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A Computational Guide to Stability Analysis of Nonlinear System: The Lotka-Volterra and SIR Models as Case Studies

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Abstract. This paper provides a structured and reproducible guide for analyzing the local stability of nonlinear dynamical systems by systematically combining analytical linearization with computational phase portrait visualization. Although these techniques are standard, introductory materials often lack a unified code-based workflow that connects abstract theory to practical, visual interpretation. This guide bridges that gap using two canonical models from different scientific domains: the Lotka-Volterra predator-prey model and the Susceptible Infected Recovered (SIR) epidemic model. For each system, we identify equilibrium points, compute the Jacobian matrix, and use eigenvalue analysis to determine local stability, and perform a sensitivity analysis to explore how dynamics are affected by key parameters. By comparing ecological and epidemiological models, we highlight how shared mathematical principles lead to distinct real-world dynamics, such as persistent oscillations versus threshold-based outbreaks. Python-generated phase portraits are used throughout to visually validate the analytical results, offering an intuitive complement to the theory. This work serves as a practical toolkit for students and researchers new to nonlinear modeling, emphasizing a clear step-by-step process essential for both educational settings and applied research.

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Key Words and Phrases: Nonlinear dynamics, stability analysis, linearization, phase portrait, Lotka-Volterra model, SIR model

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1. Introduction

In many areas of science and engineering, from population dynamics to control theory, understanding the stability of nonlinear systems is essential [1, 2]. Analyzing how a system behaves near its equilibrium points provides invaluable insight into its overall structure and long-term evolution [3, 4]. The classical tools for this task are linearization and phase portrait analysis. The theoretical foundations for this approach were laid out in inspiring texts that remain fundamental to the field today [5]. Linearization provides a precise criterion for local stability by approximating a nonlinear system near an equilibrium, while phase portraits offer an intuitive geometric understanding of the dynamic of the system [6, 7].

These foundational methods continue to be the bedrock of modern mathematical modeling. The Lotka-Volterra model, for example, is still actively used and extended to explore complex ecological interactions such as [8] and [9]. Similarly, the SIR model forms the basis for a large body of epidemiological research, providing critical insights into the spread of infectious diseases from influenza to recent pandemics [10] and [11].

Alongside this research, there is a parallel conversation on the most effective ways to teach these concepts. Many educators have highlighted the power of computational tools such as Python and MATLAB to help students visualize abstract concepts [12, 13]. However, while numerous resources focus on either the deep of theory [14–16] or advanced research applications [17], there remains a need for accessible, step by step guides that explicitly connect analytical calculations of stability with their computational visualization. This is particularly true for cross-disciplinary leaners who need to apply these methods without necessarily having a deep mathematical background. Linearization techniques can be used to approximate a linear system that closely resembles a nonlinear system at its equilibrium points [18]. Standard linear algebraic methods can be employed to analyze the Jacobian matrix in these places to determine the nature and stability of the equilibria [19, 20]. The eigenvalues of the Jacobian indicate whether an equilibrium point is a saddle, node, or spiral, as well as its stability or instability [20]. Recent applications of these methods can be found in [21–37].

To enhance the analysis, we incorporate a parameter sensitivity study, in particular, the predation rate parameter b, to investigate how changes in interaction strength affect equilibrium configurations and stability of the system. Beyond predator-prey dynamics, nonlinear modeling is also fundamental in epidemiology. The Susceptible Infected Recovered model is a cornerstone of mathematical epidemiology, describing the spread of infectious diseases through compartments that represent different health states of the population [11]. The SIR model, like the Lotka-Volterra system, is nonlinear and admits equilibrium points whose stability can be analyzed using Jacobian linearization [38]. In this work, we include a comparative analysis between the Lotka-Volterra and SIR models, highlighting how similar mathematical tools, such as local linearization, eigenvalue classification, and phase portraits, can be applied to problems from different domains. This cross-domain perspective enriches the learning process for students and emphasizes

