Available online at http://scik.org
Commun. Math. Biol. Neurosci. 2024, 2024:135
https://doi.org/10.28919/cmbn/8971
ISSN: 2052-2541

MONTE CARLO SIMULATION METHOD IN STABILITY ANALYSIS OF EPIDEMIOLOGICAL MODELS

DANI SUANDI*, MARIA ARTANTA GINTING

Computer Science Department, School of Computer Science, Bina Nusantara University, Jakarta 11480, Indonesia

Abstract. Differential equations are a very important tool for mathematical modeling to capture and describe dynamic processes in various disciplines. The most difficult challenge in differential equation-based modeling is determining the stability of the equilibrium point, especially for equilibria that cannot be found explicitly, which is usually the case in complex models with high dimensions. This paper presents an alternative method for analyzing the stability of an equilibrium point. The method presented is a numerical approach using Monte Carlo simulation. This stability analysis uses two different approaches, namely the stability ratio approach and the eigenvalue based analysis. Both approaches are tested on the SIR model whose stability has been tested. The model selected is one that can explicitly represent equilibrium. The aim is to validate the constructed method. The SIR model usually has a level of complexity in checking the stability of the internal equilibrium with the stability condition $R_0 > 1$. For parameters that allow human intervention in it, the influence of these parameters on the stability is studied. Therefore, in this numerical approach, it is necessary to build a stability domain of the interior equilibrium before implementing the Monte Carlo simulation. Simulation results show that both approaches are successful in approximating the interior equilibrium stability of epidemiological models.

Keywords: monte carlo method; stability analysis; dynamical system; epidemic model.
2020 AMS Subject Classification: 34C60, 34A34, 34D20, 90C31, 92B05, 93C15.

*Corresponding author
E-mail address: dani.suandi@binus.ac.id
Received October 18, 2024

1. INTRODUCTION

In mathematical modeling, real-world phenomena are commonly expressed and analyzed in the form of a differential equations system. It is an abstract and simplified representation of a complex system. The differential equations system describes relationship between all variables in the system and their rate of change. In dynamic model, the system states change substantially in time. The study of differential equations in dynamic model enable us to simulate, analyze, and predict the behavior of the system. In recent years, dynamic modeling using differential equations has been applied in a wide range of disciplines, such as in biology, physics, finance, and engineering where accurate simulations and predictions are necessary to describe and solve the challenges of real-world phenomena. For instance, in population dynamics, [1] discussed analytical solutions of logistic growth model with two differential equations representing coupled processes of growth and development. In 2022, [2] proposed a procedure for obtaining analytical solutions of a population model with variable carrying capacity consisting of a coupled system of nonlinear ordinary differential equations. In addition, [3] studied systems of Stieltjes differential equations and presented an application to the predator-prey model describing the dynamics of a fish population subjected to predation and seasonal fishing strategy. The qualitative analysis of the interaction between aphids and their predators, such as ladybugs, was explored in [4]. The principal findings indicated that the proliferation of insectivorous species, such as ladybirds, could serve as an alternative strategy for the management of aphid populations, thereby reducing the reliance on chemical insecticides. The differential equation method can be utilized to examine insecticide resistance in Anopheles mosquito populations. This approach has been demonstrated in [5], which focuses on resistance at a single locus, and further expanded in [6] to address resistance at two loci. A central finding of both studies is that elevated insecticide usage correlates with augmented resistance levels. In epidemiology, [7] extended SIR compartmental model to deterministic and stochastic time-delayed models in order to predict the epidemiological trend of COVID-19. Furthermore, [8] presented two nonlinear mathematical models to gain insight into the optimal vaccination strategy under different situations.

One of significant concepts in dynamical system is equilibrium problem. Equilibrium can be defined as the point in state-space where the system's states remain unchanged. This condition is also known as the steady-state. The stability of equilibrium in dynamical systems is contingent upon the trajectories that originate in proximity to the equilibrium point and subsequently diverge from it. The stability of solutions to differential and difference equations describing dynamical systems has been the subject of extensive discussion. For instance, Lyapunov stability theory has been studied in [9], [10], and [11] to investigate the stability of equilibria in nonlinear systems. Other methodologies such as Integral Quadratic Constraint (IQC) formulations and Linear Parameter Varying (LPV) techniques have been discussed by [12], [13] and [14]. However, in relatively complex models, equilibrium conditions cannot be determined explicitly, making it challenging to assess the stability of the equilibrium point. In epidemiological systems arising from compartmental deterministic modeling, [15] proposed an algorithm to obtain an analytical threshold condition for the local stability of the disease-free equilibrium. [16] then analyzed the global asymptotic stability at the disease-free equilibrium of a metapopulation model for the dynamics of malaria's spread. [17] and [18] studied the direction of Hopf bifurcations and the stability of bifurcated periodic solutions by applying the center manifold theorem and bifurcation theory. [19] analyzed the stability of disease-free equilibrium in the network-based Susceptible–Exposed–Infected–Recovered (SEIR) epidemic model. In addition, they consider several control strategies and the effects on epidemic inhibition. In this paper, we present a numerical approach to analyze equilibrium stability using Monte Carlo method for complex dynamical models.

