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Mathematical Analysis of a SEIR Model with Nonlinear Incidence Rate for COVID-19 Dynamics

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Author's contribution

The sole author designed, analysed, interpreted and prepared the manuscript.

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Abstract

In this paper, an SEIR epidemic model with nonlinear incidence is considered. First, we formulate the model and obtain its basic properties. Then, we find the equilibrium points of the model, the disease-free and the endemic equilibrium. The stability of disease-free and endemic equilibrium is associated with the basic reproduction number $\mathcal{R}$. If the basic reproduction number $\mathcal{R} < 1$, the disease-free equilibrium $\bar{\mathcal{E}}$ is locally as well as globally asymptotically stable. Moreover, if the basic reproduction number $\mathcal{R} > 1$, the disease is uniformly persistent and the unique endemic equilibrium $\mathcal{E}^*$ of the system is locally as well as globally asymptotically stable under certain conditions. Finally, the numerical results justify the analytical results.

Keywords: SEIR epidemic model; nonlinear incidence rate; local stability; global stability; Lyapunov function; LaSalle's invariance principle.

2010 Mathematics Subject Classification: 34K20; 34D23; 37B25; 49K40; 92D25.

1 Introduction

The global health crisis of the Coronavirus Covid-19 has brought out the role of mathematical models in political and health decision-making. Since the outbreak began in Wuhan, several modeling

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groups around the world have reported estimates and forecasts for the COVID-19 outbreak in the scientific literature. Depending on the models and methods used, the results obtained show large variations (estimated basic reproduction number varies from 2 to 6, peaks reached, total number of infected people varies from 50,000 to millions, etc.). This problem of variability can be partially explained by the lack of reliable data, in particular before January 23, 2019, when Wuhan, the epicenter of the epidemic, was quarantined and locked down. With the exception of confirmed case data which is used for model calibration, an inadequate choice of model used for the problem at hand, a model calibration problem, the use of data from different sources may explain these variations. Mathematical models of infectious diseases [1, 2, 3, 4, 5], initially purely theoretical tools, began to be put into practice with the problem of AIDS in the 1980s. During the Covid 19 pandemic, mathematical models experienced a boom during the taking of decision relating to public health policies and also contributed to the epidemiological surveillance of the disease. Long before that, since the Spanish influenza pandemic, compartmental models have been used to aid in contagion probability calculations. These models divide the population into epidemiological classes. Compartmental models make it possible to estimate how the number of individuals in each compartment varies over time. By abuse of notation, the letter used to represent a compartment is also used to represent the number of individuals in the compartment. For example, S is used in an equation to represent the number of susceptible individuals. A more rigorous formulation, and sometimes employed, is to use $S(t)$ instead of S, which explains that it is a function and that the number depends on time t. To know how the number of individuals in a compartment varies over time, it is necessary to know how to deduce the number of individuals from one stage to another, that is to say from time t at time $t + 1$. This difference in the number of individuals is given by the derivative. Thus, dS/dt corresponds to the balance of the number of individuals in relation to compartment S. A negative scale means that individuals leave, while a positive scale means that individuals enter. The dI/dt scale is called incidence because it represents the number of infections of the disease. The main indicator in the spread of an epidemic is the force of infection or the rate at which a susceptible person becomes infected. The prediction models are mainly based on deterministic principles such as SIR or SEIR [6, 7, 8, 9, 10, 11]. Recent SARS-CoV-2 models are often derived from the SIR model by adding a population of infected non-infectious E (or exposed) individuals who are therefore not contagious. In this article, we have introduced the SEIR model and we have discussed the effect of health measures by illustrating their impact on the epidemic evolution. Several research teams are interested in the potential of mathematical models in the development of new tools and methods to control the spread of a disease [12, 9]. To conclude, it should be remembered that models remain mathematical tools that help predict the evolution of a given epidemic; they are certainly precise and rigorous, but calculated at a given moment, with given parameters and in a rather ideal context. Modeling the incidence rate, the virus evolution (possible mutation) and all other parameters to the situation is extremely difficult. This is why, like surveys and statistics, it is necessary to use them, to know how to read them but also to understand them. We must therefore find the right balance between: seriously considering the epidemic models obtained after modeling and taking a step back from the situation.

Therefore, in the present article, we shall revisit and analyse the SEIR model for COVID-19 dynamics but with a non-linear incidence rate. The structure of this article is as follows. The basic model and its properties are discussed in Section 2. In Section 3, the local stability of the disease-free and the endemic equilibrium points is discussed. The global stability of the disease-free and the endemic equilibrium points is discussed in Section 4. Finally, in section 5, numerical results, validating the theoretical findings, are presented.