the broad applicability of nonlinear stability analysis in applied mathematics. This paper aims to bridge the pedagogical gap by proposed a clear, step by step computational workflow that unifies these techniques. We demonstrate this integrated approach using two celebrated models: the Lotka-Volterra predator-prey model and the SIR model, which are nonlinear systems widely used in ecology and theoretical biology. The goal is not to introduce new mathematical theory but rather to provide an accessible and introducible guide that empowers learners and practitioners to confidently apply stability analysis to nonlinear models. By placing these two distinct models' side by side, we emphasize the universal power of these mathematical tools and explore the rich domain-specific insights they can reveal. The remainder of this paper is structured as follows. Section 2 details the mathematical methodology. Section 3 applies this methodology to the Lotka-Volterra model, including a parameter sensitivity analysis. In Section 4, we present a complete analysis of the SIR model, setting the stage for a direct comparison. Section 5 discussed the visual results of the phase portraits for both systems. Finally, Section 6 concludes with a summary of the findings and their implications.

2. Methods

With our main goal set, this section is all about building our toolkit. To make sure our approach is perfectly clear, we have broken it down into two parts. First, in Section 2.1, we will walk gently through the essential mathematical theory behind stability analysis. Then, in Section 2.2, we will lay out the concrete step by step workflow we will follow for our case studies, showing exactly how we will put that theory into practice.

2.1. Mathematical Foundations of Stability Analysis

We consider a general n-dimensional autonomous system of first-order ordinary differential equations (ODEs):

$$\frac{dx}{dt} = f(x). \tag{1}$$

Here, $x(t) \in \mathbb{R}^n$ and $f : \mathbb{R}^n \to \mathbb{R}^n$ is a continuously differentiable function. An equilibrium point, denoted by x^*, is a point where the dynamics of the system stops, i.e., it satisfies $f(x^*) = 0$.

To study the local stability near an equilibrium, we linearize the system by approximating $f(x)$ with its first-order Taylor expansion around x^*. The result is a linear system governed by the Jacobian matrix J, which consists of all first-order partial derivatives of f:

$$J(x) = \begin{bmatrix} \frac{\partial f_1}{\partial x_1} & \frac{\partial f_1}{\partial x_2} & \cdots & \frac{\partial f_1}{\partial x_n} \\ \frac{\partial f_2}{\partial x_1} & \frac{\partial f_2}{\partial x_2} & \cdots & \frac{\partial f_2}{\partial x_n} \\ \vdots & \vdots & \ddots & \vdots \\ \frac{\partial f_n}{\partial x_1} & \frac{\partial f_n}{\partial x_2} & \cdots & \frac{\partial f_n}{\partial x_n} \end{bmatrix}. \tag{2}$$

The linearized system that describes the evolution of a small perturbation $u = x - x^*$ is given by

$$\frac{du}{dt} = J(x^*)\, u \tag{3}$$

The stability of the equilibrium point x^* is determined by the eigenvalues λ of the Jacobian matrix evaluated at the point $J(x^*)$:

$$J(x^*)v = \lambda v,$$

where v is the corresponding eigenvector.

- If all eigenvalues have negative real parts, then x^* is *locally asymptotically stable*.
- If at least one eigenvalue has a positive real part, then x^* is *unstable*.
- If all eigenvalues have non-positive real parts with at least one having a zero real part, the linear analysis is *inconclusive*, and higher-order terms are needed.

For two-dimensional systems, the trace $\mathrm{tr}(J)$ and the determinant $\det(J)$ of the Jacobian matrix can be used to classify the type of equilibrium (e.g. node, saddle, spiral, or center).

2.2. Applied Workflow

In this study, we apply this mathematical framework to our case studies using the following structured workflow:

(i) **Identify Equilibrium Points:** Analytically solve $f(x) = 0$ to find all equilibria.

(ii) **Perform Linearization:** Compute the Jacobian matrix $J(x)$ and evaluate it at each equilibrium point x^*.

(iii) **Classify Stability:** Calculate the eigenvalues of each $J(x^*)$ to determine the local stability and type of each equilibrium.

(iv) **Visualize Dynamics:** Generate phase portraits using Python to visually confirm the analytical predictions.

(v) **Conduct Sensitivity Analysis:** For the Lotka–Volterra model, investigate how varying a key parameter affects the system's dynamics.