Monte Carlo method is a probabilistic approach to the behavior of uncertain system. It has been implemented to analyze the stability of dynamical systems in various field. For instance, [20] applied the technique to find small signal stability in electric power systems with uncertain generation and demand. [21] and [22] implemented the method to determine the basin of attraction for nonlinear systems and transient stability in power systems. The Monte Carlo simulations provide a comprehensive description of system stability, nevertheless the computational resources are often considerably expensive. In this condition, some researchers proposed combining the Monte Carlo with other techniques, such as Lyapunov exponents [21] and hybrid

transient stability approaches [22] to reduce the computational time. Furthermore, [23] combined the non-intrusive generalized polynomial chaos with the indirect Lyapunov method as an efficient alternative to Monte Carlo simulation. They estimated the stability and instability regions with high accuracy and confidence levels at lower computational costs. [24] proposed a numerical scheme to investigate stability in perturbed dynamical systems which computes transient probability densities effectively. He applied the scheme in a three-dimensional system under stochastic perturbations, and presents the analysis of stability under various conditions. [25] present a numerical approach to analyze high-dimensional complex systems with asymptotic states. Incorporating machine learning, based on random sampling and clustering methods, they characterize different asymptotic states or classes and their basins of attraction. This approach provides new insights into the bifurcation structure of complex dynamical systems.

This paper is organized as follows. In Section 2, the mathematical foundation is presented. The concept of Monte Carlo simulation and the stability of dynamical systems are discussed in this section. The algorithm of Monte Carlo simulation is described in Section 3. Here, we introduce a Monte Carlo simulation method utilizing ratio stability and eigenvalue analysis. In Section 4, the application of Monte Carlo Simulation to the Susceptible-Infected-Recovered (SIR) model is discussed. Finally, the conclusion of this paper is presented in Section 5.

2. MATHEMATICAL FOUNDATION

The Monte Carlo method is a statistical technique that utilizes random sampling to obtain numerical results. It is often used in situations where it is challenging or impossible to obtain an analytical solution. The method is widely applied in various fields, such as physics, finance, engineering, and computational biology [26]. Here we will discuss the Monte Carlo method in dynamic systems, especially in epidemiological models to determine endemic stability, which is usually difficult to do analytically. However, prior to an in-depth examination of this methodology within the subsequent epidemiological model, a comprehensive overview of the Monte Carlo method and the stability of dynamical systems is provided.

2.1. Monte Carlo Simulations.

Monte Carlo simulation is fundamentally rooted in the concept of random variables and their expectations. A random variable X, defined on a probability

space $(\Omega, \mathscr{F}, \mathbb{P})$, can be thought of as a function that maps outcomes of a random process to real numbers. In [26], the expectation of a random variable, denoted by $\mathbb{E}[X]$, is a crucial measure that provides the average value one would expect over many repetitions of the random process, mathematically given by:

$$\mathbb{E}[X] = \int_{\Omega} X(\omega)\, d\mathbb{P}(\omega).$$

Monte Carlo estimation leverages this concept by approximating the expectation through repeated sampling. Specifically, by generating a large number of independent and identically distributed (i.i.d.) samples $X_1, X_2, \ldots, X_N$ of the random variable X, the Monte Carlo estimator $\hat{\mu}_N$ approximates the true expectation $\mu = \mathbb{E}[X]$ as :

$$\hat{\mu}_N = \frac{1}{N} \sum_{i=1}^{N} X_i,$$

converging towards μ as the number of samples N increases, a phenomenon supported by the Law of Large Numbers:

$$\hat{\mu}_N \xrightarrow{a.s.} \mu \quad \text{as} \quad N \to \infty.$$

The generation of random numbers is a crucial step in Monte Carlo simulations, as it enables the creation of independent and identically distributed (i.i.d.) samples. It is frequently undertaken with the objective of ensuring that they adhere to a specific probability distribution. Two distributions that are typically chosen as the constraints for generating data in the Monte Carlo simulation are uniform and normal (Gaussian) distribution. The uniform distribution is one of the simplest probability distributions which defines equal probability over a given range for a continuous distribution. The probability density function of uniform distribution on interval $[a, b]$ is described as follows

$$f_U(u) = \frac{1}{b-a}, \quad \text{for } u \in [a, b].$$

In addition, another type of distribution with its convenient in mathematical properties is normal (Gaussian) distribution. It is commonly used in modeling a wide range of phenomena, as many real-world processes can be thought of as the sum of several small, independent effects.

Probability density function of normal random variable $X \sim N(\mu, \sigma^2)$ is presented as follows:

$$f_X(x) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(-\frac{(x-\mu)^2}{2\sigma^2}\right), \quad x \in \mathbb{R},$$

where μ is the mean and σ^2 is the variance.

2.2. Stability of dynamical systems. Dynamical systems play an important role in mathematical modeling, which is used to describe the dynamics of a population or the evolution of a particular state. Typically, the system is expressed mathematically using ordinary differential equations (ODEs). In [27], these systems can be represented in the form

$$\frac{d\mathbf{y}}{dt} = \mathbf{f}(\mathbf{y}, \boldsymbol{\theta}),$$

where $\mathbf{y} \in \mathbb{R}^n$ is the state vector, $\mathbf{f} : \mathbb{R}^n \times \mathbb{R}^m \to \mathbb{R}^n$ is a vector-valued function representing the dynamics of the system and, $\boldsymbol{\theta} \in \mathbb{R}^m$ is a vector of system parameters.

