\gamma+\varepsilon)(\mu+\beta)}$$

$$I_B = \frac{1}{\rho(\mu+\gamma+\varepsilon)(\mu+\beta)}\left(\frac{\delta\varepsilon(\gamma\mu+\beta(\gamma-\varepsilon))(\gamma+\varepsilon+\mu-\rho)\mu}{(\mu+\gamma+\varepsilon)(\mu^2+(\beta+\delta+\theta)\mu+\beta\theta)} + \frac{\delta\gamma\big(\gamma\mu+\beta(\gamma-\varepsilon)\big)(\gamma+\varepsilon+\mu-\rho)+\mu}{(\mu+\gamma+\varepsilon)(\mu^2+(\beta+\delta+\theta)\mu+\beta\theta)} + \frac{\delta(\gamma\mu+\beta(\gamma-\varepsilon))(\gamma+\varepsilon+\mu-\rho)\mu^2}{(\mu+\gamma+\varepsilon)(\mu^2+(\beta+\delta+\theta)\mu+\beta\theta)} - \varepsilon^2\mu - \varepsilon\gamma\mu - \varepsilon\mu^2 + \varepsilon\mu\rho\right)$$

$$I_B = -\frac{(\gamma+\varepsilon+\mu-\rho)\mu(\varepsilon\mu + (\delta+\theta)\varepsilon - \delta\gamma)}{(\mu+\gamma+\varepsilon)\rho(\mu^2+(\beta+\delta+\theta)\mu+\beta\theta)}$$

Then substitute H into equation R to obtain the equilibrium point R:

$$\theta H - \mu R = 0$$

$$\theta\left(\frac{\big(\gamma\mu+\beta(\gamma-\varepsilon)\big)(\gamma+\varepsilon+\mu-\rho)\mu}{(\mu+\gamma+\varepsilon)\rho(\mu^2+(\beta+\delta+\theta)\mu+\beta\theta)}\right) - \mu R = 0$$

$$\frac{(\gamma\mu+\beta(\gamma-\varepsilon))(\gamma+\varepsilon+\mu-\rho)\mu\theta}{(\mu+\gamma+\varepsilon)\rho(\mu^2+(\beta+\delta+\theta)\mu+\beta\theta)} - \mu R$$

$$R = \frac{(-\beta\varepsilon+\beta\gamma+\gamma\mu)(\gamma+\varepsilon+\mu-\rho)\theta}{\rho(\beta\mu+\beta\theta+\delta\mu+\mu^2+\mu\theta)(\mu+\gamma+\varepsilon)}$$

Thus, the endemic equilibrium point in the model in this study is:

$$E_2(S,I,I,H,R) = \left\{\begin{array}{c}\left(\frac{\mu}{I_R\rho+\mu}\right),\left(-\frac{\mu(\gamma+\varepsilon+\mu-\rho)}{\rho(\mu+\gamma+\varepsilon)}\right),\\ \left(-\frac{(\gamma+\varepsilon+\mu-\rho)\mu(\varepsilon\mu+(\delta+\theta)\varepsilon-\delta\gamma)}{(\mu+\gamma+\varepsilon)\rho(\mu^2+(\beta+\delta+\theta)\mu+\beta\theta)}\right)\\ ,\left(\frac{\big(\gamma\mu+\beta(\gamma-\varepsilon)\big)(\gamma+\varepsilon+\mu-\rho)\mu}{(\mu+\gamma+\varepsilon)\rho(\mu^2+(\beta+\delta+\theta)\mu+\beta\theta)}\right),\\ \left(\frac{(-\beta\varepsilon+\beta\gamma+\gamma\mu)(\gamma+\varepsilon+\mu-\rho)\theta}{\rho(\beta\mu+\beta\theta+\delta\mu+\mu^2+\mu\theta)(\mu+\gamma+\varepsilon)}\right)\end{array}\right\}$$

Substitute the parameter values in Table 1 so that the endemic equilibrium point is obtained: $E_2(S,I,I,H,R) = (650,-554{,}7008,-29{,}48016,-24{,}93037,-39{,}88860)$.