We identify the equilibrium points, compute the Jacobian matrix at each point, and perform an eigenvalue analysis to classify their stability. Phase portraits are generated to visualize the local behavior near each equilibrium, confirming the analytical predictions.

3. Case Study: Lotka-Volterra Predator-Prey Model

Our first case study is the classical Lotka–Volterra model, which describes the dynamic relationship between a predator and its prey. For this model to be biologically meaningful, we assume that all parameters (a, b, c, d), representing birth, death, and interaction rates, are positive real constants:

$$\begin{cases} \dfrac{dx}{dt} = ax - bxy, \\ \dfrac{dy}{dt} = -cy + dxy, \end{cases} \tag{4}$$

where $x(t)$ and $y(t)$ represent the prey and predator populations, respectively, and $a, b, c, d > 0$ are constant parameters.

3.1. Equilibrium Points

The first step is to find the equilibrium points of the system by setting both derivatives to zero.

$$\begin{cases} ax - bxy = 0, \\ -cy + dxy = 0. \end{cases}$$

Factoring both equations, we obtain the following:

$$x(a - by) = 0, \qquad y(-c + dx) = 0.$$

This yields two biologically relevant equilibrium points:

- **Trivial Equilibrium:** $E_1 = (0, 0)$. This represents the complete absence of both prey and predators.
- **Co-existence Equilibrium:** $E_2 = \left(\frac{c}{d}, \frac{a}{b}\right)$. This represents a state where both populations co-exist with stable average populations.

3.2. Stability Analysis

With the equilibria identified, our next step is to use linearization to understand the stability of each point. We first compute the general Jacobian matrix for the system:

$$J(x, y) = \begin{bmatrix} a - by & -bx \\ dy & -c + dx \end{bmatrix}.$$

We now evaluate this Jacobian at each equilibrium point:

(i) Analysis in the Trivial Equilibrium $E_1 = (0, 0)$. Evaluating the Jacobian at $(0, 0)$ gives:

$$J(0,0) = \begin{bmatrix} a & 0 \\ 0 & -c \end{bmatrix}.$$

The eigenvalues are the diagonal entries: $\lambda_1 = a$ and $\lambda_2 = -c$. Since $a > 0$ and $-c < 0$, the eigenvalues are real and have opposite signs. Thus, the origin is an **unstable saddle point**. Trajectories near the origin will be pushed away, indicating that if even a few prey and predators are present, the populations will not die out.

(ii) Analysis in the Co-existence Equilibrium $E_2 = \left(\frac{c}{d}, \frac{a}{b}\right)$. Evaluating the Jacobian at this point gives:

$$J\left(\tfrac{c}{d}, \tfrac{a}{b}\right) = \begin{bmatrix} 0 & -\frac{bc}{d} \\ \frac{ad}{b} & 0 \end{bmatrix}.$$

To find the eigenvalues, we solve the characteristic equation

$$\det(J - \lambda I) = 0 \quad \Rightarrow \quad \lambda^2 + ac = 0.$$

This yields the purely imaginary eigenvalues

$$\lambda = \pm i\sqrt{ac}.$$

Purely imaginary eigenvalues correspond to a **center**. Thus, the analytical result predicts that, in the vicinity of the co-existence point, the predator and prey populations will oscillate in endless, stable cycles.

3.3. Parameter Sensitivity Analysis

A powerful feature of a good model is understanding how its predictions change when its parameters are tweaked. This is known as a *sensitivity analysis*. In our Lotka–Volterra model, a particularly interesting parameter is b, which represents the rate at which prey is consumed by predators, or the impact of each predation event. What happens to the system if this rate changes?

Let us consider the co-existence equilibrium $E_2 = \left(\frac{c}{d}, \frac{a}{b}\right)$. We can immediately see that the equilibrium predator population,

$$y^* = \tfrac{a}{b},$$

depends directly on b. If the predation rate (b) increases, the steady-state predator population (y^*) required to maintain equilibrium decreases. This reflects a more "efficient" system where fewer predators are needed to control the prey.