Identifying the stability of an equilibrium point is important in the study of mathematical models based on differential equations. Equilibrium is achieved when $\mathbf{f}(\mathbf{y}_e) = 0$, where $\mathbf{y}_e$ is the equilibrium point. The stability of equilibrium points is analyzed by linearized the system, and calculating the Jacobian matrix around the equilibrium, $\mathbf{J}(\mathbf{y}_e)$, which is defined as :

$$\mathbf{J}(\mathbf{y}_e) = \left.\frac{\partial \mathbf{f}}{\partial \mathbf{y}}\right|_{\mathbf{y}=\mathbf{y}_e} = \begin{bmatrix} \frac{\partial f_1}{\partial y_1} & \cdots & \frac{\partial f_1}{\partial y_n} \\ \vdots & \ddots & \vdots \\ \frac{\partial f_n}{\partial y_1} & \cdots & \frac{\partial f_n}{\partial y_n} \end{bmatrix}_{\mathbf{y}=\mathbf{y}_e}.$$

The system can be approximated linearly around $\mathbf{y}_e$ by:

$$\frac{d\mathbf{z}}{dt} = \mathbf{J}(\mathbf{y}_e)\mathbf{z},$$

where $\mathbf{z} = \mathbf{y} - \mathbf{y}_e$ represents a small perturbation from the equilibrium [27]. After linearizing the system, the eigenvalues of the Jacobian matrix will be investigated. The eigenvalues $\lambda_1, \lambda_2, \ldots, \lambda_n$ of the Jacobian can be used to describe the behavior system around the equilibrium. An equilibrium is asymptotically stable if all eigenvalues have negative real parts ($\Re(\lambda_i) < 0$ for all i). Asymptotically stable means that any small perturbation will decay over time, returning the system to equilibrium. Conversely, the equilibrium is unstable if at least one eigenvalue has positive real part ($\Re(\lambda_i) > 0$). In unstable condition, small perturbations will

grow, leading the system away from equilibrium. However, if eigenvalues have non-positive real parts ($\Re(\lambda_i) \leq 0$) with at least one zero, further analysis is required [27].

3. Monte Carlo Simulation Algorithm

3.1. Ratio Stability Approach. In this section, an algorithm is constructed to obtain the stability ratio value to evaluate the stability of the equilibrium of a dynamic system using Monte Carlo simulation. We aim to analyze the stability of the equilibrium point $\mathbf{y}_e$, where $\mathbf{f}(\mathbf{y}_e, \boldsymbol{\theta}) = 0$. However, the equilibrium point may not be explicitly known. Thus, we use the Monte Carlo method for a probabilistic stability analysis. The following are the steps in the stability analysis of a dynamical system through the Ratio Stability Approach.

Step 1: Perturbation of Initial Conditions and Parameters. In the first step, it is possible to commence the process by introducing a degree of variation into the initial values $\mathbf{y}_0$ and parameters $\boldsymbol{\theta}$ that are deemed suitable for analysis. In some epidemiological cases, however, the necessity for random initial values is minimal, as the initial conditions in the field are typically already known, rendering random initial values optional. In the meantime, with regard to parameter values, the uncertainty of parameter values in the field, particularly in epidemiological models, provides a rationale for introducing a degree of disturbance to the parameters. The perturbed initial condition $\mathbf{y}_0'$ and perturbed parameter $\boldsymbol{\theta}'$ are given by:

$$\mathbf{y}_0' = \mathbf{y}_0 + \delta\mathbf{y}, \tag{3.1}$$

$$\boldsymbol{\theta}' = \boldsymbol{\theta} + \delta\boldsymbol{\theta}, \tag{3.2}$$

where $\delta\mathbf{y}$ and $\delta\boldsymbol{\theta}$ are small perturbations, typically sampled from a distribution such as the normal or uniform distribution. For epidemic models, it is crucial to confirm that the generation of parameter data is focused on the region of stability being analyzed. Typically, $R_0 < 1$ indicates the stability of the disease-free equilibrium, while $R_0 > 1$ corresponds to the stability of the endemic equilibrium (interior equilibrium).

Step 2: Numerical Simulation. For each set of perturbed initial conditions and parameters, we simulate the system over a time interval $[0, T]$ using a suitable numerical integration method, such as the Runge-Kutta method. The state vector at time T is denoted as $\mathbf{y}(T)$.

Step 3: Distance from Equilibrium. We evaluate the distance between the state vector at time T and the equilibrium point $\mathbf{y}_e$. The distance d is given by:

$$d = \|\mathbf{y}(T) - \mathbf{y}_e\|, \tag{3.3}$$

where $\|\cdot\|$ is typically the Euclidean norm. Since $\mathbf{y}_e$ may not be explicitly known, it can be approximated by the final state of the simulation if the system is stable.

Step 4: Stability Condition. The system is considered stable if the distance d is below a certain threshold δ. Mathematically, this is expressed as:

$$\text{Stability} = \begin{cases} 1 & \text{if } d < \delta, \\ 0 & \text{if } d \geq \delta. \end{cases} \tag{3.4}$$

Step 5: Stability Ratio. We repeat the above steps for N simulations, each with different random perturbations. The stability ratio R_s is then computed as:

$$R_s = \frac{1}{N} \sum_{i=1}^{N} S_i, \tag{3.5}$$

where S_i is the stability indicator for the i-th simulation. The stability ratio R_s provides a probabilistic measure of the system's stability. A high R_s value (close to 1) indicates that the system is likely stable under the given perturbations, while a low R_s value suggests potential instability. The pseudo code for performing a stability analysis using the stability ratio is shown in Algorithm 1.

