

MATHEMATICAL TRANSMISSION OF SEITR EPIDEMIC MODEL IN THE PRESENCE OF AWARENESS

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Abstract

A model for the dynamic transmission of SEITR pandemics is proposed, incorporating awareness and a mass action incidence function. The stability of both endemic and disease-free equilibrium points was examined, revealing that the disease-free equilibrium is locally and globally asymptotically stable when the Basic Reproduction Number R_0 is less than 1, while the endemic equilibrium is stable when $R_0 > 1$. Additionally, it's shown that the Basic Reproduction Number (without awareness) R_{01} is greater than R_0 (with awareness), this means that when $\omega = 0$, then $R_{01} = 1.450 > R_0 = 0.870$. A Lyapunov function is constructed to demonstrate the global stability of both disease-free equilibrium $R_0 < 1$ when and the endemic equilibrium when $R_0 > 1$. Numerical simulations illustrate the impact of awareness on disease spread, highlighting the importance of awareness in informing and educating individuals about infection risks during outbreaks, thereby reducing the health burden of the epidemic by lowering its peak.

Keywords: Equilibrium Points; Effective Basic Reproduction Number; Stability; Sensitivity; Numerical Simulations

Introduction

Mathematical modeling of infectious diseases has been widely used to predict the trajectory of epidemics and inform control measures (Daley and Gani, 2005; Akinola, *et al.*, 2017; Olopade *et al.*, 2017). These models have been a vital component of public health planning and intervention, and have also contributed significantly to population biology (Kumar *et al.*, 2020). The direct model has the

potential to greatly enhance our understanding of infectious diseases and inform prevention and control strategies (Otunuga, 2017). The rate at which infections spread to susceptible individuals is a critical aspect of epidemic dynamics, with the infection rate representing the number of new cases emerging per unit of time. Various mathematical models have been employed to study the

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transmission and re-emergence of emerging diseases (LaSalle, 1976; Driessche and Watmough, 2002; Qiu, 2008; Korobeinikov, 2009; Yang and Mao, 2013; Huo *et al.*, 2016; Li *et al.*, 2016; Otunuga, 2017; Etbaigha *et al.*, 2018; Just *et al.*, 2018; Mummert and Otunuga, 2019; Kumar *et al.*, 2019; Olopade, 2021), with extensive research conducted on the dynamic spread of SIR, SIRS, SEIR, and SVEIR epidemic models.

Daniel Bernoulli was a pioneer in using mathematical modeling to study disease transmission dynamics. His ground breaking work focused on smallpox immunization, revealing that widespread vaccination would increase life expectancy from 26 years and 7 months to 29 years and 9 months (Bernoulli and Blower, 1976; Goel, 2020). Kermack and McKendrick later developed a linear incidence rate of $f(I)S = cIS$ where $f(I) = cI$ is unbounded for $I \geq 0$. Which, although accurate for a limited number of cases, has limitations when applied to widespread community transmission. In response, researchers have sought to explore non-linear infection rates to gain a deeper understanding of infectious disease transmission dynamics (Cui *et al.*, 2008; Feng *et al.*, 2011; Adesanya *et al.*, 2016; Goel, 2020; Kumar *et al.*, 2020).

Awareness plays a vital role in preventing the spread of disease, as it influences the behavior of those at risk, encouraging them to take precautions and seek information. Awareness is the most effective protection against communicable diseases, fostering reflection, education, and information sharing among the public (Feng *et al.*, 2011; Cui *et al.*, 2008; Akinwumi *et al.*, 2021). Several researchers have incorporated awareness into their epidemiological models, recognizing its impact on disease transmission (Cui *et al.* 2008; Kumar *et al.*, 2019; Goel *et al.*, 2019; 2020). Researchers have investigated the impact of awareness on epidemic dynamics through various models. For instance, Researcher (Just *et al.*, 2018) investigated the SAIS interactive model, which conveys awareness through a particular class of susceptible, and introduced awareness into the epidemic model through that class of susceptible. They demonstrate in their models that, even in the face of declining consciousness, a constant proportion of conscious people may be preserved, resulting into an epidemic threshold above the initial reproduction rate. (Kumar *et al.*, 2019) examine the impact of alertness on the subtleties of communicable illness transmission by incorporating the category of alert people into the SIR widespread classical through the assistance of the SEIR widespread perfect, (Lacitignola and Diele, 2021) employed a Z-control technique to obtain an understanding of

