Stability Analysis of a General SEIRS Epidemic Model

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ABSTRACT

In this paper, we developed a general SEIR Sepidemic model that provides knowledge about the occurrence of epidemic. The model can integrate the birth, death and examine the outcome mathematically. Along the way, we show how this simple SEIR Sepidemic model assists to lay a theoretical foundation for public health interventions.

KEYWORDS: mathematical models, SEIR Sepidemic, dynamics

INTRODUCTION

It is proved that mathematical modeling plays an important role in the disease spread and control. A better qualitative assessment can be obtained by an appropriate mathematical model for the problem. Normally mathematical models for epidemics are comprised of system of differential equations that show the rate of change of each interacting component. Numerous advantages of avoiding invasion of infection to population can be obtained by developing a good epidemic model; therefore epidemiological models attracted the attention of many researchers [1-4]. Several epidemic models are there in the literature that focuses on the dynamical properties [5-16]. In this work, we consider a single host population, the mode of transmission is direct contact, stay in latency period before becoming infectious. The infectious host can be recovered if the required immunity is provided during infectious stage.

In research literature a lot of mathematical models have been presented to study the dynamics of infectious diseases [20, 21, 23]. Khan et al. [21] presented an SEIR epidemic model with preventive vaccination. They divided the host population into four subclasses that is S-susceptible, E-exposed, I-infected and R-recovered. Kaddar et al. [20] proposed a generalized SEIRS epidemic model. The proved the global stability for a generalized SEIRS model by using the geometric approach.

In this work, we present a general SEIRS epidemic model. In our model we assume that the infections stay in the exposed classes before becoming infectious. The term \((1-\delta)\) is used which represents the number of individuals that gain natural immunity during the incubation period. Further, we two different transmission \(\alpha_1\) and \(\alpha_2\), which respectively represent the contact rate between susceptible and exposed, and susceptible and infected individuals. We denote the total host population by \(N(t)\), subdividing into four subclasses, that’s the susceptible S, latent (exposed) E, Infectious I and recovered R. Thus the total host population can be written as \(N(t) = S(t) + E(t) + I(t) + R(t)\).

Model Formulation

This section shows the mathematical formulation of the general infectious SEIR epidemic disease model. The population is categorized is four different subclasses, namely, the susceptible individuals \(S(t)\), the individuals latent (Exposed) which are not yet infectious by \(E(t)\), infected by \(I(t)\) and the individuals whose recover from infection or removed by \(R(t)\). Thus, we write \(N(t) = S(t) + E(t) + I(t) + R(t)\) the total size of host population at any time. The model that describes the assumptions above can be written through the following systems of differentials equations:

\[
\frac{dS(t)}{dt} = \Lambda - \alpha_1 S(t)E(t) - \alpha_2 S(t)I(t) - \mu S(t) + \gamma R(t), \quad S(0) = S_0 \geq 0
\]
\[
\frac{dE(t)}{dt} = \alpha_1 S(t) E(t) + \alpha_2 S(t) I(t) - (1 - \delta) E(t) - \mu E(t), \quad E(0) = E_0 \geq 0
\]
\[
\frac{dt}{dt} = (1 - \delta) E(t) - (\omega + \varepsilon + \mu) I(t), \quad t(0) = I_0 \geq 0
\]
\[
\frac{dR(t)}{dt} = \omega l(t) - \gamma R(t) - \mu R(t), \quad R(0) = R_0 \geq 0.
\]

The host population is increased by the recruitment rate \( \Lambda \), \( \alpha_1 \) and \( \alpha_2 \) respectively show the contact rate between susceptible-exposed and susceptible-infected individuals. The induced death rate is given by \( \varepsilon \), natural death rate \( \mu \), recovery rate is \( \omega \) (the recovery may be assumed here, natural or due to treatment). The individuals in the latent class gain immunity naturally at a rate \( \delta \) while loss at a rate \( \gamma \). The model (1) has the DFE, denoted by, \( E_0 = (S^0, 0, 0, 0) \) and is given by \( E_0 = (\frac{\Lambda}{\mu}, 0, 0, 0) \).

