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UTILIZING THE SEIR MATHEMATICAL MODEL FOR ANALYZING AND MITIGATING INFLUENZA SPREAD

JERREY G. LUNGAY*, ROLANDO N. PALUGA

Caraga State University, Main Campus, Ampayon, Butuan City, Philippines

jerrey.lungay@deped.gov.ph

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Abstract. Influenza, a contagious respiratory illness caused by influenza viruses, poses a significant global public health and economic burden. This study develops a deterministic SEIR (Susceptible-Exposed-Infectious-Recovered) model exclusively for influenza to analyze its transmission dynamics, progression, and recovery. By dividing the population into four compartments—susceptible (S), exposed (E_i), infected (I_i), and recovered (R_i)—and incorporating key epidemiological parameters such as transmission, progression, and recovery rates, the model provides a comprehensive mathematical framework represented by a system of nonlinear differential equations. The findings emphasize the SEIR model's critical role in guiding public health interventions, optimizing resource allocation, and informing policy decisions. As a vital tool for global health organizations like the World Health Organization and national health agencies, this model underscores the power of data-driven strategies in managing influenza outbreaks, reducing societal impacts, and saving lives.

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1. Introduction

Influenza, or the flu, is a highly contagious respiratory illness caused by influenza viruses, posing major public health and economic burdens worldwide. It affects all age groups, leading to severe illness, hospitalizations, and deaths [1]. The World Health Organization (WHO) highlights the need for continuous monitoring and research due to its high infection rates and unpredictable transmission [2]. Influenza follows seasonal patterns, with winter epidemics in temperate regions and year-round outbreaks in tropical areas, making its epidemiology crucial for effective prevention and control [3].

Globally, the virus's ability to mutate enables seasonal and pandemic outbreaks, as seen in the 2009 H1N1 pandemic [4]. WHO estimates that annual epidemics cause 3–5 million severe cases and

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290,000–650,000 respiratory deaths worldwide [1]. This highlights the need for ongoing research on epidemiological trends, prevention, and control strategies [5].

In the Philippines, influenza-like illnesses (ILIs) remain a concern due to the country's tropical climate. Seasonal outbreaks are unpredictable, and the Department of Health (DOH) reported 158,307 ILI cases from January to October 2023—a 46% increase from the previous year [6]. Regions such as I, IV-B, XII, Caraga, and the Bangsamoro Autonomous Region saw significant surges, underscoring the need for improved surveillance and localized disease modeling [6].

In the Caraga Region, acute respiratory infections were the leading reported illness in 2020, totaling over 35,600 cases [7]. Fluctuating ILI trends in recent years highlight the importance of studying influenza transmission in the region to develop targeted intervention strategies [8].

Mathematical models, especially the Susceptible-Exposed-Infectious-Recovered (SEIR) framework, have been key in analyzing influenza spread. Studies have used SEIR models to assess vaccination programs [9], zoonotic transmission [10], and population mobility's impact on outbreaks [11]. However, most rely on numerical simulations or focus on specific populations like age groups, animals, or urban areas [12].

This study proposes a novel SEIR deterministic model for influenza transmission dynamics. Unlike previous studies that rely on numerical approaches, this model adopts a deterministic framework to improve the accuracy of outbreak predictions. By refining existing SEIR models, this research aims to enhance public health strategies and policymaking for better disease control. Ultimately, the findings will contribute to a broader understanding of influenza dynamics and mitigation efforts.

2. Preliminary Concepts

Definition 2.1 (**Lipschitz Continuity**) [13] A function $f : \mathbb{R}^n \to \mathbb{R}^n$ is Lipschitz continuous if there exists a constant $L \geq 0$ such that:

$$\|f(x) - f(y)\| \leq L\|x - y\| \quad \text{for all } x, y \in \mathbb{R}^n.$$

Theorem 2.1 (**Cauchy–Lipschitz / Picard–Lindelöf Theorem: Existence and Uniqueness**) [14] Consider the initial value problem:

$$\frac{dy}{dt} = f(t, y), \quad y(t_0) = y_0,$$

where $f : \mathbb{R} \times \mathbb{R}^n \to \mathbb{R}^n$ is continuous and satisfies a Lipschitz condition with respect to y; that is, there exists a constant $L > 0$ such that:

$$\|f(t, y_1) - f(t, y_2)\| \leq L\|y_1 - y_2\| \quad \text{for all } t \in \mathbb{R},\ y_1, y_2 \in \mathbb{R}^n.$$

Theorem 2.2 (**Operations on Continuous Functions**) [13] Let $f, g : \mathbb{R}^n \to \mathbb{R}$ be continuous functions, and let $c \in \mathbb{R}$ be a constant. Then the functions cf, $f + g$, and fg are also continuous.

Definition 2.2 (The Euclidean Norm) [15] Let $u = (u_1, u_2, \ldots, u_n)$ and $v = (v_1, v_2, \ldots, v_n)$. The Euclidean distance between u and v is defined as:

$$\|u - v\| = \sqrt{\sum_{i=1}^{n} (u_i - v_i)^2}.$$

Inequality (A Special Case of the Cauchy–Schwarz Inequality) Let $u = (u_1, u_2, \ldots, u_n)$ and $v = (v_1, v_2, \ldots, v_n)$. Then

$$\sum_{i=1}^{n} |u_i - v_i| \leq \sqrt{n}\|u - v\|.$$

Definition 2.3 (Next Generation Matrix) [16] Let F be the transmission matrix representing the rate of appearance of new infections in each compartment, and let V be the transition matrix representing the rate at which individuals leave the infected compartments. The Next Generation Matrix K is defined as:

$$K = FV^{-1}.$$

Interpretation and Properties of the Next Generation Matrix

- The dominant eigenvalue of K is the basic reproduction number R_0, which represents the average number of secondary infections caused by one infected individual in a fully susceptible population.
- If $R_0 < 1$, the infection will eventually die out.
- If $R_0 > 1$, the infection can spread and potentially lead to an epidemic.

This matrix is widely used in epidemiological modeling to analyze the stability of disease-free equilibrium points and evaluate intervention strategies.

Theorem 2.3 (Routh–Hurwitz Criteria) [17] The Routh–Hurwitz Criteria is a mathematical method used to determine the stability of a linear time-invariant (LTI) system by analyzing the characteristic polynomial of its transfer function. Given a polynomial of the form

$$P(s) = a_0 s^n + a_1 s^{n-1} + \cdots + a_n,$$

where $a_0, a_1, \ldots, a_n \in \mathbb{R}$, the system is stable if and only if all roots of $P(s)$ have negative real parts. In particular:

- For a quadratic polynomial, $P(s) = s^2 + b_1 s + b_2$, the system is stable if and only if $b_1 > 0 \quad \text{and} \quad b_2 > 0.$
- For a cubic polynomial, $P(s) = s^3 + b_1 s^2 + b_2 s + b_3$, the system is stable if and only if $b_1 > 0, \quad b_2 > 0, \quad \text{and} \quad b_1 b_2 > b_3.$

These conditions are both necessary and sufficient for ensuring that all roots of the polynomial lie in the left half of the complex plane.

Theorem 2.4 (**Lyapunov Function**) [18] Consider a dynamical system described by the differential equation:

$$\dot{x} = f(x), \quad x \in \mathbb{R}^n,$$

where $f(x)$ is a continuously differentiable vector field. The equilibrium point x^* of the system is asymptotically stable if there exists a Lyapunov function $V(x)$ that satisfies the following conditions:

- $V(x)$ is continuous, differentiable, and positive definite, i.e.,

$$V(x) > 0 \quad \text{for} \quad x \neq x^*, \quad V(x^*) = 0.$$

- The time derivative of $V(x)$, denoted $\dot{V}(x)$, is negative definite (i.e., $\dot{V}(x) < 0$ for all $x \neq x^*$).

In this case, x^* is an asymptotically stable equilibrium point, meaning that the solutions to the system will approach x^* as time progresses.

Theorem 2.5 (**Integrating Factor Method**) [19] Consider a first-order linear differential equation

$$\frac{dx}{dt} + p(t)x = q(t),$$

where $p(t)$ and $q(t)$ are continuous functions. The solution is given by

$$x(t) = e^{-\int p(t)\,dt} \int e^{\int p(t)\,dt} q(t)\,dt.$$

This is the integrating factor method, where $e^{\int p(t)\,dt}$ is the integrating factor that simplifies the differential equation.

Theorem 2.6 (**LaSalle's Invariance Principle**) [20] Consider the dynamical system

$$\dot{x} = f(x), \quad x \in \mathbb{R}^n,$$

where $f(x)$ is a continuously differentiable vector field, and x^* is an equilibrium point of the system, i.e., $f(x^*) = 0$.

Let $V : \mathbb{R}^n \to \mathbb{R}$ be a continuously differentiable function (a Lyapunov function) that satisfies the following conditions:

- **Positive definiteness**: $V(x) > 0$ for $x \neq x^*$ and $V(x^*) = 0$.
- **Non-increasing derivative**: The time derivative of $V(x)$, denoted by $\dot{V}(x) = \nabla V(x) \cdot f(x)$, satisfies $\dot{V}(x) \leq 0$ for all $x \in \mathbb{R}^n$.

Then, the set

$$M = \{x \in \mathbb{R}^n : \dot{V}(x) = 0\}$$

is invariant, meaning that any trajectory that starts in M remains in M for all future times. Furthermore, if M contains the equilibrium point x^*, then all trajectories that start in M will asymptotically approach the set of equilibrium points in M.

In particular, if M consists only of the equilibrium point x^*, then all trajectories in the state space will converge to x^* as $t \to \infty$.

Definition 2.4 (**Normalized Forward Sensitivity Index** (**NFSI**)) [21] The Normalized Forward Sensitivity Index (NFSI) using the basic reproduction number (commonly denoted R_0) measures how sensitive R_0 is to changes in the model's parameters. It quantifies the relative change in R_0 due to small variations in input parameters, normalized by the value of R_0 itself.

The NFSI for a parameter x is defined as:

$$S_N(x) = \frac{\partial R_0}{\partial x} \cdot \frac{x}{R_0},$$

where:

- $\frac{\partial R_0}{\partial x}$ is the partial derivative of R_0 with respect to the parameter x,
- x is the model parameter under consideration,
- R_0 is the basic reproduction number.

This index helps evaluate the impact of changes in different model parameters (e.g., transmission rate, recovery rate) on the overall transmission potential of a disease, while accounting for the scale of R_0.

Lemma 2.1 (**Positivity of Solutions of ODE Systems**) [13] Let $u(t) = (u_1(t), u_2(t), \ldots, u_n(t))$ be the solution to a system of ordinary differential equations (ODEs) defined on a domain $D \subseteq \mathbb{R}^n$, and suppose that the initial conditions satisfy $u(0) \in \mathbb{R}^n_+$. If the vector field defining the system satisfies

$$f_i(u) \geq 0 \quad \text{whenever } u_i = 0 \text{ and } u \in \mathbb{R}^n_+,$$

then the solution $u(t)$ remains in $\mathbb{R}^n_+$ for all $t \geq 0$; that is, the non-negative orthant is positively invariant.

3. Model Formulation

This study builds upon the numerical models presented in [22], [23], [24]. Consistent with previous studies on the mathematical modeling of influenza [25], [26], [27], [28], we develop an SEIR deterministic model specifically for influenza dynamics. To construct this mathematical model, the human population is divided into four (4) mutually exclusive compartments, representing individuals' health statuses concerning influenza:

- **Susceptible individuals,** S: People who are predisposed or vulnerable to infection with influenza.
- **Exposed individuals with influenza,** E_i: People who have been exposed to influenza and can still transmit the disease.
- **Infected individuals with influenza,** I_i: People who are infectious or symptomatic with influenza and capable of transmitting the disease.

- **Recovered individuals from influenza infection,** R_i: People who have recovered from influenza, with immunity against future infection.

Hence, the total human population N at time t is given by:

$$N_i(t) = S(t) + E_i(t) + I_i(t) + R_i(t).$$

The parameters and their descriptions, commonly used in the formulation of the influenza model, are presented in Table 1. It is important to note that the formulation of the influenza model assumes that all parameters are positive constants.

Parameter	Description
ω	Recruitment rate of susceptible individuals into the population
β_i	Transmission rate of influenza
σ_i	Progression rate from E_i class to I_i class
γ_i	Recovery rate from influenza
μ	Natural mortality rate

TABLE 1. Description of the Model Parameters

Figure 1 presents a schematic diagram that illustrates the transmissions between compartments, as individuals move between states of susceptibility, exposure, infection, and recovery, based on the biological progression of influenza [29].

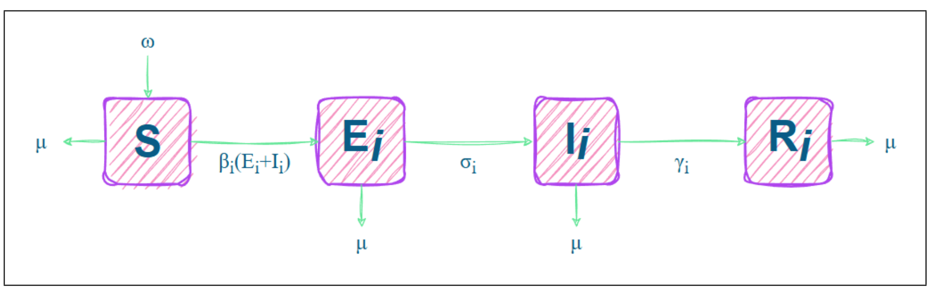

FIGURE 1. Schematic diagram of the compartmental influenza infection model

In formulating the influenza model, the parameter ω represents the inflow (or recruitment) rate into the susceptible compartment S. Susceptible individuals are exposed to influenza at a rate $\beta_i(E_i + I_i)$, transitioning into the exposed compartment E_i. Exposed individuals with influenza have a tendency to become infected with influenza at a rate σ_i, moving into the infected compartment I_i. Influenza-infected individuals recover from the disease at a rate γ_i, subsequently transitioning to the influenza-recovered compartment R_i. It is important to note that all individuals in each compartment experience natural death at a rate μ.