2 Mathematical Model and Results

We recall that the SEIR model has four population classes ($S(t)$ for susceptible, $E(t)$ for exposed, $I(t)$ for infected, and $R(t)$ for recovered class). The SEIR model, however relatively simple, therefore makes it possible to obtain a first model of an epidemic and to observe the impact of health measures on its development. In this paper, we assume that recovered individuals will not re-infect in the future. Consider ρ to be the constant recruitment rate of susceptible due to new born and immigration. The saturated incidence rate considered here is nonlinear of Monod's form $\frac{\mu I}{k+I}$ where μ and k are two constants. σ_1 is the rate at which an exposed individuals become infectious and σ_2 is the rate at which infectious agents recover their health. Therefore $1/\sigma_1$ represents the average latency time spent in compartment E and $1/\sigma_2$ represents the average duration elapsed in compartment I. d_s, d_e, d_i and d_r represents the death rates of susceptible, exposed, infected and recovered individuals, respectively.

The SEIR model for COVID-19 dynamics that we considered in this paper is given by the following ordinary differential equations:

$$\begin{cases} \dot{S} &= \rho - \frac{\mu SI}{k+I} - d_s S, \\ \dot{E} &= \frac{\mu SI}{k+I} - \sigma_1 E - d_e E, \\ \dot{I} &= \sigma_1 E - \sigma_2 I - d_i I, \\ \dot{R} &= \sigma_2 I - d_r R, \end{cases} \tag{2.1}$$

with positive initial condition $(S_0, E_0, I_0, R_0) \in \mathbb{R}^4_+$.

Table 1. Description of the variables and parameters for model (2.1)

$S(t)$	Susceptible individuals	ρ	Susceptible recruitment rate
$E(t)$	Exposed individuals	σ_1	Infection rate of exposed individuals
$I(t)$	Infected individuals	σ_2	Recover rate of infected individuals
$R(t)$	Recovered individuals	d_s	Death rate of susceptible individuals
		d_e	Death rate of exposed individuals
		d_i	Death rate of infected individuals
		d_r	Death rate of recovered individuals

In order to prove that the system (2.1) is well-posed, it is necessary that the state variables $S(t), E(t), I(t)$ and $R(t)$ remain non-negative for all $t \geq 0$. Let $d = \min(d_s, d_e, d_i, d_r)$, then

Proposition 1. The compact set $\Omega_1 = \{(S, E, I, R) \in \mathbb{R}^4_+ \ / \ S+E+I+R \leq \frac{\rho}{d}\}$ is positively invariant for system (2.1).

Proof. Since $\dot{S}_{|S=0} = \rho > 0$, $\dot{E}_{|E=0} = \frac{\mu SI}{k+I} > 0$, $\dot{I}_{|I=0} = \sigma_1 E > 0$ and $\dot{R}_{|R=0} = \sigma_2 I > 0$ then the solution of system (2.1) is non-negative.

By summing all equations of system (2.1), one obtains, for $T = S+E+I+R-\frac{\rho}{d}$, a single equation:

$$\begin{aligned} \dot{T} &= \dot{S} + \dot{E} + \dot{I} + \dot{R} \\ &= \rho - d_s S - d_e E - d_i I - d_r R \\ &\leq \rho - dS - dE - dI - dR \\ &\leq d(\frac{\rho}{d} - S - E - I - R) \\ &\leq -dT. \end{aligned}$$

Hence

$$T(t) \leq T(0)e^{-dt}. \tag{2.2}$$

Since all variables are non-negative then all variables are bounded and thus Ω_1 is invariant for model (2.1). □

For any disease, a major health issue is whether it is spreading in the population and at what speed (doubling time). This amounts to calculating the average number of people that an infectious person infects while they are contagious. This rate is called the basic reproduction number [12], and is denoted $\mathcal{R}$ (ratio). This rate is intuitively easy to understand, but if it is linked to the pathogen, its calculation is complex. $\mathcal{R}$ should be used with caution, as it can lead to misinterpretations, both on the real role that $\mathcal{R}$ has on the spread of an infectious disease and on the ability to control an epidemic. The calculation of the $\mathcal{R}$ presupposes a population where all the individuals are healthy, except the infectious individual introduced (patient zero). If $\mathcal{R} < 1$, then the infected individual infects less than one other individual on average, which means that the disease is disappearing from the population. If $\mathcal{R} > 1$, then the disease spreads in the population and becomes epidemic. Determining $\mathcal{R}$ as a function of the model parameters thus makes it possible to calculate the conditions under which the disease spreads. As van den Driessche and Watmough [13] note, "in the case of a single infected compartment, $\mathcal{R}$ is simply the product of the infection rate and its average duration". When the model is simple, it is often possible to find an exact expression for $\mathcal{R}$. In our case, the basic reproduction number $\mathcal{R}$ is given by

$$\mathcal{R} = \frac{\rho\sigma_1\mu}{kd_s(d_e+\sigma_1)(d_i+\sigma_2)}. \tag{2.3}$$

Proposition 2. System (2.1) admits a unique disease-free equilibrium $\bar{\mathcal{E}} = (\frac{\rho}{d_s}, 0, 0, 0)$ and a unique endemic equilibrium $\mathcal{E}^* = (S^*, E^*, I^*, R^*)$ with $S^*, E^*, I^*, R^* > 0$.