2. Basic Reproduction Number (R_0)

The basic reproduction number (R_0)What is the expected value of the number of cases of the population susceptible to drug addiction? The number (R_0)It is a threshold condition to determine whether a population is endemic or not addicted. In determining the basic reproduction number (R_0)The system of equations model is constructed into a Jacobian matrix and substitutes the equilibrium point where $I_R = I_B \neq 0$. So it can be solved as follows:

$$J(E_1) = \begin{bmatrix} \frac{\vartheta S}{\vartheta S} & \frac{\vartheta S}{\vartheta I_R} & \frac{\vartheta S}{\vartheta I_B} & \frac{\vartheta S}{\vartheta H} & \frac{\vartheta S}{\vartheta R} \\ \frac{\vartheta I_R}{\vartheta S} & \frac{\vartheta I_R}{\vartheta I_R} & \frac{\vartheta I_R}{\vartheta I_B} & \frac{\vartheta I_R}{\vartheta H} & \frac{\vartheta I_R}{\vartheta R} \\ \frac{\vartheta I_B}{\vartheta S} & \frac{\vartheta I_B}{\vartheta I_R} & \frac{\vartheta I_B}{\vartheta I_B} & \frac{\vartheta I_B}{\vartheta H} & \frac{\vartheta I_B}{\vartheta R} \\ \frac{\vartheta H}{\vartheta S} & \frac{\vartheta H}{\vartheta I_R} & \frac{\vartheta H}{\vartheta I_B} & \frac{\vartheta H}{\vartheta H} & \frac{\vartheta H}{\vartheta R} \\ \frac{\vartheta R}{\vartheta S} & \frac{\vartheta R}{\vartheta I_R} & \frac{\vartheta R}{\vartheta I_B} & \frac{\vartheta R}{\vartheta H} & \frac{\vartheta R}{\vartheta R} \end{bmatrix}$$

$$J(E_1) = \begin{bmatrix} -(\mu + \rho I_R) & -\rho S & 0 & 0 & 0 \\ \rho I_R & \rho S - (\mu + \gamma + \varepsilon) & 0 & 0 & 0 \\ 0 & \varepsilon & -(\mu + \beta) & \delta & 0 \\ 0 & \gamma & \beta & -(\delta + \mu + \theta) & 0 \\ 0 & 0 & 0 & \theta & -\mu \end{bmatrix}$$

equilibrium point substitution E_1 :

$$J(1,0,0,0,0) = \begin{bmatrix} -(\mu + \rho(0)) & -\rho(1) & 0 & 0 & 0 \\ \rho(0) & \rho(1) - (\mu + \gamma + \varepsilon) & 0 & 0 & 0 \\ 0 & \varepsilon & -(\mu + \beta) & \delta & 0 \\ 0 & \gamma & \beta & -(\delta + \mu + \theta) & 0 \\ 0 & 0 & 0 & \theta & -\mu \end{bmatrix}$$

$$= \begin{bmatrix} -\mu & -\rho & 0 & 0 & 0 \\ 0 & \rho - (\mu + \gamma + \varepsilon) & 0 & 0 & 0 \\ 0 & \varepsilon & -(\mu + \beta) & \delta & 0 \\ 0 & \gamma & \beta & -(\delta + \mu + \theta) & 0 \\ 0 & 0 & 0 & \theta & -\mu \end{bmatrix}$$

Furthermore, the decomposition of the Jacobian matrix to determine R_0By forming two matrices, F and V, the model system is divided into two main components, namely the rate of emergence of new infections represented by the F matrix, and the rate of individual transitions between infectious compartments and out of infectious compartments represented by the V matrix. By forming the product of the matrix FV^{-1}, The next generation matrix is obtained, where the dominant result (spectral radius) of the matrix is the value of R_0.