From the above description and the flow chart shown in Figure 1, the following system of non-linear differential equations for the influenza infection model is derived:

$$\begin{aligned} \frac{dS}{dt} &= \omega - \beta_i(E_i + I_i)S - \mu S, \\ \frac{dE_i}{dt} &= \beta_i(E_i + I_i)S - (\sigma_i + \mu)E_i, \\ \frac{dI_i}{dt} &= \sigma_i E_i - (\gamma_i + \mu)I_i, \\ \frac{dR_i}{dt} &= \gamma_i I_i - \mu R_i. \end{aligned} \tag{3.1}$$

The system (3.1) satisfies the following conditions:

$$S(t), E_i(t), I_i(t), R_i(t) \geq 0.$$

4. Positivity and Boundedness of the Solutions

Consider the system of ordinary differential equations given in (3.1),

$$\frac{du_i}{dt} = f_i(u,t), \quad i = 1,2,3,4$$

where the variables are defined as:

$$u_1 = S, \quad u_2 = E_i, \quad u_3 = I_i, \quad u_4 = R_i.$$

Then we have the following system of ordinary differential equations:

$$u' = \begin{pmatrix} \omega - \beta_i(u_2 + u_3)u_1 - \mu u_1 \\ \beta_i(u_2 + u_3)u_1 - (\sigma_i + \mu)u_2 \\ \sigma_i u_2 - (\gamma_i + \mu)u_3 \\ \gamma_i u_3 - \mu u_4 \end{pmatrix} \tag{4.1}$$

Theorem 4.1 *The solution of the influenza infection model given in* (4.1) *is non-negative, unique, and bounded in the given feasible region:*

$$\Omega = \{(u_1, u_2, u_3, u_4) \in \mathbb{R}^4_+ : u_1 + u_2 + u_3 + u_4 \leq \frac{\omega}{\mu}\}.$$

Proof: To show the non-negativity of the solutions, assume $u = (u_1, u_2, u_3, u_4) \in [0, \infty)^4$ and $u_i = 0$ for some $i = 1,2,3,4$. Suppose that at some $t = t_*$, one of the state variables first becomes zero. Without loss of generality, consider the following cases:

If $u_1(t_*) = 0$, then (by Lemma 2.1)

$$\begin{aligned} u_1'(t_*) &= \omega - \beta_i(u_2(t_*) + u_3(t_*))u_1(t_*) - \mu u_1(t_*) \\ &= \omega - \beta_i(u_2(t_*) + u_3(t_*))(0) - \mu(0) \\ &= \omega \end{aligned}$$

Since $\omega > 0$, it follows that $u_2(t_*), u_3(t_*) \geq 0$, and $u_1'(t_*) > 0$. Thus, $u_1(t) \geq 0$ for all t.

If $u_2(t_*) = 0$, then (by Lemma 2.1)

$$\begin{aligned} u_2'(t_*) &= \beta_i(u_2(t_*) + u_3(t_*))u_1(t_*) - (\sigma_i + \mu)u_2(t_*) \\ &= \beta_i((0) + u_3(t_*))u_1(t_*) - (\sigma_i + \mu)(0) \\ &= \beta_i(u_3(t_*))u_1(t_*) \end{aligned}$$

Since $\beta_i > 0$, and $u_1(t_*), u_3(t_*) \geq 0$, we have $u_2'(t_*) \geq 0$. Thus, $u_2(t) \geq 0$ for all t.

If $u_3(t_*) = 0$, then (by Lemma 2.1)

$$\begin{aligned} u_3'(t_*) &= \sigma_i u_2(t_*) - (\gamma_i + \mu)u_3(t_*) \\ &= \sigma_i u_2(t_*) - (\gamma_i + \mu)(0) \\ &= \sigma_i u_2(t_*) \end{aligned}$$

Since $\sigma_i > 0$ and $u_2(t_*) \geq 0$, it follows that $u_3'(t_*) \geq 0$. Thus, $u_3(t) \geq 0$ for all t.

If $u_4(t_*) = 0$, then (by Lemma 2.1)

$$\begin{aligned} u_4'(t_*) &= \gamma_i u_3(t_*) - \mu u_4(t_*) \\ &= \gamma_i u_3(t_*) - \mu(0) \\ &= \gamma_i u_3(t_*) \end{aligned}$$

Since $\gamma_i > 0$ and $u_3(t_*) \geq 0$, it follows that $u_4'(t_*) \geq 0$. Thus, $u_4(t) \geq 0$ for all t.

Since all state variables remain non-negative for all t, we conclude that the solution of the influenza infection model is non-negative for all $t \geq 0$.

To show boundedness, summing all equations in (4.1) gives the total population rate of change:

$$\frac{dN}{dt} \leq \omega - \mu N.$$

This implies that

$$\frac{dN}{dt} + \mu N \leq \omega.$$

Multiplying both sides by the integrating factor $e^{\int \mu dt} = e^{\mu t}$, we have

$$\begin{aligned} e^{\mu t}\frac{dN}{dt} + e^{\mu t}\mu N &\leq \omega e^{\mu t} \\ \frac{d}{dt}(e^{\mu t}N) &\leq \omega e^{\mu t}. \end{aligned}$$

Integrating both sides, we get

$$e^{\mu t}N \leq \frac{\omega}{\mu}e^{\mu t} + C_0,$$

where C_0 is a constant.

$$N \leq \frac{\omega}{\mu} + C_0 e^{-\mu t}.$$

Taking the initial condition, that is, when $t = 0$, $N(0) = \frac{\omega}{\mu} + C_0$. Thus,

$$N(t) \leq \frac{\omega}{\mu} + \left(N(0) - \frac{\omega}{\mu}\right) e^{-\mu t}$$

In effect,

$$\lim_{t\to\infty} \sup N(t) \leq \frac{\omega}{\mu} \quad \text{as } t \to \infty.$$

Hence, the solution remains bounded within the feasible region.

On the other hand, consider the function $f : \mathbb{R}^4 \times \mathbb{R} \to \mathbb{R}^4$ defined by a vector of components:

$$\frac{du_i}{dt} = f_i(u,t) = \begin{bmatrix} f_1(u,t) \\ f_2(u,t) \\ f_3(u,t) \\ f_4(u,t) \end{bmatrix},$$

where each component $f_i(u, t)$ corresponds to a differential equation describing the rate of change of each variable u_i in the system, based on the given system of ordinary differential equations. The components $f_i(u, t)$ are defined as follows:

$$\begin{aligned} f_1(u,t) &= \omega - \beta_i(u_2 + u_3)u_1 - \mu u_1, \\ f_2(u,t) &= \beta_i(u_2 + u_3)u_1 - (\sigma_i + \mu)u_2, \\ f_3(u,t) &= \sigma_i u_2 - (\gamma_i + \mu)u_3, \\ f_4(u,t) &= \gamma_i u_3 - \mu u_4. \end{aligned}$$

Each $f_i(u, t)$ is defined using the variables u_1, u_2, u_3, u_4 along with constants such as $\omega, \beta_i, \sigma_i, \gamma_i$, and μ. Since these parameters are constants, we will focus on the expressions involving the u_i terms. Thus, here's the structure of each component.

Consider the first compartment:

$$f_1(u,t) = \omega - \beta_i(u_2 + u_3)u_1 - \mu u_1.$$

This component consists of terms ω, $-\beta_i(u_2 + u_3)u_1$, and μu_1 involving u_i terms and constants. Each term in $f_1(u, t)$ is a sum or product of continuous functions, which are continuous by basic properties of functions. Therefore, based on Theorem 2.2, $f_1(u, t)$ is continuous.

The second compartment is given by:

$$f_2(u,t) = \beta_i(u_2 + u_3)u_1 - (\sigma_i + \mu)u_2.$$

This component includes terms such as $\beta_i(u_2+u_3)u_1$ and $-(\sigma_i+\mu)u_2$. Each term here is a product or sum involving continuous variables and constants, based on Theorem 2.2 ensuring that $f_2(u,t)$ is continuous.

The third compartment is given by:

$$f_3(u,t) = \sigma_i u_2 - (\gamma_i+\mu)u_3.$$

This component consists of terms such as $\sigma_i u_2$ and $-(\gamma_i+\mu)u_3$, each of which is a product of a constant with a continuous variable. Therefore, based on Theorem 2.2, $f_3(u,t)$ is continuous.

The fourth compartment is given by:

$$f_4(u,t) = \gamma_i u_3 - \mu u_4.$$

This component has terms like $\gamma_i u_3$ and $-\mu u_4$. Since each term is a product or sum of continuous functions, based on Theorem 2.2, $f_4(u,t)$ is continuous.

Since each component $f_i(u,t)$ (for $i=1,2,3,4$) consists of sums and products of continuous functions, each f_i is continuous. Therefore, the entire function $f:\mathbb{R}^4\times\mathbb{R}\to\mathbb{R}^4$ is continuous.

Now, to show Lipschitz continuity of the solutions for each compartment in the system, we need to show that the difference between two solutions, say $u=(u_1,u_2,u_3,u_4)$ and $v=(v_1,v_2,v_3,v_4)$, is bounded by a constant times the norm of the difference between the state vectors $u-v$. Thus, we will compute the differences between the functions for each compartment and show that they satisfy this condition.

The first compartment is given by:

$$f_1(u,t) = \omega - \beta_i(u_2+u_3)u_1 - \mu u_1.$$

Then,

$$\begin{aligned}
|f_1(u,t)-f_1(v,t)| &= |(\omega-\beta_i(u_2+u_3)u_1-\mu u_1)-(\omega-\beta_i(v_2+v_3)v_1-\mu v_1)|.\\
&= |\omega-\omega-\beta_i\left((u_2+u_3)u_1-(v_2+v_3)v_1\right)-\mu(u_1-v_1)|.\\
&\le \beta_i|(u_2+u_3)u_1-(v_2+v_3)v_1|+\mu|u_1-v_1|.\\
&= \beta_i|u_1u_2+u_1u_3-v_1v_2-v_1v_3|+\mu|u_1-v_1|.\\
&= \beta_i|u_1u_2-v_1v_2+u_1u_3-v_1v_3|+\mu|u_1-v_1|.\\
&= \beta_i|u_1u_2-u_1v_2+u_1v_2-v_1v_2+u_1u_3-u_1v_3+u_1v_3-v_1v_3|+\mu|u_1-v_1|.\\
&= \beta_i|u_1(u_2-v_2)+v_2(u_1-v_1)+u_1(u_3-v_3)+v_3(u_1-v_1)|+\mu|u_1-v_1|.\\
&\le \beta_i\left[u_1|u_2-v_2|+v_2|u_1-v_1|+u_1|u_3-v_3|+v_3|u_1-v_1|\right]+\mu|u_1-v_1|.\\
&\le \beta_i\left[\frac{\omega}{\mu}|u_2-v_2|+\frac{\omega}{\mu}|u_1-v_1|+\frac{\omega}{\mu}|u_3-v_3|+\frac{\omega}{\mu}|u_1-v_1|\right]+\mu|u_1-v_1|.
\end{aligned}$$

$$\leq \left(\frac{2\beta_i\omega}{\mu} + \mu\right)|u_1 - v_1| + \frac{\beta_i\omega}{\mu}|u_2 - v_2| + \frac{\beta_i\omega}{\mu}|u_3 - v_3|.$$

Let $a_1 = \frac{2\beta_i\omega}{\mu} + \mu$. Then,

$$\begin{aligned}
|f_1(u,t) - f_1(v,t)| &\leq a_1|u_1 - v_1| + a_1|u_2 - v_2| + a_1|u_3 - v_3|. \\
&\leq a_1(|u_1 - v_1| + |u_2 - v_2| + |u_3 - v_3|). \\
&\leq a_1\left(\sum_{i=1}^{4}|u_i - v_i|\right). && \text{(by Cauchy-Schwarz Inequality)} \\
&\leq a_1\sqrt{4}\|u - v\|. && \text{(by Cauchy-Schwarz Inequality)} \\
&\leq 2a_1\|u - v\|.
\end{aligned}$$