Proof. Equilibria of system (2.1) satisfy

$$\begin{cases} 0 = \rho - \dfrac{\mu SI}{k+I} - d_s S, \\ 0 = \dfrac{\mu SI}{k+I} - \sigma_1 E - d_e E, \\ 0 = \sigma_1 E - \sigma_2 I - d_i I, \\ 0 = \sigma_2 I - d_r R, \end{cases} \tag{2.4}$$

which reduces to

$$\begin{cases} S = \dfrac{\rho}{d_s + \dfrac{\mu I}{k+I}} = \dfrac{\rho(k+I)}{d_s(k+I)+\mu I}, \\ E = \dfrac{\mu SI}{(k+I)(d_e+\sigma_1)} = \dfrac{\rho\mu I}{(d_e+\sigma_1)(d_s(k+I)+\mu I)}, \\ I = \dfrac{\sigma_1 E}{d_i+\sigma_2} = \dfrac{\sigma_1\rho\mu I}{(d_i+\sigma_2)(d_e+\sigma_1)(d_s(k+I)+\mu I)}, \\ R = \dfrac{\sigma_2}{d_r} I. \end{cases} \tag{2.5}$$

From the third equation of (2.5) one deduces that

$$I(d_i+\sigma_2)(d_e+\sigma_1)(d_s(k+I)+\mu I) = \sigma_1\rho\mu I.$$

Since all parameters are non-negative then either $I = 0$ or

$$(d_i+\sigma_2)(d_e+\sigma_1)(d_s(k+I)+\mu I) = \sigma_1\rho\mu.$$

- If $I = 0$ then $S = \frac{\rho}{d_s}, E = 0$ and $R = 0$. This equilibrium known as the disease-free equilibrium denoted here by $\bar{\mathcal{E}} = (\frac{\rho}{d_s}, 0, 0, 0)$.
- If $I \neq 0$, let the function g given by

$$\begin{aligned} I &= \frac{\sigma_1\rho\mu}{(d_s+\mu)(d_i+\sigma_2)(d_e+\sigma_1)} - \frac{kd_s}{(d_s+\mu)} \\ &= \frac{kd_s}{(d_s+\mu)}\Big(\frac{\sigma_1\rho\mu}{kd_s(d_i+\sigma_2)(d_e+\sigma_1)} - 1\Big) \\ &= \frac{kd_s}{(d_s+\mu)}(\mathcal{R}-1). \end{aligned}$$

Since $\mathcal{R} > 1$, then the system admits endemic equilibrium $\mathcal{E}^* = (S^*, E^*, I^*, R^*)$ where

$$\begin{cases} I^* = \frac{kd_s}{(d_s+\mu)}(\mathcal{R}-1), \\ S^* = \frac{\rho(k+I^*)}{d_s(k+I^*)+\mu I^*}, \\ E^* = \frac{\rho\mu I^*}{(d_e+\sigma_1)(d_s(k+I^*)+\mu I^*)}, \\ R^* = \frac{\sigma_2}{d_r}I^*. \end{cases} \tag{2.6}$$

□

Next, the local stability behaviours of equilibria are discussed with respect to the value of the basic reproduction number $\mathcal{R}$.

3 Local Stability Analysis

Theorem 1. If $\mathcal{R} < 1$, then the equilibrium point $\bar{\mathcal{E}}$ is locally asymptotically stable. However, if $\mathcal{R} > 1$, $\bar{\mathcal{E}}$ is unstable.

Proof. Let (S, E, I, R) be a solution of system (2.1), then the Jacobian matrix is given by:

$$J = \begin{pmatrix} -(d_s + \frac{\mu I}{k+I}) & 0 & -\frac{\mu kS}{(k+I)^2} & 0 \\ \frac{\mu I}{k+I} & -(d_e+\sigma_1) & \frac{\mu kS}{(k+I)^2} & 0 \\ 0 & \sigma_1 & -(d_i+\sigma_2) & 0 \\ 0 & 0 & \sigma_2 & -d_r \end{pmatrix}.$$

In particular its value at the equilibrium point $\bar{\mathcal{E}}$ is

$$\bar{J} = \begin{pmatrix} -d_s & 0 & -\frac{\mu\rho}{kd_s} & 0 \\ 0 & -(d_e+\sigma_1) & \frac{\mu\rho}{kd_s} & 0 \\ 0 & \sigma_1 & -(d_i+\sigma_2) & 0 \\ 0 & 0 & \sigma_2 & -d_r \end{pmatrix}$$

The matrix $\bar{J}$ admits two eigenvalues given by $\rho_1 = -d_s < 0$ and $\rho_2 = -d_r < 0$ and two other eigenvalues of the sub-matrix

$$S_{j_0} = \begin{pmatrix} -(d_e+\sigma_1) & \frac{\mu\rho}{kd_s} \\ \sigma_1 & -(d_i+\sigma_2) \end{pmatrix}.$$