But does this change the stability of the system? We find that the eigenvalues in this equilibrium are

$$\lambda = \pm i\sqrt{ac}.$$

Notice that the parameter b does not appear in this expression at all.

This leads to a crucial insight: while the predation rate b changes the equilibrium level of the predator population, it does not change the fundamental nature of the coexistence equilibrium. The equilibrium remains a *center*, and therefore no bifurcation occurs with respect to this parameter. The tendency of the system to oscillate is a robust feature.

This will be clearly illustrated in the phase portraits presented in Section 5. To demonstrate this effect, we simulate the system for three representative values of the predation rate,

$$b \in \{0.2, 0.5, 0.8\},$$

while keeping the other parameters fixed. These simulations will show how changing b alters the shape of the orbital cycles but does not break their closed-loop structure.

4. Comparative Case Study: Susceptible-Infected-Recovered Epidemic Model

In this section, we extend our mathematical framework to analyze the classical Susceptible-Infected-Recovered *(SIR)* epidemic model. This model captures the spread of infectious diseases within a closed population by dividing the population into three compartments:

$S(t)$: number of susceptible individuals,

$I(t)$: number of infected individuals, and

$R(t)$: number of recovered (or removed) individuals.

The dynamics of the model are governed by the following system of differential equations:

$$\begin{cases} \dfrac{dS}{dt} = -\beta SI, \\ \dfrac{dI}{dt} = \beta SI - \gamma I, \\ \dfrac{dR}{dt} = \gamma I, \end{cases}$$

where $\beta > 0$ is the transmission rate and $\gamma > 0$ is the recovery rate. We will identify the equilibrium points, perform a linear stability analysis using the Jacobian matrix, and illustrate the system behavior using phase portraits.

Beyond its biological relevance, the SIR model serves as an effective pedagogical bridge between biological systems and general dynamical systems theory. By comparing this model with other biological and epidemiological frameworks, learners can better understand how concepts such as equilibrium, stability, and bifurcation transcend disciplinary

boundaries. This comparison reinforces the universality of mathematical tools used to describe population dynamics, reaction kinetics, and even ecological or biochemical interactions. In particular, analyzing the stability of disease-free and endemic equilibria provides a concrete, intuitive context through which students can grasp abstract notions of local and global stability, eigenvalue behavior, and nonlinear feedback mechanisms. Thus, the SIR model not only exemplifies epidemiological reasoning but also deepens the conceptual understanding of dynamical stability in life sciences and applied mathematics.

4.1. Equilibrium Points

Setting $\frac{dS}{dt} = 0$ and $\frac{dI}{dt} = 0$, we find two biologically relevant equilibria:

- **Disease-Free Equilibrium (DFE):**

  $$E_{\text{DFE}} = (S, I) = (N, 0),$$

  which corresponds to a state without disease in the population
  .

- **Endemic Equilibrium (EE):**

  $$E_{\text{EE}} = (S^*, I^*) = \left(\frac{\gamma}{\beta}, N - \frac{\gamma}{\beta}\right).$$

  This equilibrium is only physically meaningful if $S^* < N$, which requires

  $$\frac{\gamma}{\beta} < N \quad \text{or equivalently} \quad \frac{\beta N}{\gamma} > 1.$$

  This introduces the *basic reproduction number*

  $$R_0 = \frac{\beta N}{\gamma},$$

  which is the key threshold parameter. The endemic equilibrium exists only if $R_0 > 1$.

4.2. Stability Analysis

The Jacobian matrix for the SIR system is:

$$J(S, I) = \begin{bmatrix} -\beta I & -\beta S \\ \beta I & \beta S - \gamma \end{bmatrix}.$$

Stability of the Disease-Free Equilibrium (DFE): Evaluating the Jacobian at $E_{\text{DFE}} = (N, 0)$ gives:

$$J(N, 0) = \begin{bmatrix} 0 & -\beta N \\ 0 & \beta N - \gamma \end{bmatrix}.$$

The eigenvalues are the diagonal entries:

$$\lambda_1 = 0, \quad \lambda_2 = \beta N - \gamma = \gamma(R_0 - 1).$$

The stability is determined by λ_2:

- If $R_0 < 1$, then $\lambda_2 < 0$ and the DFE is **stable**; the disease dies.
- If $R_0 > 1$, then $\lambda_2 > 0$ and the DFE is **unstable**; an outbreak can occur.