Let $L_1 = 2a_1$. Then,

$$|f_1(u,t) - f_1(v,t)| \leq L_1\|u - v\|.$$

The second compartment is given by:

$$f_2(u,t) = \beta_i(u_2 + u_3)u_1 - (\sigma_i + \mu)u_2.$$

Then,

$$\begin{aligned}
|f_2(u,t) - f_2(v,t)| &= \left|(\beta_i(u_2 + u_3)u_1 - (\sigma_i + \mu)u_2) - (\beta_i(v_2 + v_3)v_1 - (\sigma_i + \mu)v_2)\right|. \\
&= |\beta_i((u_2 + u_3)u_1 - (v_2 + v_3)v_1) - (\sigma_i + \mu)(u_2 - v_2)|. \\
&\leq \beta_i|(u_2 + u_3)u_1 - (v_2 + v_3)v_1| + (\sigma_i + \mu)|u_2 - v_2|. \\
&= \beta_i|u_1u_2 + u_1u_3 - v_1v_2 - v_1v_3| + (\sigma_i + \mu)|u_2 - v_2|. \\
&= \beta_i|u_1u_2 - v_1v_2 + u_1u_3 - v_1v_3| + (\sigma_i + \mu)|u_2 - v_2|. \\
&= \beta_i|u_1u_2 - u_1v_2 + u_1v_2 - v_1v_2 + u_1u_3 - u_1v_3 + u_1v_3 - v_1v_3| + (\sigma_i + \mu)|u_2 - v_2|. \\
&= \beta_i|u_1(u_2 - v_2) + v_2(u_1 - v_1) + u_1(u_3 - v_3) + v_3(u_1 - v_1)| + (\sigma_i + \mu)|u_2 - v_2|. \\
&\leq \beta_i[u_1|(u_2 - v_2)| + v_2|(u_1 - v_1)| + u_1|(u_3 - v_3)| + v_3|(u_1 - v_1)|] + (\sigma_i + \mu)|u_2 - v_2|. \\
&\leq \beta_i\left[\frac{\omega}{\mu}|u_2 - v_2| + \frac{\omega}{\mu}|u_1 - v_1| + \frac{\omega}{\mu}|u_3 - v_3| + \frac{\omega}{\mu}|u_1 - v_1|\right] + (\sigma_i + \mu)|u_2 - v_2|. \\
&\leq \frac{2\beta_i\omega}{\mu}|u_1 - v_1| + \left(\frac{\beta_i\omega}{\mu} + \sigma_i + \mu\right)|u_2 - v_2| + \frac{\beta_i\omega}{\mu}|u_3 - v_3|.
\end{aligned}$$

Defining the Lipschitz constant, $a_2 = \max\left\{\frac{2\beta_i\omega}{\mu}, \sigma_i + \mu\right\}$. Now,

$$\begin{aligned}
|f_2(u,t) - f_2(v,t)| &\leq a_2|u_1 - v_1| + a_2|u_2 - v_2| + a_2|u_3 - v_3|. \\
&\leq a_2(|u_1 - v_1| + |u_2 - v_2| + |u_3 - v_3|).
\end{aligned}$$

$$
\begin{aligned}
&\leq a_2 \left(\sum_{i=1}^{4} |u_i - v_i| \right). && \text{(by Cauchy-Schwarz Inequality)} \\
&\leq a_2 \sqrt{4} \|u - v\|. && \text{(by Cauchy-Schwarz Inequality)} \\
&\leq 2a_2 \|u - v\|.
\end{aligned}
$$

Let $L_2 = 2a_2$. Then,

$$|f_2(u,t) - f_2(v,t)| \leq L_2 \|u - v\|.$$

The third compartment is given by:

$$f_3(u,t) = \sigma_i u_2 - (\gamma_i + \mu) u_3.$$

Then,

$$
\begin{aligned}
|f_3(u,t) - f_3(v,t)| &= \left| (\sigma_i u_2 - (\gamma_i + \mu) u_3) - (\sigma_i v_2 - (\gamma_i + \mu) v_3) \right|. \\
&= |\sigma_i (u_2 - v_2) - (\gamma_i + \mu)(u_3 - v_3)|. \\
&\leq \sigma_i |u_2 - v_2| + (\gamma_i + \mu) |u_3 - v_3|.
\end{aligned}
$$

Defining the Lipschitz constant, $a_3 = \max\{\sigma_i, \gamma_i + \mu\}$. Now,

$$
\begin{aligned}
|f_3(u,t) - f_3(v,t)| &\leq a_3 |u_2 - v_2| + a_3 |u_3 - v_3|. \\
&\leq a_3 (|u_2 - v_2| + |u_3 - v_3|). \\
&\leq a_3 \left(\sum_{i=1}^{4} |u_i - v_i| \right). && \text{(by Cauchy-Schwarz Inequality)} \\
&\leq a_3 \sqrt{4} \|u - v\|. && \text{(by Cauchy-Schwarz Inequality)} \\
&\leq 2a_3 \|u - v\|.
\end{aligned}
$$

Let $L_3 = 2a_3$. Then,

$$|f_3(u,t) - f_3(v,t)| \leq L_3 \|u - v\|.$$

The fourth compartment is given by:

$$f_4(u,t) = \gamma_i u_3 - \mu u_4.$$

Then,

$$
\begin{aligned}
|f_4(u,t) - f_4(v,t)| &= \left| (\gamma_i u_3 - \mu u_4) - (\gamma_i v_3 - \mu v_4) \right|. \\
&= |\gamma_i (u_3 - v_3) - \mu (u_4 - v_4)|. \\
&\leq \gamma_i |u_3 - v_3| + \mu |u_4 - v_4|.
\end{aligned}
$$

Defining the Lipschitz constant, $a_4 = \max\{\gamma_i, \mu\}$. Now,

$$
\begin{aligned}
|f_4(u,t) - f_4(v,t)| &\leq a_4|u_3 - v_3| + a_4|u_4 - v_4|. \\
&\leq a_4(|u_3 - v_3| + |u_4 - v_4|). \\
&\leq a_4\left(\sum_{i=1}^{4}|u_i - v_i|\right). && \text{(by Cauchy-Schwarz Inequality)} \\
&\leq a_4\sqrt{4}\|u - v\|. && \text{(by Cauchy-Schwarz Inequality)} \\
&\leq 2a_4\|u - v\|.
\end{aligned}
$$

Let $L_4 = 2a_4$. Then,

$$|f_4(u,t) - f_4(v,t)| \leq L_4\|u - v\|.$$

Define $L^* = \max\{L_1, L_2, L_3, L_4\}$, and set $L = 4L^*$. Then,

$$
\begin{aligned}
\|f(u,t) - f(v,t)\| &\leq L_1\|u - v\| + L_2\|u - v\| + L_3\|u - v\| + L_4\|u - v\|. \\
&\leq L^*\|u - v\| + L^*\|u - v\| + L^*\|u - v\| + L^*\|u - v\|. \\
&= 4L^*(\|u - v\|). \\
&= L\|u - v\|.
\end{aligned}
$$

Since $N(t)$ is continuous and satisfies the Lipschitz condition, the existence and uniqueness theorem (Picard-Lindelöf theorem) guarantees that the system of differential equations has a unique solution for any given initial condition. This establishes the uniqueness of solutions to the given system of ordinary differential equations.

Therefore, the solution of the system exists, is non-negative, unique, and bounded in a feasible region Ω, which concludes the proof. □

5. The Equilibrium Points and Basic Reproduction Number

Understanding the equilibrium points in epidemiological models is essential for predicting disease dynamics and implementing effective control measures. The equilibrium points—specifically, the disease-free and endemic equilibrium points—help determine the conditions under which a disease may either die out or persist in a population. By computing these equilibrium states, researchers and public health officials can assess the stability of disease outbreaks, estimate the impact of interventions, and design strategies for disease eradication or containment. The disease-free equilibrium represents a scenario where the infection is eliminated, while the endemic equilibrium describes a steady-state where the disease remains present in the population at a constant level. Analyzing these points provides valuable insights into the transmission and control of infectious diseases like influenza. For example, in the SIR model with vital dynamics, the disease-free equilibrium occurs when no infection remains, determined by the basic reproduction number R_0. If $R_0 \leq 1$, the disease dies out; if $R_0 > 1$, it persists at an endemic equilibrium [30].

In this section, we will demonstrate the existence of the equilibrium points and compute the basic reproduction number for the influenza model (3.1). Equilibrium points are values of the state variables where their rates of change are 0 over time t. Thus, we set:

$$\frac{dS}{dt} = \frac{dE_i}{dt} = \frac{dI_i}{dt} = \frac{dR_i}{dt} = 0.$$

Theorem 5.1 *The system* (3.3) *has two equilibrium points, the disease-free equilibrium point*

$$\varepsilon_{0_i} = \left(\frac{\omega}{\mu}, 0, 0, 0\right)$$

and the endemic equilibrium point

$$\varepsilon_{1_i} = (S^*, E_i^*, I_i^*, R_i^*),$$

where

$$\begin{aligned}
S^* &= \frac{(\gamma_i + \mu)(\sigma_i + \mu)}{\beta_i(\gamma_i + \mu + \sigma_i)}, \\
E_i^* &= \frac{\omega - \mu\left(\frac{(\gamma_i+\mu)(\sigma_i+\mu)}{\beta_i(\gamma_i+\mu+\sigma_i)}\right)}{\sigma_i + \mu}, \\
I_i^* &= \frac{\sigma_i\omega\beta_i(\gamma_i + \mu + \sigma_i) - \sigma_i\mu(\gamma_i + \mu)(\sigma_i + \mu)}{\beta_i(\sigma_i + \mu)(\gamma_i + \mu + \sigma_i)(\gamma_i + \mu)}, \\
R_i^* &= \frac{\gamma_i\sigma_i\omega\beta_i(\gamma_i + \mu + \sigma_i) - \gamma_i\sigma_i\mu(\gamma_i + \mu)(\sigma_i + \mu)}{\mu\beta_i(\sigma_i + \mu)(\gamma_i + \mu + \sigma_i)(\gamma_i + \mu)}.
\end{aligned}$$

Proof: To solve the equilibrium points, we need to set the equations in system (3.1) to 0, that is:

$$\omega - \beta_i(E_i + I_i)S - \mu S = 0, \tag{5.1}$$

$$\beta_i(E_i + I_i)S - (\sigma_i + \mu)E_i = 0, \tag{5.2}$$

$$\sigma_i E_i - (\gamma_i + \mu)I_i = 0, \tag{5.3}$$

$$\gamma_i I_i - \mu R_i = 0. \tag{5.4}$$

From equation (5.3), we have:

$$I_i\left(\frac{\sigma_i E_i}{I_i} - (\gamma_i + \mu)\right) = 0.$$

This yields two cases: $I_i = 0$ or $\frac{\sigma_i E_i}{I_i} - (\gamma_i + \mu) = 0$.

Case 1: If $I_i = 0$, then from equation (5.3), $E_i = 0$. Since $E_i = 0$ and $I_i = 0$, from equation (5.4), $R_i = 0$. From equation (5.1),

$$S = \frac{\omega}{\mu}.$$

This means that the environment is disease-free from influenza. Hence, the disease-free equilibrium point of system (3.1) is

$$\varepsilon_{0_i} = (S, E_i, I_i, R_i) = \left(\frac{\omega}{\mu}, 0, 0, 0\right).$$

Case 2: If $I_i \neq 0$, then $I_i = \frac{\sigma_i E_i}{\gamma_i + \mu}$. Adding equations (5.1) and (5.2), and equations (5.2) and (5.3), we derive:

$$\omega - \mu S - (\sigma_i + \mu)E_i = 0, \tag{5.5}$$

$$\beta_i(E_i + I_i)S - \mu E_i - (\gamma_i + \mu)I_i = 0. \tag{5.6}$$

From equation (5.5), we get:

$$E_i = \frac{\omega - \mu S}{\sigma_i + \mu}. \tag{5.7}$$

So,

$$I_i = \frac{\sigma_i E_i}{\gamma_i + \mu} = \frac{\sigma_i \left(\frac{\omega - \mu S}{\sigma_i + \mu}\right)}{\gamma_i + \mu} = \frac{\sigma_i(\omega - \mu S)}{(\gamma_i + \mu)(\sigma_i + \mu)}.$$

By substituting the values of E_i and I_i into equation (5.6), we obtain

$$\beta_i \left(\frac{(\omega - \mu S)(\gamma_i + \mu) + \sigma_i(\omega - \mu S)}{(\gamma_i + \mu)(\sigma_i + \mu)}\right) S - \mu \frac{(\omega - \mu S)}{(\sigma_i + \mu)} - \frac{\sigma_i(\omega - \mu S)}{(\sigma_i + \mu)} = 0.$$

$$\beta_i S(\omega - \mu S) \left(\frac{(\gamma_i + \mu) + \sigma_i}{(\gamma_i + \mu)(\sigma_i + \mu)}\right) - \frac{(\mu(\omega - \mu S) + \sigma_i(\omega - \mu S))}{(\sigma_i + \mu)} = 0.$$

$$\beta_i S(\omega - \mu S) \left(\frac{(\gamma_i + \mu) + \sigma_i}{(\gamma_i + \mu)(\sigma_i + \mu)}\right) = (\omega - \mu S) \left(\frac{\mu + \sigma_i}{\sigma_i + \mu}\right).$$

$$\beta_i S \left(\frac{(\gamma_i + \mu) + \sigma_i}{(\gamma_i + \mu)(\sigma_i + \mu)}\right) = 1.$$

$$S = \frac{(\gamma_i + \mu)(\sigma_i + \mu)}{\beta_i(\gamma_i + \mu + \sigma_i)}.$$

By equation (5.7), we get

$$\begin{aligned} E_i &= \frac{\omega - \mu \left(\frac{(\gamma_i + \mu)(\sigma_i + \mu)}{\beta_i(\gamma_i + \mu + \sigma_i)}\right)}{\sigma_i + \mu} \\ &= \frac{\omega \beta_i(\gamma_i + \mu + \sigma_i) - \mu(\gamma_i + \mu)(\sigma_i + \mu)}{\beta_i(\sigma_i + \mu)(\gamma_i + \mu + \sigma_i)} \end{aligned}$$