The trace is given by

$$\text{Trace } (S_{j_0}) = -(d_e + \sigma_1 + d_i + \sigma_2) < 0$$

and the determinant is given by

$$\text{Det } (S_{j_0}) = (d_e + \sigma_1)(d_i + \sigma_2) - \frac{\sigma_1 \mu \rho}{k d_s} = (d_e + \sigma_1)(d_i + \sigma_2)(1 - \Re).$$

Therefore all eigenvalues have negative real parts and the equilibrium $\bar{\mathcal{E}}$ is locally asymptotically if $\Re < 1$. However, if $\Re > 1$, at least one eigenvalue has non negative real part and the equilibrium $\bar{\mathcal{E}}$ is therefore unstable. □

Theorem 2. The endemic equilibrium $\mathcal{E}^*$ is locally asymptotically stable if $\Re > 1$.

Proof. For the equilibrium point $\mathcal{E}^*$, the Jacobian is given by

$$J^* = \begin{pmatrix} -(d_s + \frac{\mu I^*}{k + I^*}) & 0 & -\frac{\mu k S^*}{(k + I^*)^2} & 0 \\ \frac{\mu I^*}{k + I^*} & -(d_e + \sigma_1) & \frac{\mu k S^*}{(k + I^*)^2} & 0 \\ 0 & \sigma_1 & -(d_i + \sigma_2) & 0 \\ 0 & 0 & \sigma_2 & -d_r \end{pmatrix}$$

and its characteristic polynomial is then

$$\begin{aligned}
P(X) &= \begin{vmatrix} -(X + d_s + \frac{\mu I^*}{k + I^*}) & 0 & -\frac{\mu k S^*}{(k + I^*)^2} & 0 \\ \frac{\mu I^*}{k + I^*} & -(X + d_e + \sigma_1) & \frac{\mu k S^*}{(k + I^*)^2} & 0 \\ 0 & \sigma_1 & -(X + d_i + \sigma_2) & 0 \\ 0 & 0 & \sigma_2 & -(X + d_r) \end{vmatrix} \\
&= \begin{vmatrix} -(X + d_s) & -(X + d_e + \sigma_1) & 0 & 0 \\ \frac{\mu I^*}{k + I^*} & -(X + d_e + \sigma_1) & \frac{\mu k S^*}{(k + I^*)^2} & 0 \\ 0 & \sigma_1 & -(X + d_i + \sigma_2) & 0 \\ 0 & 0 & \sigma_2 & -(X + d_r) \end{vmatrix} \\
&= -(X + d_r) \begin{vmatrix} -(X + d_s) & -(X + d_e + \sigma_1) & 0 \\ \frac{\mu I^*}{k + I^*} & -(X + d_e + \sigma_1) & \frac{\mu k S^*}{(k + I^*)^2} \\ 0 & \sigma_1 & -(X + d_i + \sigma_2) \end{vmatrix} \\
&= (X + d_r)(X + d_s) \begin{vmatrix} -(X + d_e + \sigma_1) & \frac{\mu k S^*}{(k + I^*)^2} \\ \sigma_1 & -(X + d_i + \sigma_2) \end{vmatrix} \\
&\quad + \frac{\mu I^*}{k + I^*}(X + d_r) \begin{vmatrix} -(X + d_e + \sigma_1) & 0 \\ \sigma_1 & -(X + d_i + \sigma_2) \end{vmatrix} \\
&= (X + d_r)(X + d_s)\Big((X + d_e + \sigma_1)(X + d_i + \sigma_2) - \frac{\sigma_1 \mu k S^*}{(k + I^*)^2}\Big) \\
&\quad + \frac{\mu I^*}{k + I^*}(X + d_r)(X + d_e + \sigma_1)(X + d_i + \sigma_2).
\end{aligned}$$

Then $\rho_1 = -d_r < 0$ is an eigenvalue. The other three eigenvalues are the roots of

$$\begin{aligned}
Q(X) &= (X+d_s)\Big((X+d_e+\sigma_1)(X+d_i+\sigma_2) - \frac{\sigma_1\mu k S^*}{(k+I^*)^2}\Big) \\
&\quad + \frac{\mu I^*}{k+I^*}(X+d_e+\sigma_1)(X+d_i+\sigma_2) \\
&= X^3 + X^2(d_s+d_e+\sigma_1+d_i+\sigma_2+\frac{\mu I^*}{k+I^*}) \\
&\quad + X\Big(d_s(d_e+\sigma_1)+d_s(d_i+\sigma_2)+(d_e+\sigma_1)(d_i+\sigma_2) \\
&\quad - \frac{\sigma_1\mu k S^*}{(k+I^*)^2} + \frac{\mu I^*}{k+I^*}(d_e+\sigma_1+d_i+\sigma_2)\Big) + d_s(d_e+\sigma_1)(d_i+\sigma_2) - \frac{d_s\sigma_1\mu k S^*}{(k+I^*)^2} \\
&\quad + \frac{\mu I^*}{k+I^*}(d_e+\sigma_1)(d_i+\sigma_2) \\
&= X^3 + a_2X^2 + a_1X + a_0
\end{aligned}$$