Obtained:

$$F = \begin{bmatrix} \rho & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

$$V = \begin{bmatrix} (\mu + \gamma + \varepsilon) & 0 & 0 \\ -\varepsilon & (\mu + \beta) & -\delta \\ -\gamma & -\beta & (\delta + \mu + \theta) \end{bmatrix}$$

by completing $R_0 = FV^{-1}$.

Get it done: $V^{-1} = \frac{1}{|V|} \cdot adj(V)$

$$= \begin{bmatrix} \frac{1}{\mu+\gamma+\varepsilon} & 0 & 0 \\ \frac{\delta\varepsilon+(\delta+\theta)\varepsilon+\delta\gamma}{(\mu+\gamma+\varepsilon)(\mu^2+(\beta+\delta+\theta)\mu+\beta\theta)} & \frac{\delta+\mu+\theta}{\mu^2+(\beta+\delta+\theta)\mu+\beta\theta} & \frac{\delta}{\mu^2+(\beta+\delta+\theta)\mu+\beta\theta} \\ \frac{\gamma\mu+\beta(\gamma+\varepsilon)}{(\mu+\gamma+\varepsilon)(\mu^2+(\beta+\delta+\theta)\mu+\beta\theta)} & \frac{\beta}{\mu^2+(\beta+\delta+\theta)\mu+\beta\theta} & \frac{\mu+\beta}{\mu^2+(\beta+\delta+\theta)\mu+\beta\theta} \end{bmatrix}$$

So that:

$$R_0 = FV^{-1}$$

Obtained:

$$R_0 = \frac{\rho}{\mu+\gamma+\varepsilon}$$

Substitute the parameter values in **Table 1**, so that the reproduction number is. R_0 Is obtained: $R_0 = 0{,}00153 < 1$.

Because of the condition R_0<1, the spread of drug addiction in South Sulawesi can be controlled and will disappear at a certain time.

3. Equilibrium point stability

The endemic model in this study has determined each of the disease-free and endemic equilibrium points, next is necessary to analyze the stability of the two equilibrium points by substituting them into the Jacobian matrix.

a. Stability of the disease-free equilibrium point

Substitute the disease-free equilibrium point into the Jacobian matrix:

$$J(E_1) = \begin{bmatrix} -(\mu+\rho I_R) & -\rho S & 0 & 0 & 0 \\ \rho I_R & \rho S-(\mu+\gamma+\varepsilon) & 0 & 0 & 0 \\ 0 & \varepsilon & -(\mu+\beta) & \delta & 0 \\ 0 & \gamma & \beta & -(\delta+\mu+\theta) & 0 \\ 0 & 0 & 0 & \theta & -\mu \end{bmatrix}$$

$$J(1,0,0,0,0) = \begin{bmatrix} -(\mu+\rho(0)) & -\rho(1) & 0 & 0 & 0 \\ \rho(0) & \rho(1)-(\mu+\gamma+\varepsilon) & 0 & 0 & 0 \\ 0 & \varepsilon & -(\mu+\beta) & \delta & 0 \\ 0 & \gamma & \beta & -(\delta+\mu+\theta) & 0 \\ 0 & 0 & 0 & \theta & -\mu \end{bmatrix}$$

$$= \begin{bmatrix} -\mu & -\rho & 0 & 0 & 0 \\ 0 & \rho-(\mu+\gamma+\varepsilon) & 0 & 0 & 0 \\ 0 & \varepsilon & -(\mu+\beta) & \delta & 0 \\ 0 & \gamma & \beta & -(\delta+\mu+\theta) & 0 \\ 0 & 0 & 0 & \theta & -\mu \end{bmatrix}$$