Algorithm 1 Monte Carlo Ratio Stability Analysis

Require: Model function $f(\mathbf{y}, \boldsymbol{\theta})$

Require: Initial condition $\mathbf{y}_0$

Require: Parameter set $\boldsymbol{\theta} = \{\theta_1, \theta_2, \ldots, \theta_m\}$

Require: Number of simulations N

Require: Perturbation scale ε

Require: Time range T

Require: Stability threshold δ

Ensure: Stability Ratio R_s

Initialize stability_counter $= 0$

for $i = 1$ to N **do**

    Step 1: Perturb the initial condition (optional)

    perturbed_$\mathrm{y}_0 = \mathbf{y}_0 + \mathrm{RandomPerturbation}(\varepsilon)$

    Step 2: Perturb the parameters

    perturbed_$\boldsymbol{\theta} = \boldsymbol{\theta} + \mathrm{RandomPerturbation}(\varepsilon)$

    Step 3: Run simulation

    $\mathbf{y}(t) = \mathrm{Simulate}(f, \mathrm{perturbed\_y}_0, \mathrm{perturbed\_}\boldsymbol{\theta}, T)$

    Step 4: Evaluate distance from equilibrium

    equilibrium_y $= \mathrm{EstimateEquilibrium}(\mathbf{y}(t))$

    distance $= \|\mathbf{y}(T) - \mathrm{equilibrium\_y}\|$

    Step 5: Check stability condition

    if distance $< \delta$ **then**

        stability_counter $=$ stability_counter $+ 1$

    end if

end for

Step 6: Compute Stability Ratio

$R_s = \frac{\mathrm{stability\_counter}}{N}$

return R_s

3.2. Eigenvalue Approach. The second approach involves eigenvalue analysis of the Jacobian matrix, which is computed either at the equilibrium point or at the end of a simulation. The Jacobian matrix is obtained by linearizing the system around the equilibrium point, and its eigenvalues provide information about the local stability properties of that equilibrium. When dealing with complex or non-linear systems, the equilibrium point $\mathbf{y}_e$ might not be explicitly known, or the system's behavior might be highly sensitive to initial conditions or parameters. In such cases, the Monte Carlo method can be applied to assess stability probabilistically. In this Monte Carlo framework, initial conditions and parameters will be perturbed randomly for each simulation, and at the end of the simulation, the Jacobian matrix will be computed based on the final state. The eigenvalues of this matrix will then be analyzed to assess whether the system tends to be stable or unstable. The eigenvalues obtained from all Monte Carlo simulations are constructed into a histogram, which allows for the analysis and determination of the distribution of eigenvalues and the overall system stability tendency based on stability criteria. The steps in determining stability through the eigenvalue approach are as follows:

Step 1: Perturbation of Initial Conditions and Parameters. As with the preceding approach, the factors that have the potential to be disturbed are the initial conditions $\mathbf{y}_0$ and parameter values $\boldsymbol{\theta}$. It should be noted, however, that the initial conditions are optional. In the event that additional random deviations are introduced for the initial conditions and parameters, the resulting equation can be expressed as follows:

$$\mathbf{y}_0' = \mathbf{y}_0 + \delta\mathbf{y}, \quad \boldsymbol{\theta}' = \boldsymbol{\theta} + \delta\boldsymbol{\theta},$$

where $\delta\mathbf{y}$ and $\delta\boldsymbol{\theta}$ are random perturbations, In most cases, the data is obtained from a normal or uniform distribution. As before, it is important to focus on the stability region being analyzed to ensure that the generated parameters fall within that region.

Step 2: Simulation of the System. The subsequent phase is to execute a dynamic simulation of the system at a specified time interval, denoted by the interval T, utilising the initial conditions and parameters that have been subjected to disturbances. However, prior to conducting the simulation, it is essential to identify the parameter values that satisfy the stability or existence

conditions for the equilibrium to be verified.

$$\mathbf{y}(t) = \text{Simulate}(\mathbf{f}, \mathbf{y}'_0, \boldsymbol{\theta}', T).$$

This generates a trajectory of the system states over time.

Step 3: Jacobian Matrix and Eigenvalue Computation. In order to ascertain the stability of the equilibrium through the eigenvalues, it is necessary to approximate it by taking the final value of the simulation at $t = T$. The Jacobian matrix evaluated at this point is denoted by $\mathbf{J}(\mathbf{y}(T))$. This value is dependent upon the previously selected parameters. Then, the eigenvalues of the Jacobian matrix must be calculated in order to obtain:

$$\lambda_1, \lambda_2, \ldots, \lambda_n = \text{Eigenvalues}(\mathbf{J}(\mathbf{y}(T))).$$

Step 4: Repeated Simulations and Eigenvalue Collection. The previous procedures should be repeated for a large number of Monte Carlo simulations, denoted as N. Further, all eigenvalues obtained from each simulation will be collated to create a comprehensive dataset of eigenvalues.

Step 5: Histogram of Eigenvalues. The last step is creating a histogram of the eigenvalues obtained from the simulations. A histogram is a chart that plots the distribution of possible eigenvalues under random perturbations. It visualizes the likelihood of different stability scenarios based on the distribution of the eigenvalues. Algorithm 2 presents a comprehensive breakdown of each phase of the procedure.