where

$$\begin{aligned}
a_2 &= d_s+d_e+\sigma_1+d_i+\sigma_2+\frac{\mu I^*}{k+I^*}, \\
a_1 &= d_s(d_e+\sigma_1)+d_s(d_i+\sigma_2)+(d_e+\sigma_1)(d_i+\sigma_2) - \frac{\sigma_1\mu k S^*}{(k+I^*)^2} + \frac{\mu I^*}{k+I^*}(d_e+\sigma_1+d_i+\sigma_2), \\
a_0 &= d_s(d_e+\sigma_1)(d_i+\sigma_2) - \frac{d_s\sigma_1\mu k S^*}{(k+I^*)^2} + \frac{\mu I^*}{k+I^*}(d_e+\sigma_1)(d_i+\sigma_2).
\end{aligned}$$

Using the fact that $\frac{\mu k}{(k+I^*)^2} \le \frac{\mu}{k+I^*}$, $\frac{\sigma_1\mu S^*}{k+I^*} = (d_e+\sigma_1)(d_i+\sigma_2)$, and therefore $(d_e+\sigma_1)(d_i+\sigma_2) - \frac{\sigma_1\mu k S^*}{(k+I^*)^2} \ge 0$, we obtain

$$\begin{aligned}
a_2 &= d_s+d_e+\sigma_1+d_i+\sigma_2+\frac{\mu I^*}{k+I^*} > 0, \\
a_1 &= d_s(d_e+\sigma_1)+d_s(d_i+\sigma_2)+(d_e+\sigma_1)(d_i+\sigma_2) - \frac{\sigma_1\mu k S^*}{(k+I^*)^2} + \frac{\mu I^*}{k+I^*}(d_e+\sigma_1+d_i+\sigma_2) \\
&> d_s(d_e+\sigma_1)+d_s(d_i+\sigma_2)+\frac{\mu I^*}{k+I^*}(d_e+\sigma_1+d_i+\sigma_2) > 0, \\
a_0 &= d_s((d_e+\sigma_1)(d_i+\sigma_2) - \frac{\sigma_1\mu k S^*}{(k+I^*)^2}) + \frac{\mu I^*}{k+I^*}(d_e+\sigma_1)(d_i+\sigma_2) \\
&> \frac{\mu I^*}{k+I^*}(d_e+\sigma_1)(d_i+\sigma_2) > 0, \\
a_2a_1 - a_0 &= \Big(d_s+d_e+\sigma_1+d_i+\sigma_2+\frac{\mu I^*}{k+I^*}\Big)\Big(d_s(d_e+\sigma_1)+d_s(d_i+\sigma_2)+(d_e+\sigma_1)(d_i+\sigma_2) \\
&\quad - \frac{\sigma_1\mu k S^*}{(k+I^*)^2} + f(I^*)(d_e+\sigma_1+d_i+\sigma_2)\Big) - d_s(d_e+\sigma_1)(d_i+\sigma_2) + \frac{d_s\sigma_1\mu k S^*}{(k+I^*)^2} \\
&\quad - \frac{\mu I^*}{k+I^*}(d_e+\sigma_1)(d_i+\sigma_2) \\
&> \Big(d_s+d_e+\sigma_1+d_i+\sigma_2+\frac{\mu I^*}{k+I^*}\Big)\Big(d_s(d_e+\sigma_1)+d_s(d_i+\sigma_2)+\frac{\mu I^*}{k+I^*}(d_e+\sigma_1+d_i+\sigma_2)\Big) \\
&\quad - d_s(d_e+\sigma_1)(d_i+\sigma_2) + \frac{d_s\sigma_1\mu k S^*}{(k+I^*)^2} - \frac{\mu I^*}{k+I^*}(d_e+\sigma_1)(d_i+\sigma_2) \\
&> \Big(d_s+d_e+\sigma_1+\frac{\mu I^*}{k+I^*}\Big)\Big(d_s(d_e+\sigma_1)+d_s(d_i+\sigma_2)+\frac{\mu I^*}{k+I^*}(d_e+\sigma_1+d_i+\sigma_2)\Big) \\
&\quad + \frac{d_s\sigma_1\mu k S^*}{(k+I^*)^2} > 0.
\end{aligned}$$

Then Routh Hurwitz criterion states that all eigenvalues have negative real parts. Therefore, the equilibrium E^* (exists if $\mathcal{R}_0 > 1$) is locally asymptotically stable. The proof is completed. □

In the next section, the global stability behaviour of the equilibrium points will be carried out.