$$det(\lambda I - J(E_1)) = \left| \begin{bmatrix} \lambda & 0 & 0 & 0 & 0 \\ 0 & \lambda & 0 & 0 & 0 \\ 0 & 0 & \lambda & 0 & 0 \\ 0 & 0 & 0 & \lambda & 0 \\ 0 & 0 & 0 & 0 & \lambda \end{bmatrix} - \begin{bmatrix} -\mu & -\rho & 0 & 0 & 0 \\ 0 & \rho-(\mu+\gamma+\varepsilon) & 0 & 0 & 0 \\ 0 & \varepsilon & -(\mu+\beta) & \delta & 0 \\ 0 & \gamma & \beta & -(\delta+\mu+\theta) & 0 \\ 0 & 0 & 0 & \theta & -\mu \end{bmatrix} \right|$$

$$= \begin{vmatrix} \lambda+\mu & \rho & 0 & 0 & 0 \\ 0 & \lambda-\rho+\mu+\gamma+\varepsilon & 0 & 0 & 0 \\ 0 & -\varepsilon & \lambda+\mu+\beta & -\delta & 0 \\ 0 & -\gamma & -\beta & \lambda+\delta+\mu+\theta & 0 \\ 0 & 0 & 0 & -\theta & \lambda+\mu \end{vmatrix}$$

Substitute the parameter values in **Table 1**, thus obtained:

$$= \begin{vmatrix} \lambda+0{,}5 & 0{,}0009 & 0 & 0 & 0 \\ 0 & \lambda+0{,}5841 & 0 & 0 & 0 \\ 0 & -0{,}05 & \lambda+1 & -0{,}07 & 0 \\ 0 & -0{,}035 & -0{,}5 & \lambda+1{,}37 & 0 \\ 0 & 0 & 0 & -0{,}8 & \lambda+0{,}5 \end{vmatrix}$$

By using cofactor expansion, the determinant of the matrix above is obtained:

$$= (\lambda+0{,}5)(\lambda+0{,}5841)(\lambda^3+2{,}87\lambda^2+2{,}52\lambda+0{,}6675)$$

Thus, the eigenvalue (λ) is obtained, namely :

$\lambda_1 = -0{,}5841$
$\lambda_{2,3} = -0{,}5$
$\lambda_4 = -1{,}448106442$
$\lambda_5 = -0{,}9218935577$

Since all eigenvalues have negative real values, the stability of the disease-free equilibrium point is asymptotically stable.

b. Stability of the endemic equilibrium point.

Substitute the endemic equilibrium point into the Jacobian matrix:

$$J(E_2) = \begin{bmatrix} -(\mu+\rho I_R) & -\rho S & 0 & 0 & 0 \\ \rho I_R & \rho S-(\mu+\gamma+\varepsilon) & 0 & 0 & 0 \\ 0 & \varepsilon & -(\mu+\beta) & \delta & 0 \\ 0 & \gamma & \beta & -(\delta+\mu+\theta) & 0 \\ 0 & 0 & 0 & \theta & -\mu \end{bmatrix}$$

$J(E_2)$

$$= \begin{bmatrix} -\left(\mu+\rho\left(-\frac{\mu(\gamma+\varepsilon+\mu-\rho)}{\rho(\mu+\gamma+\varepsilon)}\right)\right) & -\rho\left(\frac{\mu}{I_R\rho+\mu}\right) & 0 & 0 & 0 \\ \rho\left(-\frac{\mu(\gamma+\varepsilon+\mu-\rho)}{\rho(\mu+\gamma+\varepsilon)}\right) & \rho\left(\frac{\mu}{I_R\rho+\mu}\right)-(\mu+\gamma+\varepsilon) & 0 & 0 & 0 \\ 0 & \varepsilon & -(\mu+\beta) & \delta & 0 \\ 0 & \gamma & \beta & -(\delta+\mu+\theta) & 0 \\ 0 & 0 & 0 & \theta & -\mu \end{bmatrix}$$