Stability of the endistic Equilibrium (EE, $R_0 > 1$): Evaluating the Jacobian at $E_{\text{EE}} = \left(\frac{\gamma}{\beta}, N - \frac{\gamma}{\beta}\right)$ gives:

$$J(E_{\text{EE}}) = \begin{bmatrix} -\beta\left(N - \frac{\gamma}{\beta}\right) & -\gamma \\ \\ \beta\left(N - \frac{\gamma}{\beta}\right) & 0 \end{bmatrix}.$$

The trace and determinant are:

$$\text{tr}(J) = -\beta\left(N - \frac{\gamma}{\beta}\right) = -\beta I^* < 0, \qquad \det(J) = \gamma\beta I^* > 0.$$

Since $\text{tr}(J) < 0$ and $\det(J) > 0$, both eigenvalues have negative real parts. Therefore, the endemic equilibrium is **locally asymptotically stable** whenever it exists. This means that if a disease becomes established ($R_0 > 1$), the system will converge to a steady state where the disease persists in the population.

5. Results and Discussion: A Visual Comparison

In this section, we will demonstrate how the analytical predication of our systems should behave, and show how this behavior looks like, thus, we will bring the theory to life by generating phase portraits for both of our models. We will first visualize each system on its own to confirm our findings, and then place them side by side to draw out the crucial insights that only a direct comparison can reveal.

5.1. Lotka-Volterra Dynamics: Persistent Oscillations

The phase portrait for the Lotka–Volterra model visually confirms the analytical findings. The equilibrium at the origin $(0, 0)$ is a **saddle point**, while the interior equilibrium $\left(\frac{c}{d}, \frac{a}{b}\right)$ is a **center**, characterized by a family of closed periodic orbits. This neutrally stable structure reflects the endless cycle of predator-prey populations in this idealized model, as depicted in Figure 1.

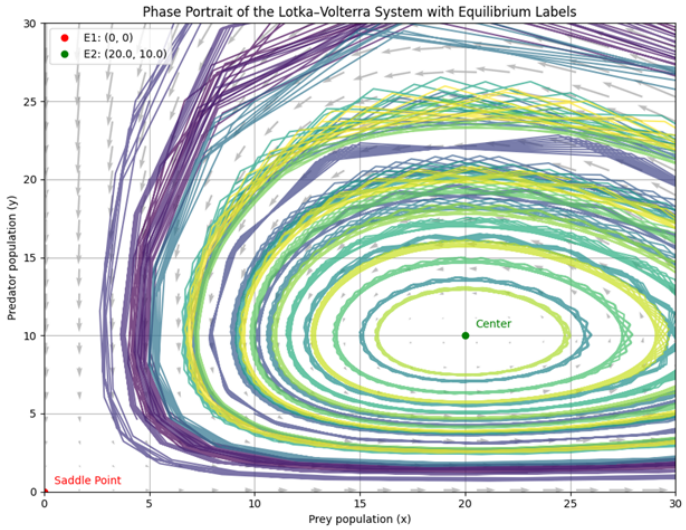

Figure 1: Phase portraits of the Lotka-Volterra predator-prey system

To further investigate the behavior of the system, we examined the sensitivity of the Lotka–Volterra model to variations in the interaction rate parameter b. This parameter directly influences the predator's efficiency in capturing prey. We considered three representative values: $b = 0.2$, 0.5, and 0.8, while keeping $a = 1$, $c = 1.5$, and $d = 0.075$ fixed.

The resulting trajectories reveal that while a higher interaction rate (b) alters the position and shape of the orbits, it does not break the underlying oscillatory dynamics. This sensitivity analysis is illustrated in Figure 2.