The total dynamics is obtained by summing the equations in (1),

\[
\frac{dN}{dt} = \Lambda N - d \leq \Lambda - \mu N.
\]

The feasible region for the model is the closed set \( \Gamma \), which is positive invariant and bounded, given by

\[
\Gamma = \left\{ (S, E, I, R): 0 \leq S, E, I, R, S + E + I + R \leq \frac{\Lambda}{\mu} \right\}.
\]

**Basic Reproduction Number \( R_0 \)**

This section describes the computation of the basic reproduction number, which is defined as the number of secondary infections generated by single infections when an infection is introduced into a purely susceptible population. The finding of the reproduction number involves the matrices, \( F \) and \( V \), see [17]. It follows from [17] that the matrix \( F \) and \( V \) can be obtained as:

\[
F = \begin{bmatrix}
0 \\
\alpha_1 SE + \alpha_2 SI \\
0 \\
0
\end{bmatrix}, \\
V = \begin{bmatrix}
\alpha_1 SE + \alpha_2 SI - \Lambda + \mu S - \gamma R \\
(1 - \delta) E + \mu E \\
-(1 - \delta) E + (\omega + \varepsilon + \mu) I \\
-\omega l + \gamma R + \mu R
\end{bmatrix}.
\]

It follows from the disease free equilibrium \( E_0 \)

\[
V^{-1} = \begin{bmatrix}
1 \\
(1 - \delta) + \mu \\
((1 - \delta) + \mu)(\omega + \varepsilon + \mu)(\omega + \varepsilon + \mu) \\
\mu((1 - \delta) + \mu)(\omega + \varepsilon + \mu)
\end{bmatrix}
\]

\[
FY^{-1} = \begin{bmatrix}
\frac{\alpha_1 \Lambda}{\mu} \\
\frac{\alpha_2 \Lambda}{\mu} \\
\frac{\alpha_1 \Lambda}{\omega + \varepsilon + \mu} + \frac{\alpha_2 \Lambda(1 - \delta)}{(\omega + \varepsilon + \mu)(\omega + \varepsilon + \mu)} \\
0
\end{bmatrix}
\]

Thus, the required basic reproduction number for model (1) is given by

\[
R_0 = \frac{\frac{\alpha_1 \Lambda}{\mu} + \frac{\alpha_2 \Lambda(1 - \delta)}{\mu((1 - \delta) + \mu)}(\omega + \varepsilon + \mu)}{\frac{\alpha_1 \Lambda(\omega + \varepsilon + \mu) + \alpha_2 \Lambda(1 - \delta)}{\mu((1 - \delta) + \mu)(\omega + \varepsilon + \mu)}}
\]

The next section describes the local stability of the system (1) at the DFE, \( E_0 \).

**Local stability:**

The present section describes the local stability of the model (1) at the disease free and endemic equilibrium.

**Theorem 1:** The model (1) is stable locally asymptotically, at the DFE \( E_0 \) whenever \( R_0 < 1 \).

**Proof:** The proof involves the linearization of the model (1) at DFE \( E_0 \) by setting equal to zero the left hand side of (1), which is given by the following Jacobian matrix:
We need to show that all the eigenvalues of \( E(%) \) are negative. The first column of \( E(%) \) contains only diagonal element which forms one negative eigenvalue \(-\), the other three eigenvalues can be obtained from the matrix \( J(E_0) \) which is

\[
J(E_0) = \begin{bmatrix}
-\mu & -\frac{\alpha_1\Lambda}{\mu} & -\frac{\alpha_2\Lambda}{\mu} & \gamma \\
\frac{\alpha_1\Lambda}{\mu} - (1 - \delta) + \mu & 0 & -\frac{\alpha_2\Lambda}{\mu} & 0 \\
0 & 1 - \delta & -(\omega + \varepsilon + \mu) & 0 \\
0 & 0 & -\omega & -(\gamma + \mu)
\end{bmatrix}.
\]

Now, again the third column of \( J(E_0) \) contains only diagonal element which forms negative eigenvalue \(-(\gamma + \mu)\), the remaining two eigenvalues can be obtained from the matrix \( J_1(E_0) \) which is

\[
J_1(E_0) = \begin{bmatrix}
\frac{\alpha_1\Lambda}{\mu} - (1 - \delta) + \mu & \frac{\alpha_2\Lambda}{\mu} & 0 \\
(1 - \delta) & -(\omega + \varepsilon + \mu) & 0 \\
0 & -\omega & -(\gamma + \mu)
\end{bmatrix}.
\]