Then,

$$I_i = \frac{\sigma_i \omega \beta_i(\gamma_i + \mu + \sigma_i) - \sigma_i \mu(\gamma_i + \mu)(\sigma_i + \mu)}{\beta_i(\sigma_i + \mu)(\gamma_i + \mu + \sigma_i)(\gamma_i + \mu)}$$

By equation (5.4),

$$R_i = \frac{\gamma_i \sigma_i \omega \beta_i(\gamma_i + \mu + \sigma_i) - \gamma_i \sigma_i \mu(\gamma_i + \mu)(\sigma_i + \mu)}{\mu \beta_i(\sigma_i + \mu)(\gamma_i + \mu + \sigma_i)(\gamma_i + \mu)}$$

Thus, the endemic equilibrium point (3.1) is

$$\varepsilon_{1_i} = (S, E_i, I_i, R_i),$$

where

$$S = \frac{(\gamma_i + \mu)(\sigma_i + \mu)}{\beta_i(\gamma_i + \mu + \sigma_i)},$$

the number of individuals still at risk of infection, determined by transmission, recovery, and natural death rates.

$$E_i = \frac{\omega - \mu\left(\frac{(\gamma_i+\mu)(\sigma_i+\mu)}{\beta_i(\gamma_i+\mu+\sigma_i)}\right)}{\sigma_i + \mu},$$

the number of individuals infected but not yet infectious, influenced by recruitment, natural death, and progression rates.

$$I_i = \frac{\sigma_i\omega\beta_i(\gamma_i + \mu + \sigma_i) - \sigma_i\mu(\gamma_i + \mu)(\sigma_i + \mu)}{\beta_i(\sigma_i + \mu)(\gamma_i + \mu + \sigma_i)(\gamma_i + \mu)},$$

the actively infected individuals spreading the disease, showing the extent of disease transmission.

$$R_i = \frac{\gamma_i\sigma_i\omega\beta_i(\gamma_i + \mu + \sigma_i) - \gamma_i\sigma_i\mu(\gamma_i + \mu)(\sigma_i + \mu)}{\mu\beta_i(\sigma_i + \mu)(\gamma_i + \mu + \sigma_i)(\gamma_i + \mu)},$$

individuals who have recovered and gained immunity, indicating the level of protection in the population.

This completes the proof for the existence of the equilibrium points for the influenza model (3.1). □

The basic reproduction number R_0 is a fundamental metric in infectious disease modeling, providing a clear threshold for determining whether an outbreak will spread or eventually die out. Unlike other analytical methods, such as stochastic modeling or network-based approaches, R_0 directly quantifies disease transmissibility and serves as the foundation for public health interventions, including vaccination, quarantine, and social distancing. Its simplicity and predictive capability make it a more essential tool in epidemic control, allowing researchers and policymakers to assess the potential impact of an infectious disease and design effective mitigation strategies. The following theorem establishes the R_0 for the influenza model (3.1).

Theorem 5.2. *The basic reproduction number of the influenza model (3.1) is captured by*

$$R_{0_i} = \frac{\beta_i\omega}{(\sigma_i + \mu)\mu} + \frac{\beta_i\omega\sigma_i}{(\sigma_i + \mu)(\gamma_i + \mu)\mu}.$$

Proof: The basic reproduction number is a mathematical notion used to quantify and describe the transmission dynamics of infectious diseases. It is calculated using the Next Generation Matrix approach [16]. To perform the next generation matrix, we need to determine the infected compartments.

Now suppose x_c be the vector of the infected states [31]. In system (3.1), the vector x_c is given by

$$x_c = \begin{pmatrix} E_i \\ I_i \end{pmatrix}.$$

By taking the first derivative of x_c, we have

$$x_c' = \begin{pmatrix} E_i' \\ I_i' \end{pmatrix} = \begin{pmatrix} \beta_i(E_i + I_i)S - (\sigma_i + \mu)E_i \\ \sigma_i E_i - (\gamma_i + \mu)I_i \end{pmatrix}.$$

Thus, x_c' can be written as

$$x_c' = \begin{pmatrix} \beta_i(E_i + I_i)S - (\sigma_i + \mu)E_i \\ \sigma_i E_i - (\gamma_i + \mu)I_i \end{pmatrix} = F - V,$$

where F refers to the transmission matrix and V refers to the transitional matrix.

Accordingly,

$$F = \begin{pmatrix} \beta_i(E_i + I_i)S \\ 0 \end{pmatrix},$$

and

$$V = \begin{pmatrix} (\sigma_i + \mu)E_i \\ -\sigma_i E_i + (\gamma_i + \mu)I_i \end{pmatrix}.$$

Solving the Jacobian of F and V evaluated at the disease-free equilibrium point $E_{0_i} = \left(\frac{\omega}{\mu}, 0, 0, 0\right)$, we get

$$F = \frac{\partial F}{\partial x}\bigg|_{E_{0_i}} = \begin{pmatrix} \beta_i S & \beta_i S \\ 0 & 0 \end{pmatrix}_{E_{0_i}} = \begin{pmatrix} \frac{\beta_i \omega}{\mu} & \frac{\beta_i \omega}{\mu} \\ 0 & 0 \end{pmatrix}.$$

$$V = \frac{\partial V}{\partial x}\bigg|_{E_{0_i}} = \begin{pmatrix} \sigma_i + \mu & 0 \\ -\sigma_i & \gamma_i + \mu \end{pmatrix}.$$

where

$$V^{-1} = \begin{pmatrix} \frac{1}{\sigma_i+\mu} & 0 \\ \frac{\sigma_i}{(\sigma_i+\mu)(\gamma_i+\mu)} & \frac{1}{\gamma_i+\mu} \end{pmatrix}.$$

Now, the next-generation matrix is given by

$$FV^{-1} = \begin{pmatrix} \frac{\beta_i \omega}{\mu} & \frac{\beta_i \omega}{\mu} \\ 0 & 0 \end{pmatrix} \begin{pmatrix} \frac{1}{\sigma_i+\mu} & 0 \\ \frac{\sigma_i}{(\sigma_i+\mu)(\gamma_i+\mu)} & \frac{1}{\gamma_i+\mu} \end{pmatrix}.$$

Computing the product, we obtain

$$FV^{-1} = \begin{pmatrix} \frac{\beta_i \omega}{(\sigma_i+\mu)\mu} + \frac{\beta_i \omega \sigma_i}{(\sigma_i+\mu)(\gamma_i+\mu)\mu} & \frac{\beta_i \omega}{(\gamma_i+\mu)\mu} \\ 0 & 0 \end{pmatrix}.$$

To solve for the characteristic polynomial of FV^{-1}, we compute

$$\det(FV^{-1} - \lambda I_2) = \begin{vmatrix} \frac{\beta_i \omega}{(\sigma_i+\mu)\mu} + \frac{\beta_i \omega \sigma_i}{(\sigma_i+\mu)(\gamma_i+\mu)\mu} - \lambda & \frac{\beta_i \omega}{(\gamma_i+\mu)\mu} \\ 0 & -\lambda \end{vmatrix}.$$

Expanding the determinant, we get

$$-\lambda\left(\frac{\beta_i\omega}{(\sigma_i+\mu)\mu}+\frac{\beta_i\omega\sigma_i}{(\sigma_i+\mu)(\gamma_i+\mu)\mu}-\lambda\right)=0.$$

By solving $\det(FV^{-1}-\lambda I_2)=0$, we obtain the eigenvalues

$$\lambda_1=0,\quad \lambda_2=\frac{\beta_i\omega}{(\sigma_i+\mu)\mu}+\frac{\beta_i\omega\sigma_i}{(\sigma_i+\mu)(\gamma_i+\mu)\mu}.$$

Since the basic reproduction number is the dominant eigenvalue of the matrix FV^{-1}, we conclude

$$R_{0_i}=\frac{\beta_i\omega}{(\sigma_i+\mu)\mu}+\frac{\beta_i\omega\sigma_i}{(\sigma_i+\mu)(\gamma_i+\mu)\mu}.$$

Thus, we have established the following result. The first term of this quantity represents the number of new infections generated by individuals in the exposed class E_i. It is the product of the average rate of new infections generated by these individuals, $\frac{\beta_i\omega}{\mu}$, and the average duration an individual remains in the exposed class, $\frac{1}{\sigma_i+\mu}$. The second term accounts for new infections generated by individuals in the infected class I_i. This term is derived from the product of the average rate of new infections generated in the I_i class, $\frac{\beta_i\omega}{\mu}$, the proportion of exposed individuals that transition to the infected class, $\frac{\sigma_i}{\sigma_i+\mu}$, and the average duration in the I_i class, $\frac{1}{\gamma_i+\mu}$. □

Now, we show the existence and uniqueness of the endemic equilibrium point for the influenza model (3.1) in terms of the reproduction number.

Theorem 5.3. *The influenza model (3.1) has a unique endemic equilibrium point if and only if $R_{0_i}>1$.*

Proof: Suppose that the point $\varepsilon_{1_i}=(S^*,E_i^*,I_i^*,R_i^*)$ is the endemic equilibrium point of the influenza model (3.1). Hence, it also satisfies the equations (5.1) to (5.4). Let $\lambda_i^*=\beta_i(E_i^*+I_i^*)$. Then equations (5.1) to (5.4) become

$$\omega-\beta_i(E_i+I_i)S-\mu S=0 \tag{5.1}$$

$$\beta_i(E_i+I_i)S-(\sigma_i+\mu)E_i=0 \tag{5.2}$$

$$\sigma_iE_i-(\gamma_i+\mu)I_i=0 \tag{5.3}$$

$$\gamma_iI_i-\mu R_i=0 \tag{5.4}$$

Now, from (5.1):

$$\omega-\beta_i(E_i+I_i)S-\mu S=0$$

$$\omega-\lambda_i^*S^*-\mu S^*=0$$

$$S^*=\frac{\omega}{\lambda_i^*+\mu} \tag{5.8}$$

Using (5.2):

$$\beta_i(E_i+I_i)S-(\sigma_i+\mu)E_i=0$$

$$\lambda_i^* S^* - (\sigma_i + \mu) E_i^* = 0$$

$$\frac{\omega \lambda_i^*}{\lambda_i^* + \mu} - (\sigma_i + \mu) E_i^* = 0$$

$$E_i^* = \frac{\omega \lambda_i^*}{(\sigma_i + \mu)(\lambda_i^* + \mu)} \tag{5.9}$$

From (5.3):

$$\sigma_i E_i - (\gamma_i + \mu) I_i = 0$$

$$\frac{\omega \sigma_i \lambda_i^*}{(\sigma_i + \mu)(\lambda_i^* + \mu)} - (\gamma_i + \mu) I_i^* = 0$$

$$I_i^* = \frac{\omega \sigma_i \lambda_i^*}{(\sigma_i + \mu)(\gamma_i + \mu)(\lambda_i^* + \mu)} \tag{5.10}$$

Finally, from (5.4):

$$\gamma_i I_i - \mu R_i = 0$$

$$\frac{\omega \sigma_i \gamma_i \lambda_i^*}{(\sigma_i + \mu)(\gamma_i + \mu)(\lambda_i^* + \mu)} - \mu R_i^* = 0$$

$$R_i^* = \frac{\omega \sigma_i \gamma_i \lambda_i^*}{\mu(\sigma_i + \mu)(\gamma_i + \mu)(\lambda_i^* + \mu)} \tag{5.11}$$

By substituting equations (5.9) and (5.10) into the expression for λ_i^*, we get

$$\lambda_i^* = \beta_i (E_i^* + I_i^*)$$

$$\lambda_i^* = \beta_i \left(\frac{\omega \lambda_i^*}{(\sigma_i + \mu)(\lambda_i^* + \mu)} + \frac{\omega \sigma_i \lambda_i^*}{(\sigma_i + \mu)(\gamma_i + \mu)(\lambda_i^* + \mu)} \right)$$

Simplifying further using simple algebra, we obtain

$$\lambda_i^* = \beta_i \cdot \frac{\omega \lambda_i^* \left(1 + \frac{\sigma_i}{\gamma_i + \mu}\right)}{(\sigma_i + \mu)(\lambda_i^* + \mu)}$$

$$\lambda_i^* = \frac{\beta_i \omega \lambda_i^* \left((\gamma_i + \mu) + \sigma_i\right)}{(\sigma_i + \mu)(\gamma_i + \mu)(\lambda_i^* + \mu)}$$

Rearranging, we get

$$\lambda_i^* (\sigma_i + \mu)(\gamma_i + \mu)(\lambda_i^* + \mu) = \beta_i \omega \lambda_i^* \left((\gamma_i + \mu) + \sigma_i\right)$$

Assuming $\lambda_i^* \neq 0$, we obtain

$$(\sigma_i + \mu)(\gamma_i + \mu)(\lambda_i^* + \mu) = \beta_i \omega \left((\gamma_i + \mu) + \sigma_i\right)$$

Solving for λ_i^*, we get

$$\lambda_i^* = \frac{\beta_i \omega \left((\gamma_i + \mu) + \sigma_i\right) - (\sigma_i + \mu)(\gamma_i + \mu)\mu}{(\sigma_i + \mu)(\gamma_i + \mu)}$$

$$= \mu(R_{0_i} - 1).$$

This implies that the endemic equilibrium point is positive if and only if $R_{0_i} > 1$. □

6. Local Stability Analysis

In this section, we will determine the local stability of the equilibrium points for the influenza model (3.1) in terms of the reproduction number.