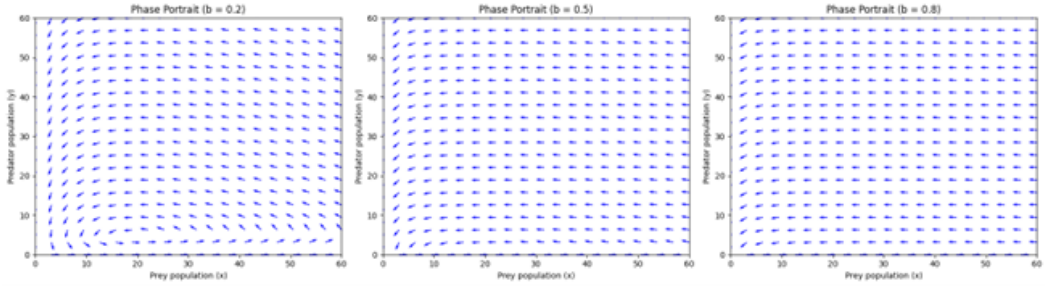

Figure 2: Sensitivity analysis

5.2. Susceptible-Infected-Recovered Dynamics: Threshold Behavior

The SIR epidemic model displays a fundamentally different behavior, governed by the threshold R_0. When $R_0 < 1$, all trajectories converge to the stable disease-free equilibrium $(N, 0)$, indicating that the disease does not spread or die out, as shown in Figure 3.

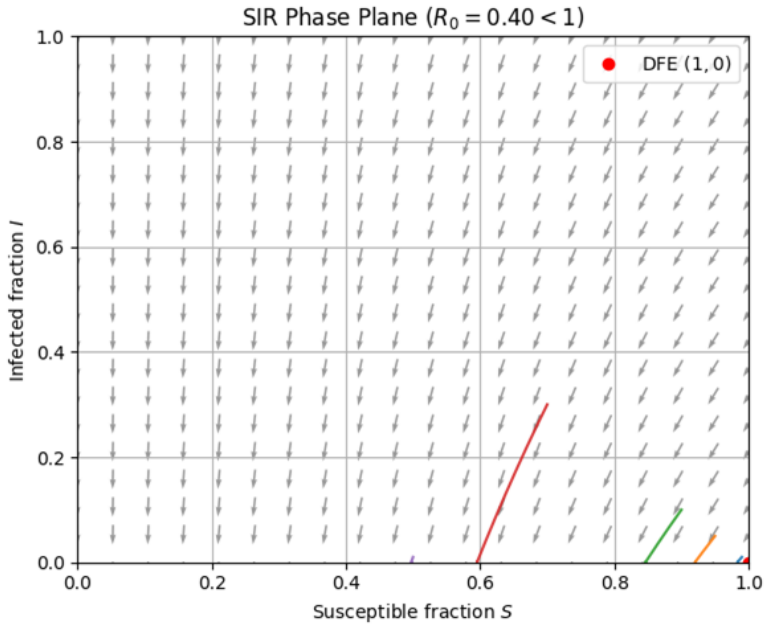

Figure 3: Phase portrait of the SIR model for $R_0 < 1$, showing convergence of all trajectories to the disease-free equilibrium $(N, 0)$.

In stark contrast, when $R_0 > 1$, the DFE becomes unstable. As shown in the phase portrait, trajectories starting near the DFE are initially repelled, leading to an outbreak where the number of infected individuals increases. These trajectories do not grow indefinitely, instead, they spiral towards the stable endemic equilibrium, which was shown to be a stable node or spiral. This shows that the disease will persist in the population at a constant level. As shown in Figure 4.