consciousness' function in controlling epidemics. By exploiting awareness' capacity to create social isolation and self-isolation among the vulnerable, they employ it as an indirect control on the group of affected people by taking it into account as a time-dependent variable with unpredictable dynamics. (Kumar and Nilam, 2019) Discusses the impact of full and partial awareness of prevalent disease among those at risk of developing Holling Type 2 cases and treatment rates. To better grasp the intricate possibilities that awareness offers to contain epidemics, several research that integrates qualitative, homogenous, prevalence models have been constructed. (Das *et al.*, 2019) Examine how social media awareness affects the dynamics of the spread of tuberculosis and provide the most effective transmission method.

A crucial element that significantly affects the pattern of infectious disease transmission is human awareness during disease outbreaks. Since the value of the basic reproduction number determines how widely a disease spreads, awareness was utilized in this research as a control technique to lessen the dynamic transmission of any disease. Hence, we proposed five (5) nonlinear differential compartmental models of SEITR to study the effect of awareness on the dynamical eradication/curtailing the infectious diseases. This is how the study is structured: in Section 2, we develop an SEITR model with awareness and a common incidence function followed by the Analysis of basic properties of model in Section 3. The numerical analysis is completed in Section 4 and the results and discussion of the fallouts then the conclusions is presented in Section 5.

Deterministic Model Formulation and Description

The total population of human $N(t)$ is been subdivided into five compartments. That is, Susceptible individuals $S(t)$, Exposed individuals $E(t)$, Infected individuals $I(t)$, Treated individuals $T(t)$ and the Recovered individuals $R(t)$, Therefore;

$$N(t) = S(t) + E(t) + I(t) + T(t) + R(t) \quad (2.1)$$

The population of the susceptible compartment will increase whenever a new person joins the population either as a result of new birth or immigration, this happens at the rate π . The population will also experience increase each time individual from the recovered compartment moves to the susceptible compartment due to treatment

wanes or loss of treatment immunity at the rate v . In the same vein, the population will experience a decrease each time there is a new infection at the rate λ and a natural death at the rate μ . Therefore, the population of the susceptible compartment will increase whenever a new person joins the population either as a result of new genetic or migration, this happens at the rate π . The populace will also experience increase each time individual from the recovered compartment moves to the vulnerable compartment owing to treatment wanes or cost of treatment immunity at the rate v . In the same vein, the population will experience a decrease each time there is a new contagion at the rate λ and a normal passing away at the rate μ . Therefore,

$$\pi - (1 - \omega)\lambda S - \mu S + vR \quad (2.2)$$

The exposed compartment will experience an increase in population whenever a person from the susceptible class come in contact with someone infected with awareness of the disease, the rate of force of infection is given to be λ , although at this stage they are not yet infectious. The population of exposed compartment is decreased when an exposed individual moves to the infectious stage at the rate κ . Natural death and immunity decreased the population at rates of μ and τ_1 , respectively. Thus,

$$(1 - \omega)\lambda S - (\kappa + \mu + \tau_1)E \quad (2.3)$$

The population of the infected compartment grows by the number of persons who move at a percentage of κ from the exposed period to the infected period, it also increases as a result of recovering individuals that relapsed due to endogenous re-infection at a rate ϕ . This population will reduced by normal passing away at the rate μ and also by passing away due to illness at the rate δ , it further reduced by natural immunity and treatment of infected individuals at the rate τ_2 and θ respectively. Therefore,