$det(\lambda I - J(E_1)) = 0$

$$\left|\begin{bmatrix}\lambda & 0 & 0 & 0 & 0\\ 0 & \lambda & 0 & 0 & 0\\ 0 & 0 & \lambda & 0 & 0\\ 0 & 0 & 0 & \lambda & 0\\ 0 & 0 & 0 & 0 & \lambda\end{bmatrix}\right.$$

$$\left.-\begin{bmatrix}-\left(\mu+\rho\left(-\frac{\mu(\gamma+\varepsilon+\mu-\rho)}{\rho(\mu+\gamma+\varepsilon)}\right)\right) & -\rho\left(\frac{\mu}{I_R\rho+\ \mu}\right) & 0 & 0 & 0\\ \rho\left(-\frac{\mu(\gamma+\varepsilon+\mu-\rho)}{\rho(\mu+\gamma+\varepsilon)}\right) & \rho\left(\frac{\mu}{I_R\rho+\ \mu}\right)-(\mu+\gamma+\varepsilon) & 0 & 0 & 0\\ 0 & \varepsilon & -(\mu+\beta) & \delta & 0\\ 0 & \gamma & \beta & -(\delta+\mu+\theta) & 0\\ 0 & 0 & 0 & \theta & -\mu\end{bmatrix}\right|$$

$$= 0$$

$$\left|\begin{bmatrix}\lambda+\mu-\frac{\mu(-\rho+\varepsilon+\mu+\gamma)}{\rho(\mu+\gamma+\varepsilon)} & \frac{\rho\mu}{I_R\rho+\ \mu} & 0 & 0 & 0\\ \frac{\mu(\gamma+\varepsilon+\mu-\rho)}{\mu+\gamma+\varepsilon} & \lambda-\frac{\rho\mu}{I_R\rho+\ \mu}+\mu+\gamma+\varepsilon & 0 & 0 & 0\\ 0 & -\varepsilon & \lambda+\mu+\beta & -\delta & 0\\ 0 & -\gamma & -\beta & \lambda+\delta+\mu+\theta & 0\\ 0 & 0 & 0 & -\theta & \lambda+\mu\end{bmatrix}\right|$$

$$= 0$$

$$\frac{1}{(\mu+\gamma+\varepsilon)(I_R\rho+\ \mu)}\big((\beta\lambda^2+2\beta\lambda\mu+\beta\lambda\theta+\beta\mu^2+\beta\mu\theta+\delta\lambda^2+2\delta\lambda\mu+\delta\mu^2+\lambda^3$$
$$+3\lambda^2\mu+\lambda^2\theta+3\lambda\mu^2+2\lambda\mu\theta+\mu^3+\mu^2\theta)(I_R\varepsilon\mu\rho^2+(2I_R)\varepsilon\lambda\mu\rho$$
$$+I_R\lambda\mu^2\rho+(2I_R)\gamma\varepsilon\lambda\rho+I_R\lambda^2\mu\rho+I_R\gamma^2\lambda\rho+I_R\gamma\mu\rho^2+I_R\gamma\lambda^2\rho+I_R\varepsilon^2\lambda\rho$$
$$+(2I_R)\gamma\lambda\mu\rho+I_R\mu^2\rho^2+I_R\varepsilon\lambda^2\rho+I_R\lambda\mu\rho^2+\gamma^2\lambda\mu+2\gamma\varepsilon\lambda\mu+\gamma\lambda^2\mu$$
$$+2\gamma\lambda\mu^2-\gamma\lambda\mu\rho+\varepsilon^2\lambda\mu+\varepsilon\lambda^2\mu+2\varepsilon\lambda\mu^2-\varepsilon\lambda\mu\rho+\lambda^2\mu^2+\lambda\mu^3)\big)=0$$

By substituting the parameter values in **Table 1**, the following characteristic equation is obtained:

$$\lambda^5+2{,}870769254\lambda^4+2{,}230157772\lambda^3-0{,}1687449458\lambda^2-0.7354524933\lambda$$
$$-0{,}1949433672=0$$

By using Maple 16 software, the value of :

$[\lambda_1 = 0{,}5400320050], [\lambda_2 = -0{,}5000000074], [\lambda_3 = -0{,}5408012491],$
$[\lambda_4 = -0{,}9218935637], [\lambda_5 = -1.448106439]$

Because there is an eigenvalue (λ) that does not have a negative real part, the stability of the endemic equilibrium point on that parameter is unstable.