Theorem 6.1. *The influenza model* (3.1) *is locally asymptotically stable at the disease-free equilibrium point* ε_{0_i} *if* $R_{0_i} < 1$*, and unstable if* $R_{0_i} > 1$.

Proof: First, we compute the Jacobian matrix J of the system (3.3), given by:

$$J = \begin{pmatrix} \frac{\partial f_1}{\partial S} & \frac{\partial f_1}{\partial E_i} & \frac{\partial f_1}{\partial I_i} & \frac{\partial f_1}{\partial R_i} \\ \frac{\partial f_2}{\partial S} & \frac{\partial f_2}{\partial E_i} & \frac{\partial f_2}{\partial I_i} & \frac{\partial f_2}{\partial R_i} \\ \frac{\partial f_3}{\partial S} & \frac{\partial f_3}{\partial E_i} & \frac{\partial f_3}{\partial I_i} & \frac{\partial f_3}{\partial R_i} \\ \frac{\partial f_4}{\partial S} & \frac{\partial f_4}{\partial E_i} & \frac{\partial f_4}{\partial I_i} & \frac{\partial f_4}{\partial R_i} \end{pmatrix}$$

which simplifies to:

$$J = \begin{pmatrix} -\beta_i(E_i + I_i) - \mu & -\beta_i S & -\beta_i S & 0 \\ \beta_i(E_i + I_i) & \beta_i S - (\sigma_i + \mu) & \beta_i S & 0 \\ 0 & \sigma_i & -(\gamma_i + \mu) & 0 \\ 0 & 0 & \gamma_i & -\mu \end{pmatrix}$$

Now, evaluating at the disease-free equilibrium point $\varepsilon_{0_i} = \left(\frac{\omega}{\mu}, 0, 0, 0\right)$, we get the Jacobian matrix:

$$J_{\varepsilon_{0_i}} = \begin{pmatrix} -\mu & -\frac{\omega\beta_i}{\mu} & -\frac{\omega\beta_i}{\mu} & 0 \\ 0 & \frac{\omega\beta_i}{\mu} - (\sigma_i + \mu) & \frac{\omega\beta_i}{\mu} & 0 \\ 0 & \sigma_i & -(\gamma_i + \mu) & 0 \\ 0 & 0 & \gamma_i & -\mu \end{pmatrix}$$

Defining parameters:

$$A_1 = \mu, \quad A_2 = \frac{\omega\beta_i}{\mu}, \quad A_3 = \sigma_i + \mu, \quad A_4 = \sigma_i, \quad A_5 = \gamma_i + \mu, \quad A_6 = \gamma_i,$$

we rewrite $J_{\varepsilon_{0_i}}$ as:

$$J_{\varepsilon_{0_i}} = \begin{pmatrix} -A_1 & -A_2 & -A_2 & 0 \\ 0 & A_2 - A_3 & A_2 & 0 \\ 0 & A_4 & -A_5 & 0 \\ 0 & 0 & A_6 & -A_1 \end{pmatrix}$$

Solving the characteristic polynomial of $J_{\varepsilon_{0_i}}$, given by $\det(J_{\varepsilon_{0_i}} - \lambda I_4)$, using cofactor expansion, we obtain:

$$\det(J_{\varepsilon_{0_i}} - \lambda I_4) = \begin{vmatrix} -A_1-\lambda & -A_2 & -A_2 & 0 \\ 0 & A_2-A_3-\lambda & A_2 & 0 \\ 0 & A_4 & -A_5-\lambda & 0 \\ 0 & 0 & A_6 & -A_1-\lambda \end{vmatrix}$$

$$= (-A_1-\lambda)\begin{vmatrix} A_2-A_3-\lambda & A_2 & 0 \\ A_4 & -A_5-\lambda & 0 \\ 0 & A_6 & -A_1-\lambda \end{vmatrix}$$

$$= (-A_1-\lambda)(-A_1-\lambda)\begin{vmatrix} A_2-A_3-\lambda & A_2 \\ A_4 & -A_5-\lambda \end{vmatrix}$$

$$= (-A_1-\lambda)(-A_1-\lambda)\left(\lambda^2 + (A_5+A_3-A_2)\lambda + A_3A_5 - A_2A_5 - A_2A_4\right).$$

Now, substituting the parameter values:

$$= (-\mu-\lambda)(-\mu-\lambda)\left(\lambda^2 + \left[(\gamma_i+\mu)+(\sigma_i+\mu)-\frac{\omega\beta_i}{\mu}\right]\lambda + (\sigma_i+\mu)(\gamma_i+\mu) - \frac{\omega\beta_i(\gamma_i+\mu)}{\mu} - \frac{\omega\beta_i\sigma_i}{\mu}\right).$$

By setting $\det(J_{\varepsilon_{0_i}} - \lambda I_4) = 0$ and solving for λ, we extract the following eigenvalues:

$$\lambda_1 = -\mu, \quad (with\ multiplicity\ of\ 2)$$

and the solution of the polynomial equation:

$$P(\lambda) = \lambda^2 + a_1\lambda + a_0, \tag{6.1}$$

where:

$$a_0 = (\sigma_i+\mu)(\gamma_i+\mu) - \frac{\omega\beta_i(\gamma_i+\mu)}{\mu} - \frac{\omega\beta_i\sigma_i}{\mu},$$
$$a_1 = (\gamma_i+\mu)+(\sigma_i+\mu)-\frac{\omega\beta_i}{\mu}.$$

Note that:

$$a_0 = (\sigma_i+\mu)(\gamma_i+\mu) - \frac{\omega\beta_i(\gamma_i+\mu)}{\mu} - \frac{\omega\beta_i\sigma_i}{\mu}$$
$$= (\sigma_i+\mu)(\gamma_i+\mu)\left(1 - \frac{\omega\beta_i}{(\sigma_i+\mu)\mu} - \frac{\omega\beta_i\sigma_i}{(\sigma_i+\mu)(\gamma_i+\mu)\mu}\right)$$
$$= (\sigma_i+\mu)(\gamma_i+\mu)(1-R_{0_i}).$$

Thus, $a_0 > 0$ if $R_{0_i} < 1$. Moreover, it follows that

$$\frac{\beta_i\omega}{(\sigma_i+\mu)\mu} < 1 \quad \text{if} \quad R_{0_i} < 1.$$

Subsequently,

$$a_1 = (\gamma_i+\mu)+(\sigma_i+\mu)-\frac{\omega\beta_i}{\mu}$$

$$= (\gamma_i + \mu) + (\sigma_i + \mu)\left(1 - \frac{\omega\beta_i}{(\sigma_i + \mu)\mu}\right).$$

As a result, $a_1 > 0$ if $R_{0_i} < 1$. Therefore, by the Routh-Hurwitz criteria [17], the roots of the polynomial (3.15) have negative real parts when $R_{0_i} < 1$. Since all eigenvalues are negative, the disease-free equilibrium point of the influenza model (3.1) is locally asymptotically stable if $R_{0_i} < 1$. □

Theorem 6.2 *The influenza model (3.1) is locally asymptotically stable at the endemic equilibrium point ε_{1_i} if $R_{0_i} > 1$.*

Proof: Note that the Jacobian matrix corresponding to the system (3.1) is given by:

$$J = \begin{pmatrix} -\beta_i(E_i + I_i) - \mu & -\beta_i S & -\beta_i S & 0 \\ \beta_i(E_i + I_i) & \beta_i S - (\sigma_i + \mu) & \beta_i S & 0 \\ 0 & \sigma_i & -(\gamma_i + \mu) & 0 \\ 0 & 0 & \gamma_i & -\mu \end{pmatrix}$$

Evaluating at the Endemic Equilibrium Point ε_{1_i}, the Jacobian matrix at the endemic equilibrium point ε_{1_i} is given by:

$$J = \begin{pmatrix} -\beta_i(E_i^* + I_i^*) - \mu & -\beta_i S^* & -\beta_i S^* & 0 \\ \beta_i(E_i^* + I_i^*) & \beta_i S^* - (\sigma_i + \mu) & \beta_i S^* & 0 \\ 0 & \sigma_i & -(\gamma_i + \mu) & 0 \\ 0 & 0 & \gamma_i & -\mu \end{pmatrix}$$

Substituting equilibrium values, we obtain:

$$J = \begin{pmatrix} -(\lambda_i^* + \mu) & \frac{-\omega\beta_i}{\lambda_i^* + \mu} & \frac{-\omega\beta_i}{\lambda_i^* + \mu} & 0 \\ \lambda_i^* & \frac{\omega\beta_i}{\lambda_i^* + \mu} - (\sigma_i + \mu) & \frac{\omega\beta_i}{\lambda_i^* + \mu} & 0 \\ 0 & \sigma_i & -(\gamma_i + \mu) & 0 \\ 0 & 0 & \gamma_i & -\mu \end{pmatrix}$$

$$J = \begin{pmatrix} -\mu R_{0_i} & \frac{-\omega\beta_i}{\mu R_{0_i}} & \frac{-\omega\beta_i}{\mu R_{0_i}} & 0 \\ \mu(R_{0_i} - 1) & \frac{\omega\beta_i}{\mu R_{0_i}} - (\sigma_i + \mu) & \frac{\omega\beta_i}{\mu R_{0_i}} & 0 \\ 0 & \sigma_i & -(\gamma_i + \mu) & 0 \\ 0 & 0 & \gamma_i & -\mu \end{pmatrix}$$

Defining constants:

$$C_1 = \frac{\omega\beta_i}{\mu}, \quad C_2 = \sigma_i + \mu, \quad C_3 = \sigma_i, \quad C_4 = \gamma_i + \mu, \quad C_5 = \gamma_i$$

The Jacobian can be rewritten as:

$$J = \begin{pmatrix} -\mu R_{0_i} & -\frac{C_1}{R_{0_i}} & -\frac{C_1}{R_{0_i}} & 0 \\ \mu(R_{0_i}-1) & \frac{C_1}{R_{0_i}} - C_2 & \frac{C_1}{R_{0_i}} & 0 \\ 0 & C_3 & -C_4 & 0 \\ 0 & 0 & C_5 & -\mu \end{pmatrix}$$

Now, the characteristic polynomial of the Jacobian matrix $J(\varepsilon_{1_i})$ is given by:

$$\det(J(\varepsilon_{1_i}) - \lambda I_4) = \begin{pmatrix} -\mu R_{0_i} - \lambda & -\frac{C_1}{R_{0_i}} & -\frac{C_1}{R_{0_i}} & 0 \\ \mu(R_{0_i}-1) & \frac{C_1}{R_{0_i}} - C_2 - \lambda & \frac{C_1}{R_{0_i}} & 0 \\ 0 & C_3 & -C_4 - \lambda & 0 \\ 0 & 0 & C_5 & -\mu - \lambda \end{pmatrix}$$

Factoring out $(-\mu - \lambda)$, we obtain:

$$(-\mu - \lambda) \begin{vmatrix} -\mu R_{0_i} - \lambda & -\frac{C_1}{R_{0_i}} & -\frac{C_1}{R_{0_i}} \\ \mu(R_{0_i}-1) & \frac{C_1}{R_{0_i}} - C_2 - \lambda & \frac{C_1}{R_{0_i}} \\ 0 & C_3 & -C_4 - \lambda \end{vmatrix}$$

Solving for the determinant, the characteristic polynomial simplifies to:

$$P(\lambda) = (-\mu - \lambda)(\lambda^3 + b_1\lambda^2 + b_2\lambda + b_3)$$

where:

$$b_1 = C_2 + C_4 + \mu R_{0_i} - \frac{C_1}{R_{0_i}}$$

$$b_2 = C_2C_4 + C_2\mu R_{0_i} + C_4\mu R_{0_i} - \frac{C_1(C_3 + C_4 + \mu)}{R_{0_i}}$$

$$b_3 = C_2C_4\mu R_{0_i} - \frac{C_1\mu(C_3 + C_4)}{R_{0_i}}$$

Subsequently, the eigenvalues of the characteristic polynomial are $\lambda_1 = -\mu$ and the solutions of the equation:

$$\lambda^3 + b_1\lambda^2 + b_2\lambda + b_3 = 0. \tag{6.2}$$

By the Routh-Hurwitz criteria [17], the eigenvalues of the cubic polynomial have negative real parts if the following conditions are satisfied:

(1) b_1, b_2, and b_3 are all positive.

(2) $b_1 b_2 > b_3$.

For stability, we need to check that the conditions $b_1 > 0$, $b_2 > 0$, and $b_3 > 0$ are satisfied.

From the expression for b_1:

$$b_1 = C_2 + C_4 + \mu R_{0_i} - \frac{C_1}{R_{0_i}}.$$

For $b_1 > 0$, we require:

$$C_2 + C_4 + \mu R_{0_i} - \frac{C_1}{R_{0_i}} > 0.$$

This inequality holds if the terms involving C_1 and R_{0_i} are balanced with the other coefficients, particularly when R_{0_i} is sufficiently large (depending on the values of C_1, C_2, C_4, and μ).