4 Global Stability Analysis

Lemma 1. $\Omega_2 = \{(S,E,I,R) \in \mathbb{R}^4_+ \ / \ S+E+I+R \leq \frac{\rho}{m}; S \leq \frac{\rho}{d_s}\}$ is a positively invariant set for system (2.1).

Proof. It is already proved that Ω_1 is a positively invariant set for system (2.1). Note that $\dot{S}(t) = \rho - d_s S - f(I)S \leq \rho - d_s S < 0$ for $S(t) > \frac{\rho}{d_s}$ therefore $\liminf S(t) \leq \frac{\rho}{d_s}$.

For all $\xi > 0$, and for all $S_0 \geq 0$, $\exists T \geq 0$ such that $S(t) \leq \frac{\rho}{d_s} + \xi$, $\forall t \geq T$. This completes the proof. □

Theorem 3. $\bar{\mathcal{E}}$ is globally asymptotically stable if $\mathcal{R} \leq 1$. However $\bar{\mathcal{E}}$ is unstable if $\mathcal{R} > 1$.

Proof. Consider the Lyapunov function:

$$\mathrm{F}_1 = \sigma_1 E + (d_e + \sigma_1) I.$$

The time-derivative of F_1 is given by:

$$\begin{aligned}
\dot{\mathrm{F}}_1 &= \sigma_1 \dot{E} + (d_e+\sigma_1)\dot{I} \\
&= \sigma_1 (\frac{\mu S I}{k+I} - (d_e+\sigma_1)E) + (d_e+\sigma_1)(\sigma_1 E - (d_i+\sigma_2)I) \\
&= \sigma_1 \frac{\mu S I}{k+I} - (d_e+\sigma_1)(d_i+\sigma_2)I \\
&\leq \frac{\sigma_1 \mu S I}{k} - (d_e+\sigma_1)(d_i+\sigma_2)I \\
&= (d_e+\sigma_1)(d_i+\sigma_2)\Big(\frac{\sigma_1 \mu S}{k(d_e+\sigma_1)(d_i+\sigma_2)} - 1\Big)I \\
&\leq (d_e+\sigma_1)(d_i+\sigma_2)\Big(\frac{\sigma_1 \mu \rho}{k d_s (d_e+\sigma_1)(d_i+\sigma_2)} - 1\Big)I \ , \text{ since } S \leq \frac{\rho}{d_s} \\
&= (d_e+\sigma_1)(d_i+\sigma_2)(\mathcal{R}-1)I, \quad \forall (S,E,I,R) \in \Omega_2.
\end{aligned}$$

If $\mathcal{R} \leq 1$, then $\dot{\mathrm{F}}_1 \leq 0 \ \forall \ S,E,I,R > 0$. Let $W_1 = \{(S,E,I,R) : \dot{\mathrm{F}}_1 = 0\}$. It can be easily shown that $W_1 = \{\bar{\mathcal{E}}\}$. Using LaSalle's invariance principle [14] (see [15, 16, 17, 9, 10, 11, 18, 19] for more applications), one can easily deduce that $\bar{\mathcal{E}}$ is GAS when $\mathcal{R} \leq 1$. Then the solution of system (2.1) converges to $\bar{\mathcal{E}}$ since $t \to +\infty$. □

Theorem 4. If $\mathcal{R} > 1$, then the endemic equilibrium $\mathcal{E}^*$ is globally asymptotically stable.

Proof. Again we use a Lyapunov function given by

$$\mathrm{F}_2 = (S - S^* \ln(\frac{S}{S^*})) + (E - E^* \ln(\frac{E}{E^*})) + \frac{d_e+\sigma_1}{\sigma_1}(I - I^* \ln(\frac{I}{I^*}))$$

The function F_2 admits its minimum value $\mathrm{F}_{min} = S^* + E^* + \frac{d_e+\sigma_1}{\sigma_1} I^*$ when $S = S^*, E = E^*, I = I^*$.

The time-derivative of F_2, along solutions of system (2.1) is given by:

$$\begin{aligned}
\dot{\mathrm{F}}_2 &= (1 - \frac{S^*}{S})\dot{S} + (1 - \frac{E^*}{E})\dot{E} + \frac{d_e+\sigma_1}{\sigma_1}(1 - \frac{I^*}{I})\dot{I} \\
&= (1 - \frac{S^*}{S})(\rho - d_s S - \frac{\mu S I}{k+I}) + (1 - \frac{E^*}{E})(\frac{\mu S I}{k+I} - (d_e+\sigma_1)E) \\
&\quad + \frac{d_e+\sigma_1}{\sigma_1}(1 - \frac{I^*}{I})(\sigma_1 E - (d_i+\sigma_2)I).
\end{aligned}$$