Algorithm 2 Monte Carlo Eigenvalue Analysis

Require: Model function $f(\mathbf{y}, \boldsymbol{\theta})$

Require: Initial condition $\mathbf{y}_0$

Require: Parameter set $\boldsymbol{\theta} = \{\theta_1, \theta_2, \ldots, \theta_m\}$

Require: Number of simulations N

Require: Perturbation scale ε

Require: Time range T

Ensure: Histogram of all eigenvalues

Initialize eigenvalue_list $= []$

for $i = 1$ to N **do**

    Step 1: Perturb the initial condition (optional)

    perturbed_$\mathrm{y}_0 = \mathbf{y}_0 + \mathrm{RandomPerturbation}(\varepsilon)$

    Step 2: Perturb the parameters

    perturbed_$\boldsymbol{\theta} = \boldsymbol{\theta} + \mathrm{RandomPerturbation}(\varepsilon)$

    Step 3: Run simulation

    $\mathbf{y}(t) = \mathrm{Simulate}(f, \mathrm{perturbed\_y}_0, \mathrm{perturbed\_}\boldsymbol{\theta}, T)$

    Step 4: Compute Jacobian at the end of the simulation

    $\mathbf{J} = \mathrm{ComputeJacobian}(f, \mathbf{y}(T), \mathrm{perturbed\_}\boldsymbol{\theta})$

    Step 5: Calculate eigenvalues of the Jacobian

    $\mathrm{eigenvalues} = \mathrm{ComputeEigenvalues}(\mathbf{J})$

    Step 6: Store all eigenvalues in eigenvalue_list

    Append eigenvalues to eigenvalue_list

end for

Step 7: Plot histogram of eigenvalue_list

PlotHistogram(eigenvalue_list)

4. Example of Application

A basic mathematical model for epidemic spread is popularly known as the Susceptible-Infected-Recovered (SIR) model. It describes the dissemination of infectious diseases within

a population. To understand the long-term behaviour of the system, we need to analyze the stability of the SIR model. Thus, we can determine whether small perturbations in initial conditions or parameters will cause the system to deviate significantly from its equilibrium state. In this study, a stability of the SIR model is analyzed using Monte Carlo simulation with two approaches: the stability ratio and the histogram of eigenvalues.

In this study, the selected model for evaluating the efficacy of the Monte Carlo method is one whose stability can be explicitly determined, rendering it an optimal choice for validation purposes. In particular, we employ the SIR (Susceptible-Infected-Recovered) model, which has been previously utilized in a case study within the research on mathematical modeling of measles outbreaks [28]. The explicit determination of stability ensures that the Monte Carlo simulations can be compared against well-established analytical results, thereby providing a robust benchmark for evaluating the method's accuracy and reliability. The objective of this study is to confirm the effectiveness of the Monte Carlo approach in capturing key dynamics, such as disease transmission and recovery rates, within a mathematically structured framework.

The model divides the population into three compartments: Susceptible ($\tilde{S}$), Infected ($\tilde{I}$), and Recovered ($\tilde{R}$), with the following set of ordinary differential equations governing the dynamics (4.1).

$$\begin{aligned} \frac{d\tilde{S}}{dt} &= \Lambda - \beta(1-u)\frac{\tilde{I}}{N} - (\mu+u)\tilde{S} \\ \frac{d\tilde{I}}{dt} &= \beta(1-u)\frac{\tilde{I}}{N} - (\gamma+\mu)\tilde{I} \\ \frac{d\tilde{R}}{dt} &= u\tilde{S} + \gamma\tilde{I} - \mu\tilde{R} \\ N(t) &= \tilde{S}(t) + \tilde{I}(t) + \tilde{R}(t) \end{aligned} \tag{4.1}$$

Here, Λ represents the recruitment rate, μ denotes the mortality rate, β stands for the transmission rate of the infection, γ refers to the recovery rate, and u signifies the vaccination control rate.

In [28], the model was simplified and reduced to a two-dimensional form, as represented by equation (4.2). The objective of this reduction was to simplify the system while maintaining its essential dynamics, thus enabling more efficient analysis and computation. By focusing on

two key variables, the simplified model captures the core behavior of the original system, facilitating the study of stability, parameter sensitivities, and other important properties without compromising the overall accuracy of the results. Furthermore, this transformation facilitates the application of numerical methods, such as Monte Carlo simulations, by reducing the computational burden.

$$\begin{aligned} \frac{dS}{dt} &= \mu - \beta(1-u)SI - (\mu+u)S \\ \frac{dI}{dt} &= \beta(1-u)SI - (\gamma+\mu)I \end{aligned} \tag{4.2}$$

It is established that the interior equilibrium derived from equation (4.2) is as follows:

$$EE := \left\{ S = \frac{\gamma+\mu}{\beta(1-u)}, \quad I = \frac{(\mathscr{R}_0-1)(\mu+\mu)}{\beta(1-u)} \right\}.$$

The stability of the interior equilibrium, as calculated in the study [28], is determined by the Basic Reproduction Number $\mathscr{R}_0$. According to the findings, the interior equilibrium remains stable if the condition $\mathscr{R}_0 > 1$ is satisfied. Mathematically, the expression for $\mathscr{R}_0$ is given by

$$\mathscr{R}_0 = \frac{\beta\mu(1-u)}{(u+\mu)(\gamma+\mu)}.$$

This threshold value,$\mathscr{R}_0$, serves as a critical parameter for understanding disease dynamics: if $\mathscr{R}_0 > 1$ the disease can spread and maintain an endemic equilibrium, while if $\mathscr{R}_0 < 1$, the infection will die out over time.