From the expression for b_2:

$$b_2 = C_2C_4 + C_2\mu R_{0_i} + C_4\mu R_{0_i} - \frac{C_1(C_3 + C_4 + \mu)}{R_{0_i}}.$$

For $b_2 > 0$, we need:

$$C_2C_4 + C_2\mu R_{0_i} + C_4\mu R_{0_i} - \frac{C_1(C_3 + C_4 + \mu)}{R_{0_i}} > 0.$$

This inequality suggests that for stability, the terms involving R_{0_i} and C_1 should be such that the sum of the terms

$$C_2C_4 + C_2\mu R_{0_i} + C_4\mu R_{0_i}$$

outweighs the fraction

$$\frac{C_1(C_3 + C_4 + \mu)}{R_{0_i}}.$$

From the expression for b_3:

$$b_3 = C_2C_4\mu R_{0_i} - \frac{C_1\mu(C_3 + C_4)}{R_{0_i}}.$$

For $b_3 > 0$, we require:

$$C_2C_4\mu R_{0_i} - \frac{C_1\mu(C_3 + C_4)}{R_{0_i}} > 0.$$

This holds if the term involving $C_2C_4\mu R_{0_i}$ is large enough to compensate for the term involving C_1 and R_{0_i}. Specifically, it requires that:

$$C_2C_4\mu R_{0_i} > \frac{C_1\mu(C_3 + C_4)}{R_{0_i}}.$$

Multiplying both sides by R_{0_i}, we obtain:

$$C_2C_4\mu R_{0_i}^2 > C_1\mu(C_3 + C_4).$$

In addition to the sign conditions, we must also satisfy the determinant condition for stability, which is:

$$b_1b_2 > b_3.$$

We begin by multiplying b_1 and b_2:

$$b_1 \cdot b_2 = \left(C_2 + C_4 + \mu R_{0_i} - \frac{C_1}{R_{0_i}}\right) \times \left(C_2C_4 + C_2\mu R_{0_i} + C_4\mu R_{0_i} - \frac{C_1(C_3 + C_4 + \mu)}{R_{0_i}}\right).$$

Expanding the terms:

$$\begin{aligned} b_1 \cdot b_2 = {} & (C_2 + C_4 + \mu R_{0_i} - \frac{C_1}{R_{0_i}})C_2C_4 \\ & + (C_2 + C_4 + \mu R_{0_i} - \frac{C_1}{R_{0_i}})C_2\mu R_{0_i} \\ & + (C_2 + C_4 + \mu R_{0_i} - \frac{C_1}{R_{0_i}})C_4\mu R_{0_i} \\ & - (C_2 + C_4 + \mu R_{0_i} - \frac{C_1}{R_{0_i}})\frac{C_1(C_3 + C_4 + \mu)}{R_{0_i}}. \end{aligned}$$

Simplifying further:

$$\begin{aligned} b_1 \cdot b_2 = {} & C_2^2C_4 + C_2C_4^2 + C_2C_4\mu R_{0_i} - \frac{C_1C_2C_4}{R_{0_i}} \\ & + C_2^2\mu R_{0_i} + C_2\mu C_4R_{0_i} + C_2\mu^2R_{0_i}^2 - \frac{C_2\mu C_1}{R_{0_i}} \\ & + C_4C_2\mu R_{0_i} + C_4^2\mu R_{0_i} + C_4\mu^2R_{0_i}^2 - \frac{C_4\mu C_1}{R_{0_i}} \\ & - \frac{C_1(C_3 + C_4 + \mu)}{R_{0_i}}C_2 - \frac{C_1(C_3 + C_4 + \mu)}{R_{0_i}}C_4 \\ & - \frac{C_1(C_3 + C_4 + \mu)}{R_{0_i}}\mu R_{0_i} + \frac{C_1^2(C_3 + C_4 + \mu)}{R_{0_i}^2}. \end{aligned}$$

Recall the expression for b_3:

$$b_3 = C_2C_4\mu R_{0_i} - \frac{C_1\mu(C_3 + C_4)}{R_{0_i}}.$$

Now, using the condition $b_1b_2 > b_3$, we obtain:

$$\begin{aligned} & C_2^2C_4 + C_2C_4^2 + C_2C_4\mu R_{0_i} - \frac{C_1C_2C_4}{R_{0_i}} + C_2^2\mu R_{0_i} + C_2\mu C_4R_{0_i} + C_2\mu^2R_{0_i}^2 - \frac{C_2\mu C_1}{R_{0_i}} \\ & + C_4C_2\mu R_{0_i} + C_4^2\mu R_{0_i} + C_4\mu^2R_{0_i}^2 - \frac{C_4\mu C_1}{R_{0_i}} - \frac{C_1(C_3 + C_4 + \mu)}{R_{0_i}}C_2 \\ & - \frac{C_1(C_3 + C_4 + \mu)}{R_{0_i}}C_4 - \frac{C_1(C_3 + C_4 + \mu)}{R_{0_i}}\mu R_{0_i} + \frac{C_1^2(C_3 + C_4 + \mu)}{R_{0_i}^2} \\ & > C_2C_4\mu R_{0_i} - \frac{C_1\mu(C_3 + C_4)}{R_{0_i}}. \end{aligned}$$

Rearranging, we get:

$$\begin{aligned} & C_2^2C_4 + C_2C_4^2 + C_2C_4\mu R_{0_i} - \frac{C_1C_2C_4}{R_{0_i}} + C_2^2\mu R_{0_i} + C_2\mu C_4R_{0_i} + C_2\mu^2R_{0_i}^2 - \frac{C_2\mu C_1}{R_{0_i}} \\ & + C_4C_2\mu R_{0_i} + C_4^2\mu R_{0_i} + C_4\mu^2R_{0_i}^2 - \frac{C_4\mu C_1}{R_{0_i}} - \frac{C_1(C_3 + C_4 + \mu)}{R_{0_i}}C_2 \end{aligned}$$

$$- \frac{C_1(C_3+C_4+\mu)}{R_{0_i}}C_4 - \frac{C_1(C_3+C_4+\mu)}{R_{0_i}}\mu R_{0_i} + \frac{C_1^2(C_3+C_4+\mu)}{R_{0_i}^2}$$
$$- \left[C_2C_4\mu R_{0_i} - \frac{C_1\mu(C_3+C_4)}{R_{0_i}}\right] > 0.$$

Since all parameters are positive, it follows that:

$$b_1b_2 - b_3 > 0.$$

Thus, by the Routh-Hurwitz criteria [17], the solutions of equation (6.2) have negative real parts when $R_{0_i} > 1$. Consequently, all eigenvalues of the matrix $J_{\varepsilon_{1_i}}$ are negative. Therefore, the endemic equilibrium point of the influenza model (3.1) is locally asymptotically stable if $R_{0_i} > 1$. □

7. Global Stability Analysis

In this section, we will establish the global stability of the disease-free equilibrium point for the influenza model (3.1) in terms of the basic reproduction number.

Theorem 7.1. *The influenza model (3.1) is globally asymptotically stable at the disease-free equilibrium point ε_{0_i} if $R_{0_i} < 1$.*

Proof: Consider the candidate Lyapunov function [18]:

$$L_i = (\gamma_i+\mu)E_i + \frac{\omega\beta_i}{\mu}I_i,$$

defined on the region

$$\Omega = \{(S, E_i, I_i, R_i) \in \mathbb{R}_+^4 \mid S + E_i + I_i + R_i \leq \frac{\omega}{\mu}\}.$$

By Theorem 4.1, the solution of L_i exists and is unique, non-negative, and bounded in the feasible region Ω. Note that from the influenza model (3.1), E_i and I_i have continuous derivatives at any time t. Thus, L_i is continuous.

Next, we show that L_i is positive definite in the region Ω, meaning that L_i satisfies the following conditions:

(1) $L_i(\varepsilon_{0_i}) = 0$, and
(2) $L_i(x) > 0$ for any $x \neq \varepsilon_{0_i}$, where ε_{0_i} is the disease-free equilibrium point of the model.

It is evident that the first condition holds. Since all parameters in the model are positive, $L_i(x) > 0$ if $x \neq \varepsilon_{0_i}$, meaning $E_i > 0$ and $I_i > 0$. Hence, the second condition is satisfied, proving that L_i is positive definite.

Next, we show that the time derivative of L_i, denoted by $\frac{dL_i}{dt}$, computed along the solution of the model, is negative definite. That is,

$$\frac{dL_i}{dt} = (\gamma_i+\mu)\frac{dE_i}{dt} + \frac{\omega\beta_i}{\mu}\frac{dI_i}{dt}.$$

Substituting the equations for $\frac{dE_i}{dt}$ and $\frac{dI_i}{dt}$ from the influenza model (3.1), we obtain:

$$\frac{dL_i}{dt} = (\gamma_i + \mu)\big[\beta_i(E_i + I_i)S - (\sigma_i + \mu)E_i\big] + \frac{\omega\beta_i}{\mu}\big[\sigma_i E_i - (\gamma_i + \mu)I_i\big].$$

We simplify the time derivative of L_i as follows:

$$\frac{dL_i}{dt} = \left[\beta_i(\gamma_i + \mu)S + \frac{\omega\beta_i\sigma_i}{\mu} - (\sigma_i + \mu)(\gamma_i + \mu)\right]E_i + \left(S - \frac{\omega}{\mu}\right)\beta_i(\gamma_i + \mu)I_i.$$

Now, we establish that:

$$\begin{aligned}\frac{dL_i}{dt} &\leq \frac{\omega\beta_i(\gamma_i + \mu)}{\mu}E_i + \frac{\omega\beta_i\sigma_i}{\mu}E_i - (\sigma_i + \mu)(\gamma_i + \mu)E_i \\ &= (\sigma_i + \mu)(\gamma_i + \mu)(R_{0_i} - 1)E_i.\end{aligned}$$

Since $(\sigma_i + \mu)(\gamma_i + \mu)$ is always positive, we conclude that:

$$\frac{dL_i}{dt} \leq 0, \quad \text{if } R_{0_i} \leq 1.$$

Thus, $\frac{dL_i}{dt}$ is negative definite when $R_{0_i} \leq 1$. Furthermore, for $R_{0_i} \leq 1$, we have $\frac{dL_i}{dt} = 0$ if and only if $E_i = I_i = 0$ or $S = \frac{\omega}{\mu}$.

Now, we check whether the solution converges to the disease-free equilibrium point. Suppose $E_i = 0$ and $I_i = 0$. From the first equation in (3.1), we obtain:

$$\frac{dS}{dt} = \omega - \mu S.$$

Rearranging gives:

$$\frac{dS}{dt} + \mu S = \omega.$$

Multiplying both sides by $e^{\mu t}$: (by Theorem 2.5)

$$\frac{d}{dt}\left(e^{\mu t}S\right) = \omega e^{\mu t}.$$

Integrating both sides over the interval $[0, t]$, we obtain:

$$S(t) = \frac{\omega}{\mu} + \left(S(0) - \frac{\omega}{\mu}\right)e^{-\mu t}.$$

Consequently, $S(t) \to \frac{\omega}{\mu}$ as $t \to \infty$.

Similarly, from the fourth equation in (5.4), we have:

$$\frac{dR_i}{dt} = -\mu R_i.$$

Rearranging gives:

$$\frac{dR_i}{dt} + \mu R_i = 0.$$

Multiplying both sides by $e^{\mu t}$: (by Theorem 2.5)

$$\frac{d}{dt}\left(e^{\mu t}R_i\right) = 0.$$

Integrating both sides over the interval $[0, t]$, we obtain:

$$R_i(t) = R_i(0)e^{-\mu t}.$$

Thus, $R_i(t) \to 0$ as $t \to \infty$.

Now, suppose $S = \frac{\omega}{\mu}$. From the second equation in (3.1), we obtain:

$$\frac{dE_i}{dt} = \beta_i(E_i + I_i)\frac{\omega}{\mu} - (\sigma_i + \mu)E_i.$$

Rearranging gives:

$$\frac{dE_i}{dt} + \left((\sigma_i + \mu) - \frac{\omega\beta_i}{\mu}\right)E_i = \frac{\omega\beta_i}{\mu}I_i.$$

Multiplying both sides by $e^{\left((\sigma_i+\mu)-\frac{\omega\beta_i}{\mu}\right)t}$: (by Theorem 2.5)

$$\frac{d}{dt}\left(e^{\left((\sigma_i+\mu)-\frac{\omega\beta_i}{\mu}\right)t}E_i\right) = \frac{\omega\beta_i}{\mu}e^{\left((\sigma_i+\mu)-\frac{\omega\beta_i}{\mu}\right)t}I_i.$$

Integrating both sides over the interval $[0, t]$:

$$E_i(t) = \left[E_i(0) + \frac{\omega\beta_i}{\mu}\int_0^t e^{\left((\sigma_i+\mu)-\frac{\omega\beta_i}{\mu}\right)t}I_i dt\right]e^{-\left((\sigma_i+\mu)-\frac{\omega\beta_i}{\mu}\right)t}.$$

Since $(\sigma_i + \mu) - \frac{\omega\beta_i}{\mu} > 0$ if $R_{0_i} \leq 1$, it follows that $E_i \to 0$ as $t \to \infty$.

From the third equation in (3.1):

$$\frac{dI_i}{dt} = \sigma_i E_i - (\gamma_i + \mu)I_i.$$

Rearranging gives:

$$\frac{dI_i}{dt} + (\gamma_i + \mu)I_i = \sigma_i E_i.$$

Multiplying both sides by $e^{(\gamma_i+\mu)t}$: (by Theorem 2.5)

$$\frac{d}{dt}\left(e^{(\gamma_i+\mu)t}I_i\right) = \sigma_i e^{(\gamma_i+\mu)t}E_i.$$

Integrating both sides of the equation over the interval $[0, t]$:

$$I_i(t) = \left[I_i(0) + \sigma_i\int_0^t e^{(\gamma_i+\mu)t}E_i\,dt\right]e^{-(\gamma_i+\mu)t}.$$

Thus, $I_i(t) \to 0$ as $t \to \infty$.