Applying the steady state conditions for $\mathcal{E}^*$

$$\rho = d_s S^* + \frac{\mu S^* I^*}{k + I^*},\ \frac{\mu S^* I^*}{k + I^*} = (d_e + \sigma_1)E^*,\ \sigma_1 E^* = (d_i + \sigma_2)I^*,$$

we get

$$\begin{aligned}
\dot{\mathrm{F}}_2 &= (1 - \frac{S^*}{S})\Big(d_s S^* - d_s S + \frac{\mu S^* I^*}{k + I^*} - \frac{\mu SI}{k + I}\Big) + \frac{\mu SI}{k + I} - (d_e + \sigma_1)E - \frac{\mu SI}{k + I}\frac{E^*}{E} \\
&\quad + (d_e + \sigma_1)E^* + \frac{d_e + \sigma_1}{\sigma_1}\Big(\sigma_1 E - (d_i + \sigma_2)I - \sigma_1 E\frac{I^*}{I} + (d_i + \sigma_2)I^*\Big) \\
&= (1 - \frac{S^*}{S})(d_s S^* - d_s S) + \frac{\mu S^* I^*}{k + I^*} - \frac{\mu S^* I^*}{k + I^*}\frac{S^*}{S} + \frac{\mu S^* I}{k + I} - \frac{\mu SI}{k + I}\frac{E^*}{E} \\
&\quad + (d_e + \sigma_1)E^* - \frac{d_e + \sigma_1}{\sigma_1}(d_i + \sigma_2)I - (d_e + \sigma_1)E\frac{I^*}{I} + \frac{d_e + \sigma_1}{\sigma_1}(d_i + \sigma_2)I^* \\
&= d_s(1 - \frac{S^*}{S})(S^* - S) + \frac{\mu S^* I^*}{k + I^*} - \frac{\mu S^* I^*}{k + I^*}\frac{S^*}{S} + \frac{\mu S^* I}{k + I} - \frac{\mu SI}{k + I}\frac{E^*}{E} + \frac{\mu S^* I^*}{k + I^*} \\
&\quad - \frac{\mu S^* I^*}{k + I^*}\frac{I}{I^*} - \frac{\mu S^* I^*}{k + I^*}\frac{E}{E^*}\frac{I^*}{I} + \frac{\mu S^* I^*}{k + I^*} \\
&= d_s(1 - \frac{S^*}{S})(S^* - S) + \frac{\mu S^* I^*}{k + I^*}\Big(4 - \frac{S^*}{S} - \frac{E}{E^*}\frac{I^*}{I} - \frac{k + I}{k + I^*} - \frac{S}{S^*}\frac{E^*}{E}\frac{k + I^*}{k + I}\frac{I}{I^*}\Big) \\
&\quad + \frac{\mu S^* I^*}{k + I^*}\Big(\frac{I}{I^*} - \frac{I(k + I^*)}{I^*(k + I)}\Big)\Big(\frac{I^*(k + I)}{I(k + I^*)} - 1\Big).
\end{aligned}$$

By using the rule

$$x_1 + x_2 + x_3 + x_4 \geq 4\sqrt[4]{x_1 \cdot x_2 \cdot x_3 \cdot x_4},\quad x_1, x_2, x_3, x_4 \geq 0 \tag{4.1}$$

then $\Big(4 - \frac{S^*}{S} - \frac{E}{E^*}\frac{I^*}{I} - \frac{k + I}{k + I^*} - \frac{S}{S^*}\frac{E^*}{E}\frac{k + I^*}{k + I}\frac{I}{I^*}\Big) \leq 0.$

Now, using the fact that $\Big(\frac{I}{I^*} - \frac{I(k + I^*)}{I^*(k + I)}\Big)\Big(\frac{I^*(k + I)}{I(k + I^*)} - 1\Big) \leq 0$. Therefore $\dot{\mathrm{F}}_2 \leq 0$. Thank's to Lyapunov theorem, $\mathcal{E}^*$ is stable.

It remains to show that $\mathcal{E}^*$ is asymptotically stable using the Lasalle invariance principle.

Then $\dot{\mathrm{F}}_2(S, E, I, R) = 0$ if and only if $S = S^*$ and $\frac{E}{E^*} = \frac{I}{I^*}$. Let $a = \frac{E}{E^*} = \frac{I}{I^*}$, then $E = aE^*$ and $I = aI^*$.

The endemic equilibrium satisfies

$$\begin{cases}
\rho = d_s S^* + \dfrac{\mu S^* I^*}{k + I^*}, \\
\dfrac{\mu S^* I^*}{k + I^*} = (d_e + \sigma_1)E^*, \\
\sigma_1 E^* = (d_i + \sigma_2)I^*, \\
\sigma_2 I^* = d_r R^*,
\end{cases} \tag{4.2}$$

Then $a = 1$. Therefore $I = I^*$ and $E = E^*$.

Finally $\dot{\mathrm{F}}_2(S, E, I, R) = 0$ if and only if $S = S^*, E = E^*, I = I^*$ and $R = R^*$.