4. Numerical Simulation with the Adam Moulton Method

Based on the parameter values in **Table 1**, numerical simulations will be carried out using the Adams-Moulton method, as for the initial values used by the SI_RI_BHR Model, namely:

Table 2. Total Population and Initial Value of Research Variables

Variables	Description	Total Population	Initial Value	Source
S	Vulnerable Population	9361856	0.999571	BPS Sulsel, 2023
I_R	Mild Influence	2212	0.000236	BNN Sulsel, 2023
I_B	Severe Addiction	943	0.000101	BNN Sulsel, 2023
H	Rehabilitation	575	0.000061	BNN Sulsel, 2023
R	Healed	288	0.000031	Assumption

open source software R

Equations (2) to **(6)** will be solved using the Adams-Moulton method. But before that, the fifth-order Runge-Kutta method is first used to calculate the initial solution value of the system. This stage is calculated with RStudio software, with a time step of h = 0.1 and using the initial values and parameters that have been determined, five initial solution values are obtained through the fifth-order Runge-Kutta method. Obtained value k_1, k_2, k_3, k_4 and k_5 In RStudio are :

Table 3. Values of k_1, k_2, k_3, k_4 and k_5 In RStudio

	k_1	k_2	k_3	k_4	k_5	
S	0.00021429	0.00021161	0.00021163	0.00020900	0.00020641	0.00020385
IR	-0.000137	-0.000135	-0.000135	-0.000133	-0.000131	-0.000130
IB	-0.000084	-0.000083	-0.000083	-0.000081	-0.000079	-0.000077
H	-0.000024	-0.000025	-0.000025	-0.000025	-0.000025	-0.000025
R	0.0000333	0.0000323	0.0000323	0.0000314	0.0000305	0.0000296

open source software R

After calculating the value k_1, k_2, k_3, k_4, k_5The next step is to calculate the y_n Value using the following formula:

$$y_{n+1} = y_n + \frac{h}{90}(7k_1 + 32k_3 + 12k_4 + 32k_5 + 7k_6)h$$

Where h is the time step, and k_1, k_2, k_3, k_4, k_5 and k_6 Is the value calculated in the previous step for each variable? With RStudio, the initial solution y_n is obtained in **Table 3** below.

Table 4: Initial Solution with the Fifth Order Runge-Kutta Method

Variables	y_0	y_1	y_2	y_3	y_4
S	0.999571	0.99959201	0.99961198	0.99963098	0.99964905
IR	0.000236	0.00022253	0.00020983	0.00019786	0.00018657
IB	0.000101	0.00009280	0.00008532	0.00007847	0.00007221
H	0.000061	0.00005847	0.00005585	0.00005319	0.00005053
R	0.000031	0.00003418	0.00003701	0.00003949	0.00004165

open source software R

Determination of the solution with Adams-Bashforth uses the predictor equation. The system of equations **Equations (2)** to **(6)** is substituted into the predictor equation to obtain a numerical solution as the Adams-Bashforth-Moulton prediction value.