The eigenvalues of \( J_2(E_0) \) are the roots of the characteristic equation

\[
\lambda^2 + \left(\omega + \varepsilon + \mu - \left(\frac{\alpha_1\Lambda}{\mu} - (1 - \delta) + \mu\right)\right)\lambda + \left((1 - \delta) + \mu\right)\left(\lambda + \left(1 - \delta\right) + \mu\right) = 0
\]

\[
\Rightarrow \lambda^2 + \left(\omega + \varepsilon + \mu - \left(\frac{\alpha_1\Lambda}{\mu} - (1 - \delta) + \mu\right)\right)\lambda + \left((1 - \delta) + \mu\right)\left(\lambda + \left(1 - \delta\right) + \mu\right)(1 - R_0) = 0
\]

\[
\Rightarrow A_2\lambda^2 + A_1\lambda + A_0 = 0,
\]

Where \( A_2 = 1, \ A_1 = (\omega + \varepsilon + \mu) - \left(\frac{\alpha_1\Lambda}{\mu} - (1 - \delta) + \mu\right), \)

\( A_0 = (1 - \delta + \mu)\left(\omega + \varepsilon + \mu\right)(1 - R_0) \). The above quadratic equations will give two negative eigenvalues if and only if \( R_0 < 1 \) and \( \omega + \varepsilon + \mu + (1 - \delta) + \mu > \frac{\alpha_1\Lambda}{\mu} \). We see that in the above polynomial \( A_2 = 1, A_1 \) will be positive only when \( \omega + \varepsilon + \mu + (1 - \delta) + \mu > \frac{\alpha_1\Lambda}{\mu} \) and \( A_0 \) will be positive if \( R_0 < 1 \). Thus for these two conditions all the roots of the polynomial will be negative. Hence the model (1) at the DFE \( E_0 \) is stable locally asymptotically whenever \( R_0 < 1 \) and \( \omega + \varepsilon + \mu + (1 - \delta) + \mu > \frac{\alpha_1\Lambda}{\mu} \).

Endemic Equilibrium

The endemic equilibria of the model (1) at endemic equilibrium \( E^3 = (S^*, E^*, I^*, R^*) \) is given by

\[
S^* = \frac{(1 - \delta + \mu)(\delta + \mu + \omega)}{(\delta + \mu + \omega)\alpha_1 + (1 - \delta)\alpha_2}, \ E^* = \frac{I^*(\delta + \mu + \omega)}{(1 - \delta)}, \ R^* = \frac{\omega I^*}{\gamma + \mu}
\]

\[
I^* = \frac{\mu(1 - \delta + \mu)(\delta + \mu + \omega)(\gamma + \mu)(R_0 - 1)}{((\delta + \mu + \omega)\alpha_1 + (1 - \delta)\alpha_2)(\gamma + \mu)(1 - \delta + \mu)(\delta + \mu + \omega)(1 + \gamma - \delta + \mu)\omega)}.
\]

A unique positive endemic equilibrium exists if and only if \( R_0 > 1 \). The following theorem analyzes the local stability of the endemic equilibrium.
Theorem 2: The model (1) at the endemic equilibrium $E^\dagger$ is stable locally asymptotically if $R_0 > 1$ and the conditions of Routh-Hurwitz criteria is satisfied.

Proof: At the endemic equilibrium $E^\dagger$ we obtain the following jacobian matrix,

$$
J (E^\dagger) = \begin{bmatrix}
-(\alpha_1 E^\dagger + \alpha_2 I^\dagger + \mu) & -\alpha_3 S^\dagger & -\alpha_2 S^\dagger & \gamma \\
\alpha_1 E^\dagger + \alpha_2 I^\dagger & \alpha_1 S^\dagger - (1 - \delta) - \mu & \alpha_2 S^\dagger & 0 \\
0 & 1 - \delta & -(\omega + \varepsilon + \mu) & 0 \\
0 & \omega & -(\gamma + \mu) & 0
\end{bmatrix}
$$

The Jacobian matrix $J (E^\dagger)$ has the following characteristics equation:

$$
\lambda^4 + l_1 \lambda^3 + l_2 \lambda^2 + l_3 \lambda + l_4 = 0,
$$

Where

$$
l_1 = \delta + 3 \mu + \omega + 3 \mu (\delta + 2 \mu + \omega) - \delta (\delta + 3 \mu + \omega) + \gamma (1 - \delta + \delta + 3 \mu + \omega) + \left( -S^\dagger (\gamma + \delta + 3 \mu + \omega) + E^\dagger (1 + \gamma - \delta + \delta + 3 \mu + \omega) \right) \alpha_1
$$

$$
+ I^\dagger \alpha_2 + \left( S(-1 + \delta) + I^\dagger (\gamma - \delta + \delta + 3 \mu + \omega) \right) \alpha_2
$$