$$\kappa E - (\mu - \delta + \tau_2 + \theta)I + \phi R \quad (2.4)$$

The population of the treated persons increased owing to the fact that treatment of diseased persons at the rate θ . It decreases each time an individual recovers and is moved to the recuperated period at the rate γ , the populace is further abridged by the normal passing away at the rate μ . Thus,

$$\theta I - (\mu + \gamma)T \quad (2.5)$$

Recovery amount of persons are on the increase owing to fact of the fact of the natural immunity of unprotected and diseased persons at the rate τ_1 and τ_2 correspondingly. The recovered class also increased due to individuals who have been treated and fully recovered at the rate γ , it later reduced due individuals that loss treatment immunity, normal passing away and relapsed individuals at the rate v, μ and ϕ respectively. Consequently,

$$\tau_1 E + \tau_2 I + \gamma T - (\mu + v + \phi)R \quad (2.6)$$

The force of infection that is associated to the disease is denoted by λ and is given by mass action function;

$$\lambda = \frac{\beta(E+bl)}{N} \quad (2.7)$$

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The model variables are described in Table 1, and the model parameters are summarised in Table 2.

Based on the flow chart in Figure 1 and underlying assumptions considered, the population dynamics are modelled using a system of non-linear differential equations with mass action function:

$$\begin{aligned} S' &= \pi - (1 - \omega)\lambda S - \mu S + vR \\ E' &= (1 - \omega)\lambda S - (\kappa + \mu + \tau_1)E \\ I' &= \kappa E - (\mu + \delta + \tau_2 + \theta)I + \phi R \\ T' &= \theta I - (\mu + \gamma)T \\ R' &= \tau_1 E + \tau_2 I + \gamma T - (\mu + v + \phi)R \end{aligned} \quad (2.8)$$

For simplicity, equation (2.8) becomes

$$\begin{aligned} S' &= \pi - (1 - \omega)\lambda S - \mu S + vR \\ E' &= (1 - \omega)\lambda S - K_1 E \\ I' &= \kappa E - K_2 I + \phi R \\ T' &= \theta I - K_3 T \\ R' &= \tau_1 E + \tau_2 I + \gamma T - K_4 R \end{aligned} \quad (2.9)$$

Where

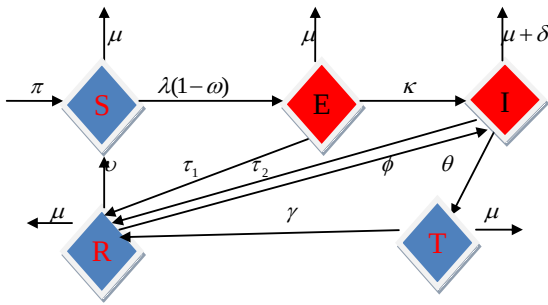
$$\begin{aligned} K_1 &= \kappa + \mu + \tau_1, K_2 = \mu + \delta + \tau_2 + \theta \\ K_3 &= \mu + \gamma, K_4 = \mu + v + \phi \end{aligned}$$

Table 1. Account of variables

Variables	Description
S	Vulnerable
E	Exposed
I	Infected
T	Treated
R	Recovered

Table 2. Descriptions of Factors and Standards Used for model formulation

Parameters	Description	Value and Source
π	Enrollment Rate	50 (Assumed)
ω	Awareness	(Varied $0 \leq \omega \leq 1$)
θ	Treatment rate	0.03 (Zarroug <i>et al.</i> , 2016)
μ	Natural Death	0.005 (Ajao <i>et al.</i> , 2023)
ν	Immunity loss	0.01 (Akinola <i>et al.</i> , 2021))
κ	Progression to Infected	0.01 (Musa <i>et al.</i> , 2020)
δ	Death due to Infection	0.0028 (Omale <i>et al.</i> , 2019)
τ_1	Natural recovery of Exposed	0.06 (Zarroug <i>et al.</i> , 2016)
B	Modification parameter	1 (Assumed)
τ_2	Natural recovery of Infected	0.06 (Roosa & Chowell, 2019)
γ	Recovery of Treated	0.02 (Zarroug <i>et al.</i> , 2016)
β	Effective contact rate	0.04 (Jiankai Huang 2022)
ϕ	Relapse rate	0.02 (Assumed)

**Figure 1. Model Flowchart**

And the initial values

$$S \geq 0, E \geq 0, I \geq 0, T \geq 0, R \geq 0 \quad (2.10)$$

Analysis of basic property of the model

All of the model's associated parameters are non-negative because the model (10) tracks human populations.