$$S_{n+1}^{(0)} = S_n + \frac{h}{720}(1901f_n - 2774f_{n-1} - 2616f_{n-2} - 1274f_{n-3} + 251f_{n-4}) = 0.99964905$$

$$I_{R_{n+1}}^{(0)} = I_{R_n} + \frac{h}{720}(1901f_n - 2774f_{n-1} - 2616f_{n-2} - 1274f_{n-3} + 251f_{n-4}) = 0.00018657$$

$$I_{B_{n+1}}^{(0)} = I_{B_n} + \frac{h}{720}(1901f_n - 2774f_{n-1} - 2616f_{n-2} - 1274f_{n-3} + 251f_{n-4}) = 0.00007221$$

$$I_{H_{n+1}}^{(0)} = H_n + \frac{h}{720}(1901f_n - 2774f_{n-1} - 2616f_{n-2} - 1274f_{n-3} + 251f_{n-4}) = 0.00005053$$

$$I_{R_{n+1}}^{(0)} = R_n + \frac{h}{720}(1901f_n - 2774f_{n-1} - 2616f_{n-2} - 1274f_{n-3} + 251f_{n-4}) = 0.00004165$$

Furthermore, the corrector equation is solved in the same way as the predictor equation, but by using the prediction value that has been obtained previously. Thus, the correction value is obtained, which is the value of the numerical solution using the Adams-Bashforth-Moulton method, as follows:

$$S_{n+1}^{(0)} = S_n + \frac{h}{720}(251f_{n+1} + 646f_n - 264f_{n-1} + 106f_{n-2} + 19f_{n-3}) = 0.99964905$$

$$I_{R_{n+1}}^{(0)} = I_{R_n} + \frac{h}{720}(251f_{n+1} + 646f_n - 264f_{n-1} + 106f_{n-2} + 19f_{n-3}) = 0.00018657$$

$$I_{B_{n+1}}^{(0)} = I_{B_n} + \frac{h}{720}(251f_{n+1} + 646f_n - 264f_{n-1} + 106f_{n-2} + 19f_{n-3}) = 0.00007221$$

$$I_{H_{n+1}}^{(0)} = H_n + \frac{h}{720}(251f_{n+1} + 646f_n - 264f_{n-1} + 106f_{n-2} + 19f_{n-3}) = 0.00005053$$

$$I_{R_{n+1}}^{(0)} = R_n + \frac{h}{720}(251f_{n+1} + 646f_n - 264f_{n-1} + 106f_{n-2} + 19f_{n-3}) = 0.00004165$$

The results of the iteration of the numerical solution of the SIRIBHR model of the spread of drug addiction in South Sulawesi until t = 42 months for each population rate will be shown in a graphical plot. The iteration results for all population rates will be shown in the following figure.