$$
l_2 = \mu (\delta (2 - 2 \delta + 3 \mu) + \mu (3 - 3 \delta + 4 \mu) + (2 - 2 \delta + 3 \mu) \omega) + \gamma (3 \mu^2 + \delta (1 - \delta + 2 \mu + \omega) (1 - \delta) + 2 \mu (1 - \delta + \omega))
$$

$$
+ (-S^\dagger (\gamma + \delta + 2 \mu + \omega) + \mu (2 \delta + 3 \mu + 2 \omega))
$$

$$
+ E^\dagger (\delta + 2 \mu + \omega - \delta (\delta + 2 \mu + \omega) + \mu (2 \delta + 3 \mu + 2 \omega)) \alpha_1
$$

$$
+ \left( S^\dagger (-1 + \delta) (\gamma + 2 \mu) + I^\dagger (\delta + 2 \mu + \omega) - \delta (\delta + 2 \mu + \omega) + \gamma (1 - \delta + \delta + 2 \mu + \omega) + \mu (2 \delta + 3 \mu + 2 \omega) \right) \alpha_2
$$

$$
l_3 = E^\dagger (\gamma + \mu) + E^\dagger (1 - \delta + \mu) (\delta + \mu) + E^\dagger (1 + \gamma - \delta + \mu) \omega - S^\dagger \mu (\gamma + \mu) (\delta + \mu + \omega) \alpha_1
$$

$$
+ \left( S^\dagger (-1 + \delta) \mu (\gamma + \mu) + I^\dagger (\gamma + \mu) (1 - \delta + \mu) (\delta + \mu) + I^\dagger \mu (1 + \gamma - \delta + \mu) \omega \alpha_2 \right) + (1 - \delta + \mu) \mu (\gamma + \mu) (\delta + \mu + \omega)
$$

The characteristics equation above will give four eigenvalues with negative real parts if and only the conditions of Routh-Hurwitz criteria: that is, the coefficients $l_1, l_2, l_3$ and $l_4$ are positive and $l_1 l_2 l_3 - l_4^2 > 0$. Thus, Routh-Hurwitz criteria ensures the system (1) at endemic equilibrium $E^\dagger$ is stable locally asymptotically whenever $R_0 > 1$ and the Routh-Hurwitz criteria is satisfied.

Global Dynamics

In the given section we reduce the model (1) by using $S + E + I + R = N = 1$, and making the assumptions $R = (1 - S - E - I)$, and then we obtain the following reduced model:

$$
\frac{dS(t)}{dt} = \Lambda - \alpha_1 S(t) E(t) - \alpha_2 S(t) I(t) - \mu S(t) + \gamma (1 - S(t) - E(t) - I(t)), \quad S(0) = S_0 \geq 0
$$

$$
\frac{dE(t)}{dt} = \alpha_1 S(t) E(t) + \alpha_2 S(t) I(t) - (1 - \delta) E(t) - \mu E(t), \quad E(0) = E_0 \geq 0
$$

$$
\frac{dI(t)}{dt} = (1 - \delta) E(t) - (\omega + \varepsilon + \mu) I(t), I(0) = I_0 \geq 0
$$

The DFE and EE of the model (2) is now denoted by $E_2 = \left( \frac{\Lambda \gamma}{\mu + \gamma}, 0, 0 \right)$ and $E_3 = \left( S^*, E^*, I^* \right)$. For the global dynamics we will study the model (2). We follow [24] to present the global stability of system (2). We rewrite the model (2) in the following form

$$
\frac{dY}{dt} = F(Y, V)
$$

$$
\frac{dV}{dt} = G(Y, V), G(Y, 0) = 0,
$$
where \( Y = S \) and \( Z = (V, I) \) respectively denotes the population of uninfected (susceptible) and infected individuals (exposed and infected) with \( X \in \mathbb{R} \) and \( Z \in \mathbb{R}^2 \). The model (2) will be stable globally asymptotically when the conditions given in the following are hold.

\[ C_1 \quad \text{For} \quad \frac{dY}{dt} = F(Y, 0) = 0, Y_0 \text{ is stable globally asymptotically.} \]

\[ C_2 \quad G(Y, V) = LV - \hat{G}(Y, V), \quad \text{where} \quad \hat{G}(Y, V) \geq 0, \quad \text{for}(Y, V) \in \Gamma, \]

where \( L = D_g(Y_0, 0) \), shows an M-matrix and \( \Gamma \) is the biologically feasible region. Following the method in [24], we present the following theorem for the global stability of DFE of the model (2).