The following non-negativity conclusion is valid as a result.

Positivity and Boundedness

Theorem 3.1

The research shows that some parameters are non-negative for the model of systems of equations to be mathematically correct and epidemiologically significant $\forall t > 0$.

Let:

$$\{S(0) \geq 0, E(0) \geq 0, I(0) \geq 0, T(0) \geq 0, R(0) \geq 0\} \in \Gamma$$

Then, the solution:

$\{S(t), E(t), I(t), T(t), R(t)\}$ of the model system equation (9) are positive $\forall t \geq 0$.

Proof:

The equations from the system (2.9) were applied to the theorem (3.1) to prove it. As determined by the model's first equation:

$$\frac{dS}{dt} \geq -((1-\omega)\lambda + \mu)S \quad (3.1)$$

Using the variable separable method, It then follows that:

$$\frac{dS}{S} \geq -((1-\omega)\lambda + \mu)dt \quad (3.2)$$

Integrating both sides and taking the exponential log of both sides, weget

$$S \geq e^{\int_0^t -((1-\omega)\lambda + \mu)dt}$$

Since $t = 0$, with the initial conditions in (2.10) to have

$$S(t) \geq S(0)e^{\int_0^t -((1-\omega)\lambda + \mu)dt} \quad (3.3)$$

Since $e^{\int_0^t -((1-\omega)\lambda + \mu)dt} > 0$ and $S(0) \geq 0$, then:
 $S(t) \geq 0$, if $t = 0$ and $t \rightarrow \infty$

Therefore:

$$S(t) \geq 0 \forall t \geq 0.$$

Similarly, $E \geq 0, I \geq 0, T \geq 0$, and $R \geq 0 \forall t \geq 0$.

Therefore, the model is well-defined from both an arithmetic and epidemiological perspective

Lemma 3.1.

The closed set

$$D = \left\{ (S, E, I, T, R) \in R_+^5 : S + E + I + T + R \leq \frac{\pi}{\mu} \right\}$$

is invariant.

Proof. The result of the addition of the equations in (2.9) is,

$$dN/dt = \pi - \mu N - \delta I \quad (3.4)$$

At disease free, since $dN/dt \leq \pi - \mu N$, then,
 $dN/dt \leq 0$ if $N \geq \mu N$.

In light of this, we apply a common comparison theorem, $N \leq N(0)e^{-\mu t} + (\pi/\mu)(1 - e^{-\mu t})$

Such that $N(t) \leq \frac{\pi}{\mu}$ if $N(0) \leq \frac{\pi}{\mu}$ for all $t > 0$.

The solution alongside initial conditions in the domain D belongs to D for all $t > 0$ (i.e., the ω - limits sets of the system in (9) are contained in D). Hence, the model is epidemiologically and mathematically well-posed in D .

The Basic Reproduction Number, (R_0)

The disease-free Equilibrium (DFE) of the model (8) is given as ;

$$E_0 = (S^*, E^*, I^*, T^*, R^*) = \left(\frac{\pi}{\mu}, 0, 0, 0, 0\right) \quad (3.5)$$

The basic reproduction number, R_0 , in an epidemiological study, is used to show how an infection is transmissible. It represents the typical number of new contagions that an infected separable can spread through out transmission. The Basic Reproduction Number is calculated using the method of the next-generation matrix approach in (Driessche and Watmough, 2002; Ajao *et al.*, 2023; Adesola *et al.*, 2024; Odebiyi *et al.*, 2024) and $R_0 = \rho(FV^{-1})$, F is the new contagion term V is the other remaining transmission terms. Given the matrices F and V below,

$$F_1 = \begin{pmatrix} \frac{\beta(1-\omega)\pi}{\mu} & \frac{b\beta(1-\omega)\pi}{\mu} \\ 0 & 0 \end{pmatrix} V_1 = \begin{pmatrix} K_1 & 0 \\ -\kappa & K_2 \end{pmatrix} \quad (3.6)$$