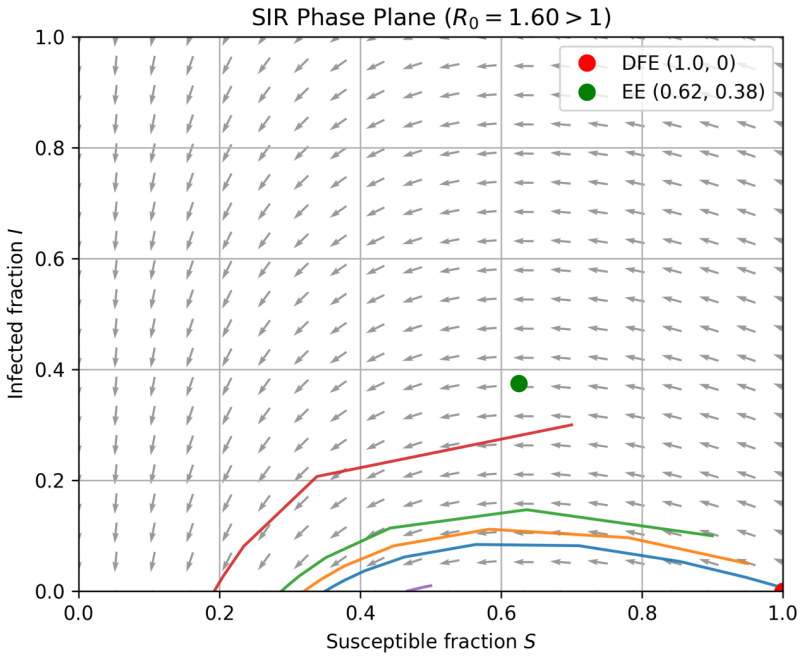

Figure 4: SIR System with $R_0 > 1$.

5.3. Comparative Analysis of Stability

The side-by-side analysis reveals a crucial distinction rooted in the stability of the non-trivial equilibria. In the Lotka–Volterra model, the interior equilibrium is a neutrally stable center, leading to persistent oscillations whose amplitudes depend strongly on initial conditions. This cyclical dynamic reflects the endless predator–prey cycles of the idealized system.

In contrast, the SIR epidemic model demonstrates a qualitatively different form of stability behavior. The Disease-Free Equilibrium (DFE) corresponds to the state $(S, I, R) = (1, 0, 0)$, whose Jacobian matrix yields one zero eigenvalue $\lambda_1 = 0$. The presence of a zero eigenvalue implies that the linear stability analysis is inconclusive in this direction. Formally, confirming the local stability of the DFE when $R_0 < 1$ requires a nonlinear analysis, such as through the *Center Manifold Theorem* or a sufficiently constructed *Lyapunov function*. This observation underscores that, while linearization provides valuable insight, it may not fully capture the dynamical behavior of the system near critical thresholds.

Moreover, when R_0 crosses the critical value $R_0 = 1$, the SIR model undergoes a *transcritical bifurcation*. At this point, the DFE loses stability and an endemic equilibrium emerges, exchanging stability properties with the DFE. This bifurcation marks the fundamental epidemiological transition between disease elimination ($R_0 < 1$) and sustained infection ($R_0 > 1$). Thus, while both models share a common analytical framework, their stability properties highlight profoundly different biological realities—endless oscil-

lations in predator–prey dynamics versus a bifurcation-driven transition and asymptotic convergence in epidemic dynamics.

6. Conclusion

This paper has presented a structured, computational guide to local stability analysis, a cornerstone of nonlinear dynamics. By combining Jacobian-based linearization with phase portrait visualization, we developed a cohesive workflow and applied it to two classical models: the Lotka–Volterra predator–prey system and the SIR epidemic model.

Our analysis of the Lotka–Volterra system demonstrated the emergence of persistent predator–prey oscillations, corresponding to a neutrally stable center. In contrast, complete analysis of the SIR model revealed a critical threshold phenomenon governed by the basic reproduction number R_0. When $R_0 < 1$, the system converges to disease-free equilibrium, whereas for $R_0 > 1$, trajectories approach a stable endemic equilibrium. The direct comparison between the two models proved particularly insightful, showing how subtle differences in nonlinear structure can lead to profoundly different long-term behaviors: persistent oscillations versus convergence to a steady state.

The primary contribution of this work is pedagogical. It offers a clear and reproducible template for students, educators, and practitioners who are new to nonlinear modeling. By bridging abstract theory with computational practice, this guide fosters a deeper and more intuitive understanding of how mathematical tools can be used to explore complex systems in ecology, epidemiology, and beyond.

Future work could extend this guide to include bifurcation analysis, systems exhibiting limit cycles, stochastic effects, or the dynamics of higher–dimensional models. Such extensions would further enrich the study of nonlinear systems and broaden the applicability of this framework to more realistic scenarios.

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