**Theorem 3:** The DFE of the model (2) is stable globally asymptotically whenever \( R_0 < 1 \).

**Proof:** Choose \( Y = S \) and \( V = (E, I) \) and \( U = (Y_0, 0) \), where \( Y_0 = S_0 = \frac{\lambda + \gamma}{\mu + \gamma} \).

The conditions mentioned above can be applied to model (2) as:

\[ \frac{dY}{dt} = F(Y, 0) = \Lambda - \mu S_0 + (1 - S_0) \]

This section describes the global stability of the endemic equilibrium of the model (2). For the proof we use the geometric approach method [19]. Many authors used this method in his papers, see [20-23].

Theorem: The endemic equilibrium of the reduced model (2) is globally asymptotically stable if \( R_0 > 1 \).

**Proof:** The endemic equilibrium of the model (2) is given by

\[ E^* = \left( \frac{S_2}{1 - \delta - \mu + \alpha_1 S_1}, \frac{S_2}{1 - \delta - \mu + \alpha_2 S_1}, \frac{S_2}{1 - \delta - \mu - \omega + \alpha_2 S_1} \right) \]

The second additive compound matrix associated to \( E^* \) is

\[ J^{[2]} = \begin{bmatrix} f_1 & S_{a_2} & S_{a_2} \\ (1 - \delta) & f_2 & -S_{a_2} \\ 0 & 0 & f_3 \end{bmatrix} \]

\[ f_1 = -\mu - E \alpha_1 - l \alpha_2 + 1 + \delta - \mu + S \alpha_1, f_2 = -\mu - E \alpha_1 - l \alpha_2 - (\epsilon + \mu + \omega), f_3 = -1 + \delta - \mu + S \alpha_1 - (\epsilon + \mu + \omega). \]

Choose the function \( H = \begin{bmatrix} 1 & 0 & 0 \\ 0 & E & 0 \\ 0 & 0 & E \end{bmatrix} \), and \( H^{-1} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & \frac{1}{E} & 0 \\ 0 & 0 & \frac{1}{E} \end{bmatrix} \), \( H_f = \begin{bmatrix} 0 & 0 \frac{-E' + E'}{l^2} \frac{1}{l^2} \frac{-E' + E'}{l^2} \frac{1}{l^2} \frac{-E' + E'}{l^2} \frac{1}{l^2} \frac{-E' + E'}{l^2} \frac{1}{l^2} \frac{-E' + E'}{l^2} \frac{1}{l^2} \frac{-E' + E'}{l^2} \frac{1}{l^2} \frac{-E' + E'}{l^2} \frac{1}{l^2} \frac{-E' + E'}{l^2} \frac{1}{l^2} \frac{-E' + E'}{l^2} \frac{1}{l^2} \frac{-E' + E'}{l^2} \frac{1}{l^2} \frac{-E' + E'}{l^2} \frac{1}{l^2} \end{bmatrix} \).

So that \( H_f H^{-1} = \begin{bmatrix} 0 & 0 & 0 \\ \frac{-E'}{l^2} - \frac{1}{l^2} & 0 & 0 \\ \frac{-E'}{l^2} - \frac{1}{l^2} & 0 & 0 \end{bmatrix} \).

Then \( H J^{[2]} H^{-1} = \begin{bmatrix} (1 - \delta)E & \frac{a_2 S_1}{E} & \frac{a_2 S_1}{E} \\ \frac{1}{E} & -\epsilon - 2\mu - \omega - E \alpha_1 - l \alpha_2 & -S \alpha_1 \\ 0 & E \alpha_1 + l \alpha_2 & -1 + \delta - \epsilon - 2\mu - \omega + S \alpha_1 \end{bmatrix} \).

So \( M = H_f H^{-1} + H J^{[2]} H^{-1} = \begin{bmatrix} f_{11} & f_{12} & f_{13} \\ (1 - \delta)E & \frac{a_2 S_1}{E} & \frac{a_2 S_1}{E} \\ 0 & E \alpha_1 + l \alpha_2 & f_{33} \end{bmatrix} \)

where

\[ f_{11} = -1 + \delta - 2\mu - E \alpha_1 + S \alpha_1 - l \alpha_2, f_{22} = -\epsilon - 2\mu - \omega - E \alpha_1 - l \alpha_2 + \frac{E'}{l} - \frac{1}{l}, \]

\[ f_{33} = -1 + \delta - \epsilon - 2\mu - \omega + S \alpha_1. \]
\[ f_{31} = -1 + \delta - \epsilon - 2\mu - \omega + S\alpha_1 + \frac{E'}{E} - \frac{I'}{I}. \]