Therefore, $R_0 = \rho(FV^{-1})$

$$R_0 = \frac{\beta\pi(1-\omega)(b\kappa+K_2)}{\mu K_1 K_2} \quad (3.7)$$

It is easy to predict whether contagion drives blow out exponentially or expires after some time or continues endlessly without spreading further, as measured by the value of the replica amount, when $R_0 < 1$, the disease will expire because every infected person will transmit the disease to less than one person in the transmittable period. When $R_0 = 1$, the infection resolves to convert widespread and will stay with each infected person transmitting to one new person. When $R_0 > 1$, a disease will spread and the number of infected people will grow exponentially which will lead to a pandemic as is seen in the corona-virus

The Basic Reproduction Number (R_{01}) Without Awareness

The special case of Basic Reproduction Number when awareness $\omega = 0$ the basic

reproduction number in the absence of awareness i.e. $\omega = 0$ is calculated using the same method;

Therefore, $R_{01} = \rho(FV^{-1})$

$$R_{01} = \frac{\beta\pi(b\kappa+K_2)}{\mu K_1 K_2} \quad (3.8)$$

It is very obvious that, the Basic Reproduction Number R_{01} (without awareness) is greater than the Basic Reproduction Number R_0 (with awareness) i.e. $R_{01} > R_0$. This shows that awareness of the disease is a crucial instrument in its dynamic control or complete eradication.

Local Stability of Disease-Free Equilibrium

Theorem 1: The disease-free equilibrium of the awareness model equation (2.9) is locally stable if $R_0 < 1$ and unstable if $R_0 > 1$.

Proof: The Jacobian matrix below, corresponding to disease-free equilibrium E_0 , is constructed to ascertain the local stability E_0 . Assuming that the disease-free equilibrium is stable

$$J(E_0) = \begin{pmatrix} \frac{\pi}{\mu}, 0, 0, 0, 0 \\ -\mu & \frac{-\beta\pi(1-\omega)}{\mu} & \frac{-\beta\pi b(1-\omega)}{\mu} & 0 & 0 \\ 0 & \frac{-\beta\pi b(1-\omega)}{\mu} & -K_1 & \frac{-\beta\pi b(1-\omega)}{\mu} & 0 \\ 0 & \kappa - K_2 & 0 & \varphi & 0 \\ 0 & 0 & 0 & -K_3 & 0 \\ 0 & \tau_1 & \tau_2 & \gamma & -K_4 \end{pmatrix}$$

The eigenvalues are $-\mu$, $-K_3$ and $-K_4$ and the remaining eigenvalues can be determined from the characteristic equation given below;

$$\lambda^2 - \left(\frac{\pi\beta\omega - \pi\beta - \mu K_1 - \mu K_2}{\mu}\right)\lambda - (1 - \omega)\beta\pi(b\kappa + K_2) + \mu K_1 K_2 = 0 \quad (3.10)$$

$$\text{Let } b_2 = 1, b_1 = \frac{\pi\beta\omega - \pi\beta - \mu K_1 - \mu K_2}{\mu},$$

$$\text{and } b_0 = -(1 - \omega)\beta\pi(b\kappa + K_2) + \mu K_1 K_2 = 0$$

Likewise, based on Routh Hurwitz criterion if $b_2 > 0, b_1 > 0$ and $b_0 > 0$, then, we have

$$-(1 - \omega)\beta\pi(b\kappa + K_2) > -K_1 K_2 \quad (3.11)$$

$$\text{Hence, } \frac{\beta\pi(1-\omega)(b\kappa+K_2)}{\mu K_1 K_2} < 1 \quad (3.12)$$

Then the remaining three eigen-values will also have negative real roots. Hence, the disease-free equilibrium is asymptotically steady when $R_0 < 1$. This theorem suggests that the disease is manageable if the initial sizes of the model's sub

populations are in the region of the disease-free equilibrium.