The Monte Carlo Simulation approach will be employed to examine the region established under conditions that ensure the stability of the interior equilibrium. This will permit an investigation of the stability's behavior across a range of parameters. Subsequently, we will apply the stability ratio algorithm and/or utilize the eigenvalue histogram method, as previously described, to assess the model's stability in a more comprehensive manner. These approaches will facilitate the quantification of stability characteristics through the analysis of the distribution of eigenvalues, thereby offering further insight into the influence of perturbations on equilibrium and the stability of the system under varying conditions. The objective is to achieve a deeper understanding of the stability landscape and verify the robustness of the equilibrium across different scenarios by combining these techniques.

1. Stability Ratio Approach Results. The first approach entails the calculation of the stability ratio through the utilization of Monte Carlo simulations. In this approach, the parameters of the SI model, β and u, are subjected to random perturbation, and the system is then simulated to ascertain whether the equilibrium remains stable or becomes disrupted. The parameter values from [28] serve as the basis for this simulation, with $\mu = \gamma = 0.01$. Meanwhile, the values of β and u are generated using a uniform distribution, with 1000 samples each. The range for β is set between 0.4 and 1, while for u, the range is between 0.01 and 0.4. The stability of the system is contingent upon the population's ability to return to an equilibrium state following minor disturbances. The stability ratio is defined as the proportion of simulations wherein the system maintains stability relative to the total number of simulations conducted. The results of the simulation conducted using this approach are presented in Figure 4.1.

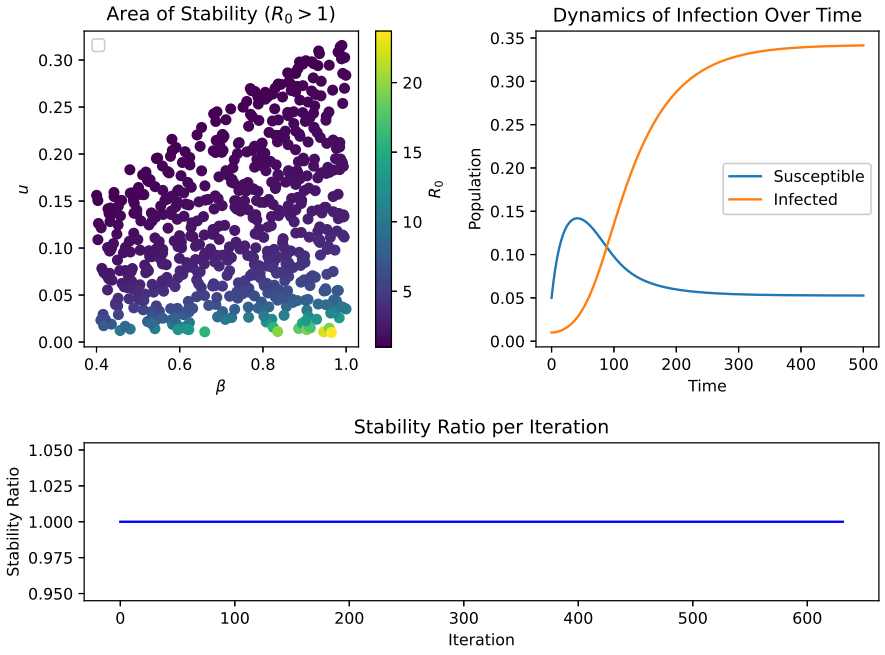

FIGURE 4.1. Simulation Result of Monte Carlo Simulation through stability ratio Approach

Figure 4.1 presents three different graphs: a stability region plot, an infection dynamics plot over time, and a stability ratio plot. The results obtained from randomly generated parameters for β and u are filtered based on the condition $\mathscr{R}_0 > 1$, which satisfies the stability criterion for

the interior equilibrium, and these are shown in the first graph. The second graph, illustrating the infection dynamics over time, is based on one of the parameter samples i.e $\beta = 0.4$ and $u = 0.05$. This helps to depict the final state of the simulation, where the solution path converges towards the interior equilibrium. The 1000 iterations with various parameter values indicate that the stability ratio is consistently one, confirming that the condition $\mathscr{R}_0 > 1$ guarantees the stability of the interior equilibrium.

2. Eigenvalue Approach Results. The second method involves analyzing the eigenvalues of the Jacobian matrix. In this approach, the same set of parameters as previously used are generated and filtered according to the stability conditions of the equilibrium under consideration, specifically the interior equilibrium. Once the randomly generated parameters are filtered, a simulation is conducted, which includes examining the eigenvalues of the Jacobian matrix at the final state of the simulation. The real parts of these eigenvalues are subsequently presented in the form of a histogram. The results of this simulation approach are displayed in Figure 4.2.