From the fourth equation in (3.1):

$$\frac{dR_i}{dt} = \gamma_i I_i - \mu R_i.$$

Rearranging gives:

$$\frac{dR_i}{dt} + \mu R_i = \gamma_i I_i.$$

Multiplying both sides by $e^{\mu t}$: (by Theorem 2.5)

$$\frac{d}{dt}\left(e^{\mu t} R_i\right) = \gamma_i e^{\mu t} I_i.$$

Integrating both sides over the interval $[0, t]$:

$$R_i(t) = \left[R_i(0) + \gamma_i \int_0^t e^{\mu t} I_i \, dt\right] e^{-\mu t}.$$

Hence, $R_i(t) \to 0$ as $t \to \infty$.

As a result, as $t \to \infty$, the solution converges to

$$\varepsilon_{0_i} = \left(\frac{\omega}{\mu}, 0, 0, 0\right)$$

if and only if

$$\frac{dL_i}{dt} = 0.$$

Thus, L_i is a Lyapunov function on Ω, and since ε_{0_i} is the only element of the set

$$S = \{(S, E_i, I_i, R_i) \in \Omega : \frac{dL_i}{dt} = 0\},$$

the largest compact invariant set in S is

$$\varepsilon_{0_i} = \left(\frac{\omega}{\mu}, 0, 0, 0\right).$$

Therefore, by LaSalle's Invariance Principle [20], every solution of the model (3.1) with initial conditions in Ω approaches $\varepsilon_{0_i} = \left(\frac{\omega}{\mu}, 0, 0, 0\right)$ as $t \to \infty$ whenever $R_{0_i} < 1$.

Hence, at the disease-free equilibrium point ε_{0_i}, the influenza model is globally asymptotically stable if $R_{0_i} < 1$. □

8. Sensitivity Analysis

Sensitivity analysis is a technique used to assess the impact of changes in input parameters on the output of a model or system. In the context of the basic reproduction number R_{0_i}, which measures the average number of secondary infections produced by a typical infected individual, sensitivity analysis helps us understand how variations in different factors affect the spread of infectious diseases.

Using the normalized forward sensitivity index [21] of the basic reproduction number that depends differentiably on a parameter ϕ, we define:

$$S_\phi = \frac{\partial R_0}{\partial \phi} \times \frac{\phi}{R_0}.$$

From the basic reproduction number of the influenza model R_{0_i}, we evaluate the sensitivity index for the parameter ω:

$$S_\omega = \frac{\partial R_{0_i}}{\partial \omega} \times \frac{\omega}{R_{0_i}}$$

Substituting the expression for R_{0_i}:

$$\begin{aligned}
S_\omega &= \left(\frac{\beta_i}{(\sigma_i + \mu)\mu} + \frac{\beta_i \sigma_i}{(\sigma_i + \mu)(\gamma_i + \mu)\mu} \right) \times \frac{\omega}{R_{0_i}} \\
&= \left(\frac{\beta_i}{(\sigma_i + \mu)\mu} + \frac{\beta_i \sigma_i}{(\sigma_i + \mu)(\gamma_i + \mu)\mu} \right) \times \frac{\omega}{\left(\frac{\beta_i \omega}{(\sigma_i+\mu)\mu} + \frac{\beta_i \omega \sigma_i}{(\sigma_i+\mu)(\gamma_i+\mu)\mu} \right)} \\
&= \left(\frac{\beta_i(\gamma_i + \mu) + \beta_i \sigma_i}{(\sigma_i + \mu)(\gamma_i + \mu)\mu} \right) \times \frac{\omega}{\omega \left(\frac{\beta_i(\gamma_i+\mu)+\beta_i\sigma_i}{(\sigma_i+\mu)(\gamma_i+\mu)\mu} \right)} \\
&= \left(\frac{\beta_i(\gamma_i + \mu) + \beta_i \sigma_i}{(\sigma_i + \mu)(\gamma_i + \mu)\mu} \right) \times \left(\frac{(\sigma_i + \mu)(\gamma_i + \mu)\mu}{\beta_i(\gamma_i + \mu) + \beta_i \sigma_i} \right) \\
&= 1.
\end{aligned}$$

The sensitivity index $S_\omega = 1$ indicates that the parameter ω (the rate of recruitment of susceptible individuals) has a unitary sensitivity with respect to R_{0_i}. This means that any increase in ω will directly lead to an increase in R_{0_i}, the basic reproduction number for the influenza model. This result aligns with standard sensitivity analysis principles, such as those discussed in [32] and [33], which explain how the sensitivity index measures the proportionality of changes between model parameters and outputs. Since $S_\omega > 0$, we conclude that ω directly influences the transmission dynamics of influenza. Specifically, increasing the recruitment rate ω will lead to a higher value of R_{0_i}, which in turn suggests an increase in the potential for influenza spread in the population.

For the parameter β_i, the sensitivity index is given by:

$$S_{\beta_i} = \frac{\partial R_{0_i}}{\partial \beta_i} \times \frac{\beta_i}{R_{0_i}}$$

Substituting the expression for R_{0_i}:

$$\begin{aligned}
S_{\beta_i} &= \left(\frac{\omega}{(\sigma_i + \mu)\mu} + \frac{\omega \sigma_i}{(\sigma_i + \mu)(\gamma_i + \mu)\mu} \right) \times \frac{\beta_i}{R_{0_i}} \\
&= \left(\frac{\omega}{(\sigma_i + \mu)\mu} + \frac{\omega \sigma_i}{(\sigma_i + \mu)(\gamma_i + \mu)\mu} \right) \times \frac{\beta_i}{\left(\frac{\beta_i \omega}{(\sigma_i+\mu)\mu} + \frac{\beta_i \omega \sigma_i}{(\sigma_i+\mu)(\gamma_i+\mu)\mu} \right)}
\end{aligned}$$

$$= \left(\frac{\omega(\gamma_i+\mu)+\omega\sigma_i}{(\sigma_i+\mu)(\gamma_i+\mu)\mu} \right) \times \frac{\beta_i}{\left(\frac{\beta_i[\omega(\gamma_i+\mu)+\omega\sigma_i]}{(\sigma_i+\mu)(\gamma_i+\mu)\mu} \right)}$$
$$= \left(\frac{\omega(\gamma_i+\mu)+\omega\sigma_i}{(\sigma_i+\mu)(\gamma_i+\mu)\mu} \right) \times \left(\frac{(\sigma_i+\mu)(\gamma_i+\mu)\mu}{\omega(\gamma_i+\mu)+\omega\sigma_i} \right)$$
$$= 1.$$

Since $S_{\beta_i} = 1$, the parameter β_i directly influences the transmission dynamics of influenza. Specifically, any increase in β_i (the transmission rate) will lead to an increase in R_{0_i}, indicating that the disease will spread more rapidly in the population. Thus, controlling β_i, through measures such as reducing contact rates or improving infection control, can directly reduce the potential for transmission of the disease.

For the parameter σ_i, the sensitivity index is given by:

$$S_{\sigma_i} = \frac{\partial R_{0_i}}{\partial \sigma_i} \times \frac{\sigma_i}{R_{0_i}}$$

Substituting the derivative:

$$S_{\sigma_i} = \left(-\frac{\omega\beta_i}{(\sigma_i+\mu)^2\mu} + \frac{\omega\beta_i(\gamma_i+\mu)\mu^2}{[(\sigma_i+\mu)(\gamma_i+\mu)\mu]^2} \right) \times \frac{\sigma_i}{R_{0_i}}$$

Substituting the expression for R_{0_i}:

$$S_{\sigma_i} = \left(\frac{-\omega\beta_i\gamma_i(\gamma_i+\mu)}{[(\sigma_i+\mu)(\gamma_i+\mu)\mu]^2} \right) \times \frac{\sigma_i}{\left(\frac{\beta_i\omega}{(\sigma_i+\mu)\mu} + \frac{\beta_i\omega\sigma_i}{(\sigma_i+\mu)(\gamma_i+\mu)\mu} \right)}$$
$$= \left(\frac{-\omega\beta_i\gamma_i(\gamma_i+\mu)}{[(\sigma_i+\mu)(\gamma_i+\mu)\mu]^2} \right) \times \frac{\sigma_i}{\left(\frac{\beta_i\omega((\gamma_i+\mu)+\sigma_i)}{(\sigma_i+\mu)(\gamma_i+\mu)\mu} \right)}$$
$$= \left(\frac{-\omega\beta_i\gamma_i(\gamma_i+\mu)}{[(\sigma_i+\mu)(\gamma_i+\mu)\mu]^2} \right) \times \left(\frac{\sigma_i(\sigma_i+\mu)(\gamma_i+\mu)\mu}{\beta_i\omega((\gamma_i+\mu)+\sigma_i)} \right)$$
$$= \frac{\gamma_i\sigma_i(\gamma_i+\mu)^2}{(\sigma_i+\mu)\mu((\gamma_i+\mu)+\sigma_i)}.$$

The sign of S_{σ_i} provides insight into how the parameter σ_i influences the basic reproduction number R_{0_i}. If $S_{\sigma_i} > 0$, this implies that increasing σ_i (the rate at which infected individuals recover or are removed from the infectious pool) decreases the basic reproduction number R_{0_i}, thereby slowing the spread of the disease. On the other hand, if $S_{\sigma_i} < 0$, it would imply that increasing σ_i leads to an increase in R_{0_i}, causing a faster spread of the disease. However, this scenario is rare in this context, as higher recovery rates typically help control outbreaks rather than accelerate them.

For the parameter γ_i, the sensitivity index is given by:

$$S_{\gamma_i} = \frac{\partial R_{0_i}}{\partial \gamma_i} \times \frac{\gamma_i}{R_{0_i}}$$

Substituting the derivative:

$$S_{\gamma_i} = \left(-\frac{\omega\beta_i\sigma_i(\sigma_i+\mu)\mu}{[(\sigma_i+\mu)(\gamma_i+\mu)\mu]^2}\right) \times \frac{\gamma_i}{R_{0_i}}$$

Substituting the expression for R_{0_i}:

$$\begin{aligned}
S_{\gamma_i} &= \left(-\frac{\omega\beta_i\sigma_i(\sigma_i+\mu)\mu}{[(\sigma_i+\mu)(\gamma_i+\mu)\mu]^2}\right) \times \frac{\gamma_i}{\left(\frac{\beta_i\omega}{(\sigma_i+\mu)\mu} + \frac{\beta_i\omega\sigma_i}{(\sigma_i+\mu)(\gamma_i+\mu)\mu}\right)} \\
&= \left(-\frac{\omega\beta_i\sigma_i(\sigma_i+\mu)\mu}{[(\sigma_i+\mu)(\gamma_i+\mu)\mu]^2}\right) \times \frac{\gamma_i}{\left(\frac{\beta_i\omega((\gamma_i+\mu)+\sigma_i)}{(\sigma_i+\mu)(\gamma_i+\mu)\mu}\right)} \\
&= \left(-\frac{\omega\beta_i\sigma_i(\sigma_i+\mu)\mu}{[(\sigma_i+\mu)(\gamma_i+\mu)\mu]^2}\right) \times \left(\frac{\gamma_i(\sigma_i+\mu)(\gamma_i+\mu)\mu}{\beta_i\omega((\gamma_i+\mu)+\sigma_i)}\right) \\
&= \frac{-\gamma_i\sigma_i}{\mu((\gamma_i+\mu)+\sigma_i)}.
\end{aligned}$$

The sensitivity index S_{γ_i} provides insight into how the parameter γ_i affects the basic reproduction number R_{0_i}. Since $S_{\gamma_i} < 0$, this indicates that increasing γ_i (which represents faster recovery or removal of infected individuals) decreases the basic reproduction number R_{0_i}. A negative value of S_{γ_i} suggests that increasing the recovery rate reduces the number of secondary infections generated by each infected individual, thereby slowing the transmission of the disease.

For the parameter μ, the sensitivity index is given by:

$$S_\mu = \frac{\partial R_{0_i}}{\partial \mu} \times \frac{\mu}{R_{0_i}}$$

Substituting the derivative:

$$S_\mu = \left(-\frac{\omega\beta_i(\sigma_i+2\mu)}{[(\sigma_i+\mu)\mu]^2} - \frac{\omega\beta_i\sigma_i(\mu(\gamma_i+\sigma_i+2\mu)+(\sigma_i+\mu)(\gamma_i+\mu))}{[(\sigma_i+\mu)(\gamma_i+\mu)\mu]^2}\right) \times \frac{\mu}{R_{0_i}}$$

Substituting the expression for R_{0_i}:

$$\begin{aligned}
S_\mu &= \left(-\frac{\omega\beta_i(2\sigma_i\gamma_i+(2+2\gamma_i+\sigma_i)\mu+(3+2\sigma_i)\mu^2)}{[(\sigma_i+\mu)(\gamma_i+\mu)\mu]^2}\right) \times \frac{\mu}{\left(\frac{\beta_i\omega}{(\sigma_i+\mu)\mu} + \frac{\beta_i\omega\sigma_i}{(\sigma_i+\mu)(\gamma_i+\mu)\mu}\right)} \\
&= \left(-\frac{\omega\beta_i(2\sigma_i\gamma_i+(2+2\gamma_i+\sigma_i)\mu+(3+2\sigma_i)\mu^2)}{[(\sigma_i+\mu)(\gamma_i+\mu)\mu]^2}\right) \times \frac{\mu}{\left(\frac{\beta_i\omega((\gamma_i+\mu)+\sigma_i)}{(\sigma_i+\mu)(\gamma_i+\mu)\mu}\right)} \\
&= \left(-\frac{\omega\beta_i(2\sigma_i\gamma_i+(2+2\gamma_i+\sigma_i)\mu+(3+2\sigma_i)\mu^2)}{[(\sigma_i+\mu)(\gamma_i+\mu)\mu]^2}\right) \times \left(\frac{\mu(\sigma_i+\mu)(\gamma_i+\mu)\mu}{\beta_i\omega((\gamma_i+\mu)+\sigma_i)}\right) \\
&= -\frac{(\gamma_i+\mu)(2\sigma_i\gamma_i+(2+2\gamma_i+\sigma_i)\mu+(3+2\sigma_i)\mu^2)}{((\sigma_i+\mu)(\gamma_i+\mu)\mu)((\gamma_i+\mu)+\sigma_i)}.
\end{aligned}$$

Since $S_\mu < 0$, increasing the natural mortality rate μ reduces R_{0_i}, thereby slowing the spread of the disease. This is expected because individuals with higher mortality will spend less time in the infectious state, reducing opportunities for transmission.