Global stability of disease-free equilibrium

Theorem 3.3: The disease-free equilibrium E_0 of the system (2.9) is a worldwide asymptotically steady symmetry model if $R_0 < 1$.

Proof: Taking a look at the Lyapunov function

$$F = k(b\theta + K_3)E + \mu K_1(K_3 + \theta)I + \mu K_1 K_2 T \quad (3.13)$$

Taking time derivative of F

$$\dot{F} = k(b\theta + K_3)\dot{E} + \mu K_1(K_3 + \theta)\dot{I} + \mu K_1 K_2 \dot{T} \quad (3.14)$$

Replacing the state variable

$$\dot{F} = k(b\theta + K_3)((1 - \omega)\lambda S - K_1 E) + \mu K_1(K_3 + \theta)(\kappa E - K_2 I) + \mu K_1 K_2(\theta I - K_3 T) \quad (3.15)$$

$$\text{at DFE } S = N = \frac{\pi}{\mu},$$

$$\lambda = \frac{\beta(E + bI)}{N} = \frac{\beta I(K_3 + b\theta)}{NK_3} \quad (3.16)$$

rearranging and replacing (3.16) in (3.15) to have

$$\begin{aligned} \dot{F} = & \frac{k(b\theta + K_3)(1 - \omega)\beta(b\theta + K_3)S}{NK_3} - \\ & E(kK_1(b\theta + K_3) - K_1\kappa(K_3 + \theta)) - \\ & I(\mu K_1 K_2(K_3 + \theta) - \theta\mu K_1 K_2) - T\mu K_1 K_2 K_3 \end{aligned} \quad (3.17)$$

And further simplification to have

$$\begin{aligned} F \leq & \frac{\beta I(K_3 + b\theta)(1 - \omega)\kappa(K_3 + b\theta)}{K_3} - \\ & IK_1 K_2(K_3 + b\theta) \\ \leq & I \left(\frac{\beta(K_3 + b\theta)(1 - \omega)\kappa(K_3 + b\theta)}{K_3 K_1 K_2(K_3 + b\theta)} - 1 \right) \\ \leq & IK_1 K_2(K_3 + b\theta)(R_0 - 1) \end{aligned} \quad (3.18)$$

Due to the positivity of all the parameter, it can be inferred that $\frac{dF}{dt} \leq 0$, for $R_0 < 1$ reaching $\frac{dV}{dt} = 0$ only when $E = I = T = 0$, leading to $S \rightarrow S_0$ and $R \rightarrow R_0$ as $t \rightarrow \infty$. Consequently, according to LaSalle's invariance principle, every solution of the system with initial conditions D converges to the disease-free equilibrium.

Lemma 3.2: The model (2.9) has at least one endemic equilibrium given by

$$E_1 = (S^*, E^*, I^*, T^*, R^*) \text{ whenever } R_0 > 1$$

Global Stability of Endemic Equilibrium

Theorem 3.4: the equation (2.9) is globally stable if $S = S^*, E = E^*, I = I^*, T = T^*, R = R^*$ and stable in D whenever $R_0 > 1$. It is unstable when $R_0 \leq 1$.