Let \( M = \begin{bmatrix} M_{11} & M_{12} \\ M_{21} & M_{22} \end{bmatrix} \) where \( M_{11} = -1 + \delta - 2\mu - E\alpha_1 + S\alpha_1 - I\alpha_2, M_{12} = \max\left[ \frac{\alpha_2 S}{E} \right], M_{22} = \begin{bmatrix} -\epsilon - 2\mu - \omega - E\alpha_1 - I\alpha_2 + \frac{E'}{E} - \frac{I'}{I} & -S\alpha_1 \\ E\alpha_1 + I\alpha_2 & -1 + \delta - \epsilon - 2\mu - \omega + S\alpha_1 + \frac{E'}{E} - \frac{I'}{I} \end{bmatrix} \).

Now consider the norm in \( R^3 \) as \( |(m_1, m_2, m_3)| = \max\{|m_1|, |m_2|, |m_3|\}, \) where \((m_1, m_2, m_3)\) represent the vector in \( R^3 \). The Lozinski associated to the above norm is shown by \( \chi \). Thus it follows from [18]:

\[ \chi(M) \leq \sup\{b_1, b_2\} = \sup\{\chi_1(M_{11}) + |M_{12}|, \chi_1(M_{22}) + |M_{21}|\}. \]

Therefore

\[ b_1 = \chi_1(M_{11}) + |M_{12}| = -(1 - \delta + \mu) - \mu - E\alpha_1 + S\alpha_1 - I\alpha_2 + \frac{\alpha_2 S I}{E} \leq \frac{E'}{E} - \mu - I\alpha_2 - E\alpha_1 \leq \frac{E'}{E} - \mu. \]

Using the fact \( \frac{E'}{E} = \frac{\alpha_2 S I}{E} + S\alpha_1 - (1 - \delta + \mu). \)

And \( b_2 = \chi_1(M_{22}) + |M_{21}| = \max\left\{ -(\epsilon + \mu + \omega) - \mu + \frac{E'}{E} - \frac{I'}{I}, -(1 - \delta + \mu) - \mu, -(\epsilon + \mu + \omega) + \frac{E'}{E} - \frac{I'}{I}, \right\} + \frac{(1 - \delta)E}{I} \leq \frac{E'}{E} - \frac{I'}{I} - \mu + \frac{(1 - \delta)E}{I} \leq \frac{E'}{E} - \mu. \)

Using the fact \( \frac{I'}{I} = \frac{(1 - \delta)E}{I} - (\epsilon + \mu + \omega). \)

So, \( \chi(M) = \sup\{b_1, b_2\} = \frac{E'}{E} - \mu. \)

Every solution \((S(t), E(t), I(t))\) of proposed system (2) with \( S(0), E(0), I(0) \) belong to some compact absorbing set (say \( \Theta \)). It follows

\[ \chi(M) = \sup\{b_1, b_2\} = \frac{E'}{E} - \mu = \frac{1}{t} \int_0^t \chi(M) ds \leq \frac{1}{t} \ln \frac{E(t)}{E(0)} - \mu \leq -\frac{\mu}{2}. \]

**Numerical results**

We find the numerical solution of the proposed model (1) by choosing the base line for the susceptible population \( S=50, \) Exposed population \( E=10, \) Infected population \( I=10, \) Recovered population \( R=10. \) The parameters and their values are given as \( \alpha_1 = 0.01, \) \( \alpha_2 = 0.05, \) \( \alpha_3 = 0.0025, \) \( \epsilon = 0.078, \) \( \omega = 0.2, \) \( \gamma = 0.4 \) and \( \delta = 0.4. \)

Figure 1 shows the behavior of distinct classes of the model.
Conclusion

In this work, we studied a general SEIRS epidemic model of infectious disease. The transmission rate between susceptible-exposed and susceptible-infected was assumed. We investigated that the model is stable at the infection free state when the associated basic reproduction number less than unity. A stable endemic equilibrium was obtained for the case when the basic reproduction number exceeds than unity. Further, the stability of the reduced model was investigated. The disease free stability is examined by Castillo-Chavez method. Using the geometric approach method, the endemic equilibrium of the reduced model is derived, which is found to be stable globally asymptotically when the basic reproduction number exceeds than unity.

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