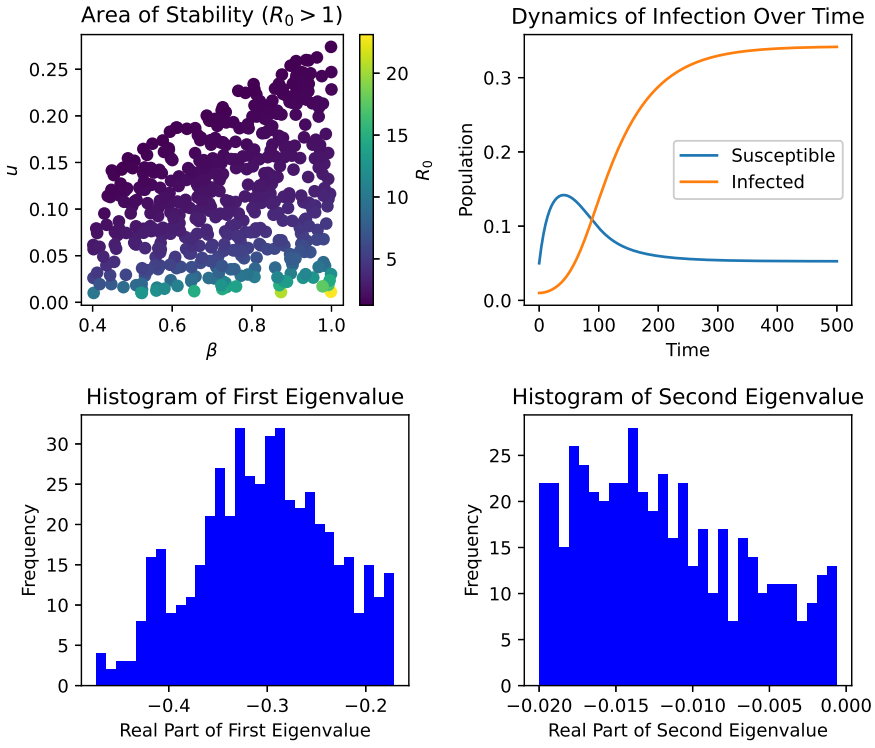

FIGURE 4.2. Simulation Result of Monte Carlo Simulation through Eigen Values Approach

Figure 4.2 illustrates the stability region, the system dynamics over time, and the histogram of all possible eigenvalues. The first two graphs are consistent with the previous approach, displaying the stability region of the interior equilibrium and the system's solution trajectory. The third result, presented as a histogram of the real parts of all eigenvalues, indicates that all eigenvalues possess negative real parts. Meanwhile, the solution trajectory demonstrates convergence towards the interior equilibrium. This suggests that the region where $\mathscr{R}_0 > 1$ serves as a stability region for the interior equilibrium.

5. CONCLUSION

High-dimensional dynamical systems, where equilibrium points are not explicitly known, present significant challenges for analytical stability determination. In such cases, numerical methods can be invaluable for confirming the stability of equilibrium points, particularly those that are not explicitly identifiable. Two distinct approaches to Monte Carlo simulations have been employed for the assessment of stability in endemic models. The results of these simulations illustrate the efficacy of numerical techniques in elucidating the intricate stability characteristics of these systems. The stability ratio approach provides a probabilistic measure of stability across a multitude of perturbations, whereas the eigenvalue analysis offers a more profound insight into the local stability properties in the vicinity of equilibrium points. The combination of these two approaches—stability ratio and eigenvalue analysis—offers a robust method for evaluating the stability of the epidemic model in the presence of random perturbations. By analyzing both the stability ratio and the distribution of eigenvalues, a comprehensive understanding of how this epidemiological system behaves under various conditions can be obtained, as well as an estimation of the likelihood that the system will remain stable or become unstable when faced with uncertainties. This implementation will furnish researchers with invaluable instruments for forecasting and administering disease outbreaks within the context of population dynamics.

DATA AVAILABILITY

The Python source code utilized in this study is publicly accessible. The code is accessible via GitHub at https://github.com/DaniSuandi174/MonteCarloSimulationForEpidemicModel.git,

and may be downloaded free of charge. The repository contains comprehensive instructions for executing the code, along with any requisite dependencies and datasets utilized within the program.

AUTHORSHIP

Dani Suandi: Writing – original draft, Methodology, Investigation, Formal analysis, Conceptualization, Supervision. Maria Artanta Ginting: Writing – review & editing, Formal analysis,Visualization.

ACKNOWLEDGMENTS

This work is supported by Bina Nusantara University as a part of Bina Nusantara University's BINUS International Research - Basic entitled *Investigation and Formulation of Optimal Strategies for the Control of the Spread of Infectious Diseases in the Agricultural Sector* with contract number: 096/VRRTT/VII/2024 and contract date 02 July 2024.

CONFLICT OF INTERESTS

The authors declare that there is no conflict of interests.

REFERENCES

[1] J.H.M. Thornley, J.J. Shepherd, J. France, An open-ended logistic-based growth function: analytical solutions and the power-law logistic model, Ecol. Model. 204 (2007), 531–534. https://doi.org/10.1016/j.ecolmodel.2006.12.026.

[2] M. Rodrigo, D. Zulkarnaen, Mathematical models for population growth with variable carrying capacity: analytical solutions, AppliedMath 2 (2022), 466–479. https://doi.org/10.3390/appliedmath2030027.

[3] L. Maia, N. El Khattabi, M. Frigon, Systems of Stieltjes differential equations and application to a predator-prey model of an exploited fishery, Discrete Contin. Dyn. Syst. 43 (2023), 4244–4271. https://doi.org/10.3934/dcds.2023086.

[4] D. Suandi, D. Aldila, V. Noviantri, et al. Mathematical modelling that characterizes the qualitative behavior of the interactions of aphids and ladybugs as insectivorous animals, Commun. Math. Biol. Neurosci., 2023 (2023), 106. https://doi.org/10.28919/cmbn/8185.

[5] D. Suandi, K.P. Wijaya, M. Apri, et al. A one-locus model describing the evolutionary dynamics of resistance against insecticide in anopheles mosquitoes, Appl. Math. Comput. 359 (2019), 90–106. https://doi.org/10.1016/j.amc.2019.03.031.

[6] D. Suandi, K.P. Wijaya, M. Amadi, et al. An evolutionary model propounding anopheles double resistance against insecticides, Appl. Math. Model. 106 (2022), 463–481. https://doi.org/10.1016/j.apm.2022.01.025.