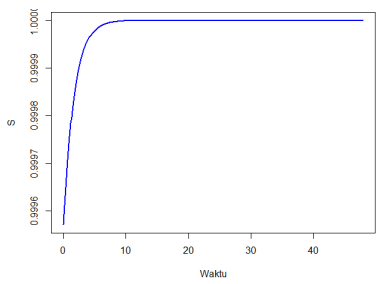

Figure 2. S population graph plot
open source software R

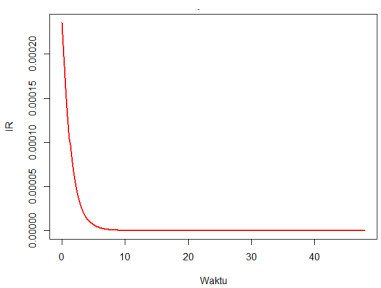

Figure 3. IR Population graph plot
open source software R

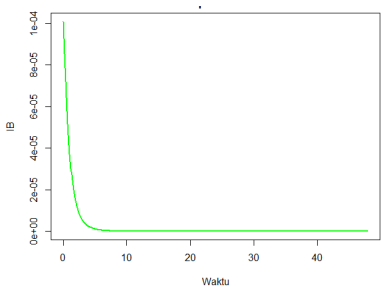

Figure 4. IB Population graph plot
open source software R

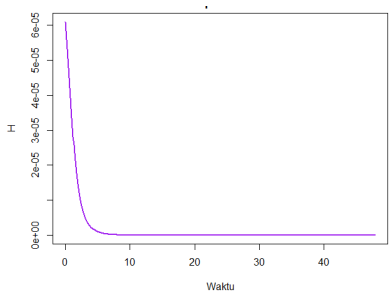

Figure 5. H Population graph plot
open source software R

The population graphs of individuals with mild addiction (I_R), severe addiction (I_B), and those undergoing rehabilitation (H) all show a sharp decline from the beginning of the simulation to close to zero, indicating that the number of individuals in these categories is drastically reduced to almost no new cases in the long run. Meanwhile, the population of recovered individuals (R) experienced a brief increase in the initial phase as a reflection of the recovery process, then declined exponentially to near zero, indicating the exit of individuals from the system or that the entire population has returned to an addiction-free state. The overall simulation results confirm that the mathematical model used, together with the Adam-Moulton numerical method, can represent the dynamics of drug addiction spread and control accurately, and by the predictions of stability theory.

The results of this study are in line with various previous studies that use mathematical models to analyze the spread of disease or social behavior, but this research makes a new contribution by focusing on drug addiction and solving it numerically using the Adams Moulton method. Unlike previous studies that generally only discuss model analysis or exact solutions, this study develops a more realistic SIIHR compartmental model by considering the rehabilitation and recovery process, and applies a multistep numerical approach to simulate population dynamics more accurately. The finding that the addiction-free equilibrium point is stable and the value of $R_0 < 1$ reinforces the theoretical assumption that the spread of addiction can be controlled, while showing that the numerical method used is effective in describing the long-term behavior of the system.

4. CONCLUSION

Based on the results of research and interpretation in the discussion, and in line with the formulation of the problem, the conclusions that can be given by the author in this study are:

1. The mathematical model of the drug addiction problem in South Sulawesi is:

$$\frac{\delta S}{\delta t} = \mu - (\mu + \rho I_R)S$$
$$\frac{\delta I_R}{\delta t} = \rho S I_R - (\mu + \gamma + \varepsilon) I_R$$
$$\frac{\delta I_B}{\delta t} = \varepsilon I_R + \delta H - (\mu + \beta) I_\beta$$
$$\frac{\delta H}{\delta t} = \beta I_B + \gamma I_R - (\delta + \mu + \theta) H$$
$$\frac{\delta R}{\delta t} = \theta H - \mu R$$

2. The mathematical model with the Adams-Moulton method is:

$$S_{n+1}^{(0)} = S_n + \frac{h}{720}(251f_{n+1} + 646f_n - 264f_{n-1} + 106f_{n-2} + 19f_{n-3}) = 0.99964905$$

$$I_{R_{n+1}}^{(0)} = I_{R_n} + \frac{h}{720}(251f_{n+1} + 646f_n - 264f_{n-1} + 106f_{n-2} + 19f_{n-3}) = 0.00018657$$

$$I_{B_{n+1}}^{(0)} = I_{B_n} + \frac{h}{720}(251f_{n+1} + 646f_n - 264f_{n-1} + 106f_{n-2} + 19f_{n-3}) = 0.00007221$$

$$I_{H_{n+1}}^{(0)} = H_n + \frac{h}{720}(251f_{n+1} + 646f_n - 264f_{n-1} + 106f_{n-2} + 19f_{n-3}) = 0.00005053$$

$$I_{R_{n+1}}^{(0)} = R_n + \frac{h}{720}(251f_{n+1} + 646f_n - 264f_{n-1} + 106f_{n-2} + 19f_{n-3}) = 0.00004165$$

Numerical solutions obtained using the Adams-Moulton method for the drug addiction problem show stable and accurate results in modeling the dynamics of addiction spread and control. The method can handle the differential equations in the model well, resulting in solutions that converge towards the addiction-free equilibrium point, where the population of susceptible individuals increases while the number of addicted and rehabilitated individuals decreases to near zero.

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