Conclusion: The recruitment rate ω and the effective transmission rate β_i have a strong positive influence on the propagation of the disease. Conversely, the parameters σ_i, γ_i, and μ play a significant role in reducing the burden of influenza infection in the population. Increasing these parameters leads to a decrease in the basic reproduction number, which in turn reduces the prevalence of the disease within the population.

9. Numerical Simulations

This section presents the numerical simulations done in Maple software, which will illustrate and support the established results in the previous sections. The parameter values used in the simulation are found in Table 2.

Description	**Parameters**	**Value**	**Unit**	**Source**
Recruitment rate	ω	3	day^{-1}	Assumed
Transmission rate of influenza	β_i	0.0011	day^{-1}	Assumed
Progression rate from E_i class to I_i class	σ_i	0.5000	day^{-1}	[34]
Recovery rate from influenza	γ_i	0.1998	day^{-1}	[35]
Natural mortality rate	μ	0.0400	day^{-1}	Assumed

Table 2. Parameter Values for the Influenza Model

Some of the parameter values in Table 2 were assumed for modeling purposes to maintain simplicity while ensuring that the basic reproduction number R_0 stays below 1, ensuring the stability of the disease-free equilibrium. The following explains the rationale behind each assumption:

Recruitment Rate $\omega = 3\,\textbf{day}^{-1}$:
The recruitment rate $\omega = 3\,\text{day}^{-1}$ was assumed to maintain a moderate and realistic inflow of susceptible individuals into the population. This value was specifically chosen so that the computed basic reproduction number $R_0^i \approx 0.4713$ remains less than 1, which satisfies the condition for the local asymptotic stability of the disease-free equilibrium. Since R_0^i is directly proportional to ω, increasing it would result in a higher reproductive number, potentially making the disease endemic. Thus, setting $\omega = 3$ strikes a balance between biological realism and the mathematical goal of exploring a stable disease-free scenario.

Transmission Rate $\beta_i = 0.0011\,\textbf{day}^{-1}$:
The transmission rate governs how efficiently the disease spreads between susceptible and infected individuals. The value $\beta_i = 0.0011\,\text{day}^{-1}$ was assumed to reflect typical influenza transmission rates in a controlled or seasonal setting, resulting in a basic reproduction number R_0 that stays below 1. This ensures that the disease will not spread indefinitely in the population under these conditions.

Natural Mortality Rate $\mu = 0.0400$ **day**$^{-1}$:

This value represents the background death rate in the population, which includes deaths unrelated to influenza infection, such as those caused by aging, accidents, or other health conditions. The assumption of $\mu = 0.0400\,\text{day}^{-1}$ (or $\frac{1}{25}\,\text{day}^{-1}$) reflects the normal rate of mortality, ensuring the population size remains realistic and doesn't grow indefinitely. It helps simulate the continuous loss of individuals from the population due to non-disease factors, enabling a more accurate representation of the influenza dynamics without allowing for unrealistic population growth.

Simulation 1. Consider the parameter values in Table 2 with $\omega = 3$. We obtain $R_{0_i} = 0.4713302753$ and the disease-free equilibrium point is $\varepsilon_{0_i} = (S, E_i, I_i, R_i) = \left(\frac{\omega}{\mu}, 0, 0, 0\right) = (75, 0, 0, 0)$. To support our result, we take the following initial conditions:

$$(a)\ \ (S, E_i, I_i, R_i) = (100, 50, 10, 1) \qquad (b)\ \ (S, E_i, I_i, R_i) = (200, 60, 20, 2)$$

$$(c)\ \ (S, E_i, I_i, R_i) = (300, 70, 30, 3) \qquad (d)\ \ (S, E_i, I_i, R_i) = (500, 90, 50, 4)$$

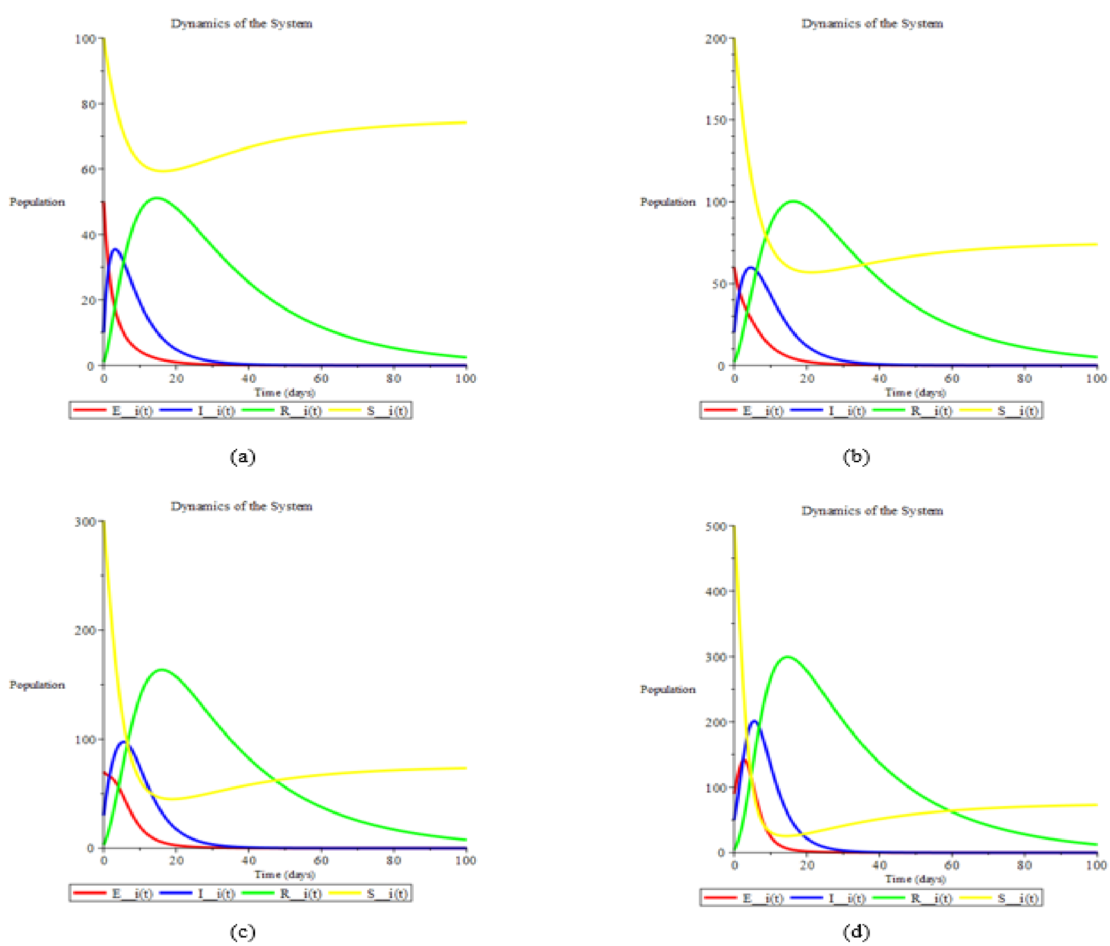

FIGURE 2. (Simulation 1) The Influenza model is locally asymptotically stable at ε_{0_i} when $R_{0_i} < 1$.

Figure 2 shows that for different initial conditions, the lines of the solutions converge to $\varepsilon_{0_i} = (75, 0, 0, 0)$. This implies that the influenza model is locally asymptotically stable at the disease-free equilibrium point when $R_{0_i} < 1$.

Simulation 2. Consider the same parameter values as in Simulation 1, except for the increased value of $\beta_i = 0.0060$. As a result, R_{0_i} becomes 2.5708924106, and the disease-free equilibrium point remains unchanged at $\varepsilon_{0_i} = (S, E_i, I_i, R_i) = \left(\frac{\omega}{\mu}, 0, 0, 0\right) = (75, 0, 0, 0)$.

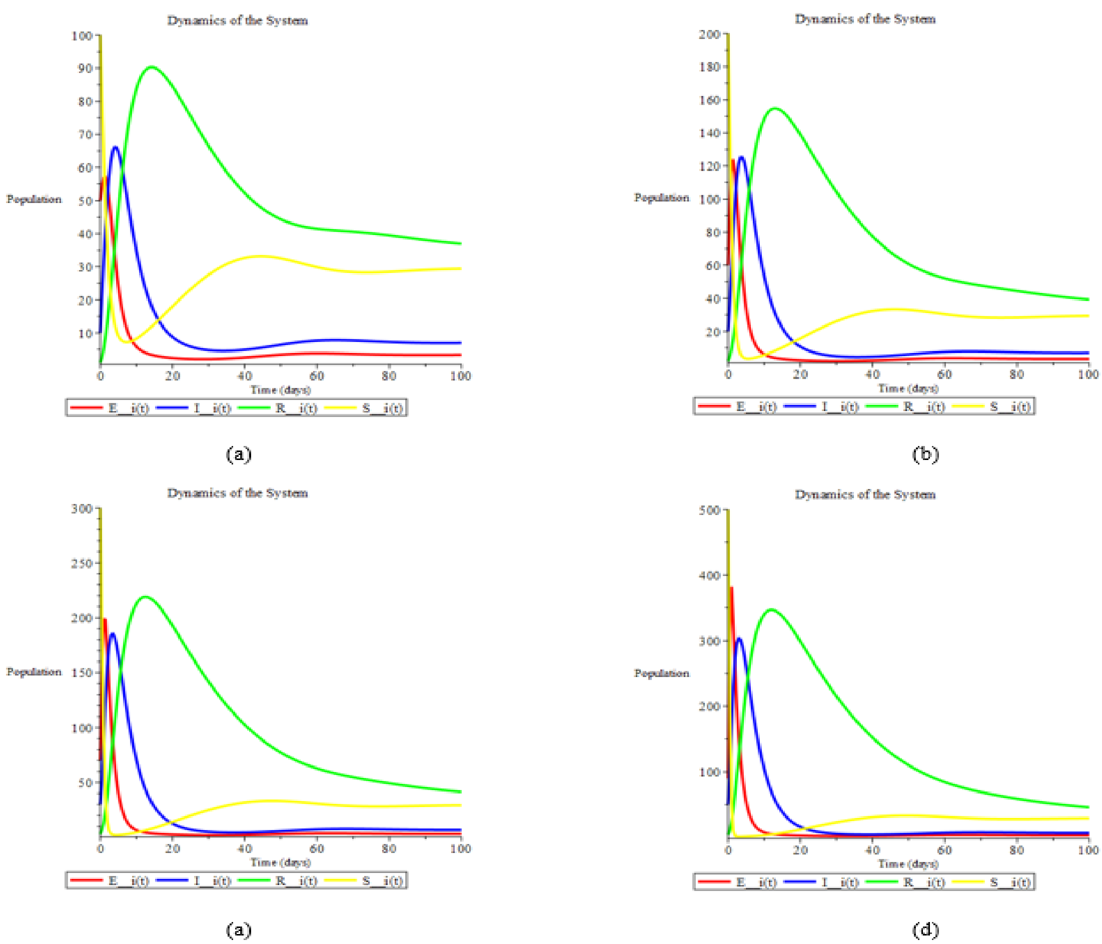

FIGURE 3. (Simulation 2) The influenza model is locally asymptotically stable at ε_{1_i} when $R_{0_i} > 1$.

By using the same initial conditions as in Simulation 1, we observe from Figure 2 that the lines of the solutions do not converge to $\varepsilon_{0_i} = (75, 0, 0, 0)$. This indicates that the influenza model is unstable at the disease-free equilibrium point when $R_{0_i} > 1$. Moreover, since we have obtained $R_{0_i} = 2.570892410$ and the endemic equilibrium $\varepsilon_{1_i} = (29, 3, 7, 35)$ now exists, we observe that the lines of the solutions converge to $\varepsilon_{1_i} = (29, 3, 7, 35)$. Therefore, the influenza model is locally asymptotically stable at the endemic point whenever $R_{0_i} > 1$.

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Ethical Considerations. This study employed a mathematical modeling approach (SEIR model) to analyze the transmission dynamics of influenza. No experiments were conducted involving human participants or animals. All data utilized were secondary, aggregated, and publicly available, ensuring that no personal or sensitive information was disclosed. The paper adhered to ethical standards for academic integrity, data privacy, and responsible scientific reporting.

Conflicts of Interest. The authors declare that there are no conflicts of interest regarding the publication of this paper.

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