[7] M. Mahrouf, A. Boukhouima, H. Zine, et al. Modeling and forecasting of COVID-19 spreading by delayed stochastic differential equations, Axioms 10 (2021), 18. https://doi.org/10.3390/axioms10010018.

[8] G. González-Parra, M.R. Cogollo, A.J. Arenas, Mathematical modeling to study optimal allocation of vaccines against COVID-19 using an age-structured population, Axioms 11 (2022), 109. https://doi.org/10.3390/axioms11030109.

[9] C. Pukdeboon, A review of fundamentals of lyapunov theory, J. Appl. Sci. 10 (2011), 55–61.

[10] S. Sastry, Lyapunov stability theory, in: Nonlinear Systems, Springer, New York, 1999: pp. 182–234. https://doi.org/10.1007/978-1-4757-3108-8_5.

[11] A. Papachristodoulou, S. Prajna, On the construction of Lyapunov functions using the sum of squares decomposition, in: Proceedings of the 41st IEEE Conference on Decision and Control, 2002., IEEE, Las Vegas, NV, USA, 2002: pp. 3482–3487. https://doi.org/10.1109/CDC.2002.1184414.

[12] A. Megretski, A. Rantzer, System analysis via integral quadratic constraints, IEEE Trans. Autom. Control 42 (1997), 819–830. https://doi.org/10.1109/9.587335.

[13] A.N. Vargas, C.M. Agulhari, R.C.L.F. Oliveira, V.M. Preciado, Robust stability analysis of linear parameter-varying systems with markov jumps, IEEE Trans. Autom. Control 67 (2022), 6234–6239. https://doi.org/10.1109/TAC.2021.3132231.

[14] P.J.W. Koelewijn, Analysis and control of nonlinear systems with stability and performance guarantees: A linear parameter-varying approach, Phd Thesis, Eindhoven University of Technology, (2023).

[15] J.C. Kamgang, G. Sallet, Computation of threshold conditions for epidemiological models and global stability of the disease-free equilibrium (DFE), Math. Biosci. 213 (2008), 1–12. https://doi.org/10.1016/j.mbs.2008.02.005.

[16] J.-H. Noubissi, J.C. Kamgang, Stability analysis of a metapopulation model for the dynamics of malaria's spread including climatic factors, Heliyon 10 (2024), e31666. https://doi.org/10.1016/j.heliyon.2024.e31666.

[17] J.-F. Zhang, W.-T. Li, X.-P. Yan, Hopf bifurcation and stability of periodic solutions in a delayed eco-epidemiological system, Appl. Math. Comput. 198 (2008), 865–876. https://doi.org/10.1016/j.amc.2007.09.045.

[18] Z. Hu, Z. Teng, L. Zhang, Stability and bifurcation analysis in a discrete sir epidemic model, Math. Comput. Simul. 97 (2014), 80–93. https://doi.org/10.1016/j.matcom.2013.08.008.

[19] J. Zhou, Y. Zhao, Y. Ye, Complex dynamics and control strategies of SEIR heterogeneous network model with saturated treatment, Physica A 608 (2022), 128287. https://doi.org/10.1016/j.physa.2022.128287.

[20] Z. Xu, Z.Y. Dong, P. Zhang, Probabilistic small signal analysis using Monte Carlo simulation, in: IEEE Power Engineering Society General Meeting, 2005, IEEE, San Francisco, CA, USA, 2005: pp. 1707–1713. https://doi.org/10.1109/PES.2005.1489425.

[21] A.R. Armiyoon, C.Q. Wu, An innovative approach for identifying boundaries of a basin of attraction for a dynamical system using monte carlo techniques and lyapunov exponents, in: 53rd IEEE Conference on Decision and Control, IEEE, Los Angeles, CA, USA, 2014: pp. 6299–6304. https://doi.org/10.1109/CDC.2014.7040376.

[22] C.M.M. Ferreira, J.A. Dias Pinto, F.P.M. Barbosa, Dynamic security analysis of an electric power system using a combined monte carlo-hybrid transient stability approach, in: 2001 IEEE Porto Power Tech Proceedings (Cat. No.01EX502), IEEE, Porto, Portugal, 2001: p. 6. https://doi.org/10.1109/PTC.2001.964742.

[23] L. Nechak, S. Berger, E. Aubry, Non-intrusive generalized polynomial chaos approach to the stability analysis of uncertain nonlinear dynamic systems, in: Eighth International Multi-Conference on Systems, Signals & Devices, IEEE, Sousse, 2011: pp. 1–6. https://doi.org/10.1109/SSD.2011.5767403.

[24] M. Labou, Numerical schemes for stability in probability of perturbed dynamical systems, Int. Appl. Mech. 48 (2012), 465–483. https://doi.org/10.1007/s10778-012-0534-x.

[25] M. Gelbrecht, J. Kurths, F. Hellmann, Monte carlo basin bifurcation analysis, New J. Phys. 22 (2020), 033032. https://doi.org/10.1088/1367-2630/ab7a05.

[26] D. Landau, K. Binder, A guide to Monte Carlo simulations in statistical physics, Cambridge University Press, 2021.

[27] S. Lynch, Dynamical systems with applications using MAPLE, Springer, 2010.

[28] D. Suandi, Optimal control problem of vacination for the spread of measles diseases model, J. Ris. Apl. Mat. 2 (2018), 76–83. https://doi.org/10.26740/jram.v2n2.p76-83.