Therefore, the largest invariant set contained in the set $\{(S, E, I, R)\,|\dot{\mathrm{F}}_2 = 0\}$ is reduced to the singleton set $\{\mathcal{E}^*\}$. Applying LaSalle's invariance principle [14] (see [18, 19, 20, 21, 22, 23] for other applications), one can deduce that $\mathcal{E}^*$ is GAS when $\mathcal{R} > 1$. □

5 Numerical Simulations

The aim of this work is to study and analyze the dynamic behavior of an SEIR epidemic model with a nonlinear incidence rate. Consider system (2.1) with the parameters given in Table 1.

Table 2. Values of the parameters for numerical investigations

Parameter	ρ	d_s	d_e	d_i	d_r	σ_1	σ_2
Value	1000	6	9	4	8	2	10

We give some numerical simulations confirming the global stability of the equilibria of system (2.1).

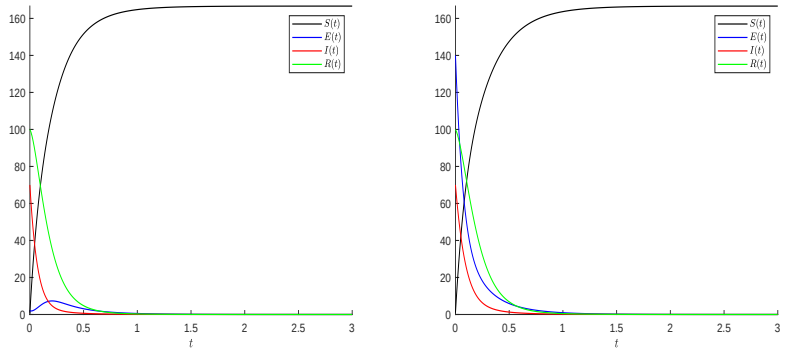

Fig. 1. $\bar{\mu} = 2$ **and** $k = 8$ **then** $\Re = 0.54 < 1$. $(S_0, E_0, I_0, R_0) = (1, 2, 70, 100)$ **(left) and** $(S_0, E_0, I_0, R_0) = (1, 140, 70, 100)$ **(right)**

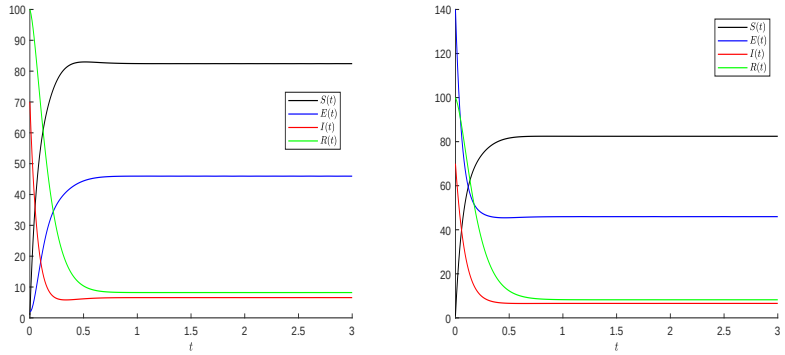

Fig. 2. $\bar{\mu} = 8$ **and** $k = 2$ **then** $\Re = 8.66 > 1$. $(S_0, E_0, I_0, R_0) = (1, 2, 70, 100)$ **(left) and** $(S_0, E_0, I_0, R_0) = (1, 140, 70, 100)$ **(right)**

In the two first cases where $\mathcal{R} < 1$, , it can be seen from these figures that all solutions approach the disease-free equilibrium point $\bar{\mathcal{E}} = (\frac{\rho}{d_s}, 0, 0, 0)$ under the mentioned initial conditions (Fig. 1) which confirms the global stability of $\bar{\mathcal{E}}$ once $\mathcal{R} \leq 1$.

In the last two cases where $\mathcal{R} > 1$, the figures (Fig. 2) confirm that the endemic equilibrium $\mathcal{E}^*$ is globally asymptotically stable, and all solutions converge to $\mathcal{E}^*$ under the mentioned initial conditions.

6 Conclusion

In this paper, we have considered a deterministic differential equation standing for a SEIR epidemic model. Firstly, we have proved the global positivity of the solution (see Proposition 1) then the basic reproduction number $\mathcal{R}$ was calculated. The model admits at most two equilibria: the disease-free equilibrium $\bar{\mathcal{E}}$ and the endemic equilibrium $\mathcal{E}^*$ (see Proposition 2). The local stability of the two equilibria was carried out (see Theorem 1 and Theorem 2) and the global stability of the two equilibria was studied (see Theorem 3 and Theorem 4). $\bar{\mathcal{E}}$ is locally and globally asymptotically stable when the reproduction number $\mathcal{R} \leq 1$. If $\mathcal{R} > 1$, $\mathcal{E}^*$ exists and is unique and it is locally and globally asymptotically stable.

Competing Interests

Author has declared that no competing interests exist.

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