Proof: By constructing a quadratic Lyapunov function as follows, it is demonstrated from the constructed Lyapunov function in (Korobeinikov, 2009; Olaniyi *et al.*, 2023). This is defined by

$$F(S^*, E^*, I^*, T^*, R^*) = \frac{1}{2}(S - S^*) + \frac{1}{2}(E - E^*) + \frac{1}{2}(I - I^*) + \frac{1}{2}(T - T^*) + \frac{1}{2}(R - R^*) \quad (3.19)$$

Calculating the derivative of F directly gives,

$$\begin{aligned} F &= \left[\frac{(S - S^*) + (E - E^*) + (I - I^*)}{(T - T^*) + (R - R^*)} + \frac{d}{dt} \right] (S + E + I + T + R) \\ &= \left[\frac{(S - S^*) + (E - E^*) + (I - I^*)}{(T - T^*) + (R - R^*)} + \mu(S + E + I + T + R) \right] (\pi \\ &\leq -\mu \left[\frac{(S - S^*) + (E - E^*) + (I - I^*)}{(T - T^*) + (R - R^*)} \right] \left((S + E + I + T + R) - \frac{\pi}{\mu} \right) \end{aligned} \quad (3.20)$$

Since $N^* = \frac{\pi}{\mu}$ this implies that

$$\begin{aligned} F &\leq -\mu \left[\frac{(S - S^*) + (E - E^*) + (I - I^*)}{(T - T^*) + (R - R^*)} \right] \left(\frac{(S + E + I + T + R) - \pi}{S^* + E^* + I^* + T^* + R^*} \right) \end{aligned} \quad (3.21)$$

And then

$$\begin{aligned} F &\leq -\mu \left[\frac{(S - S^*) + (E - E^*)}{(I - I^*) + (T - T^*) + (R - R^*)} \right] \left(\frac{(S - S^*) + (E - E^*)}{(T - T^*) + (R - R^*)} + \frac{(I - I^*)}{(T - T^*) + (R - R^*)} \right) \\ &\leq -\mu \left[\frac{(S - S^*) + (E - E^*) + (I - I^*)}{(T - T^*) + (R - R^*)} \right]^2 \end{aligned} \quad (3.22)$$

Thus, the continuously differentiable function F, is defined as a Lyapunov function due to its negative semi-definite time derivative

Specifically, $\frac{dF}{dt} \leq 0$, noting that $\frac{dV}{dt} = 0$, if and only if $S = S^*, E = E^*, I = I^*, T = T^*, R = R^*$. Therefore, the largest compact invariant set:

$\{(S^*, E^*, I^*, T^*, R^*) \in \Gamma : \frac{dF}{dt} = 0\}$ is the singleton $\{E_1\}$. Hence, by La Salle's invariances principle,

standard, this shows E_1 globally asymptotically stable.

Sensitivity Analysis

Sensitivity analysis is employed to examine the threshold amount's sensitivity to the basic reproduction number's parameters. This investigation aims to identify which parameters have the most significant impact on the basic reproduction number and cause the greatest decrease in it. By understanding the parameters' influence, we can focus intervention techniques on the most effective disease control methods. The research highlights the importance of each variable in disease transmission. Below, we calculate the normalized forward sensitivity index of the reproduction number with respect to its parameters.

Assuming a variable 'P' depends differentiably on a parameter 'w', then, normalized forward sensitivity index of 'p' with respect to 'w' is denoted by X_p , which is defined as

$$X_p = \frac{p}{w} \frac{\partial w}{\partial p} \quad (3.25)$$

As we have explicitly for R_0 , We determine the sensitivity of R_0 analytically as

$$X_w^{R_0} = \frac{dR_0}{dw} \times \frac{w}{R_0} \quad (3.26)$$

Table 3. Sensitivity Index of Parameters in (R_0)

Parameter	Sensitivity Index Expression	Sensitivity Value
π	$\frac{1}{\tau_1}$	1
τ_1	$-\frac{\tau_1}{K_1}$	-0.541
τ_2	$-\frac{b\kappa\tau_2}{K_2(b\kappa + K_2)}$	-0.003
μ	$\frac{((b\kappa - \mu + K_2)K_1 + \mu(b\kappa + K_2))\pi}{(-1 + \omega)\beta - \mu^3 K_1^2}$	-1.453
κ	$\frac{\mu^2 K_1^2 K_2}{b\kappa}$	-0.001
ω	$\frac{b\kappa + K_2}{\omega}$	-0.667
β	$-\frac{1 - \omega}{b\kappa\delta}$	1
δ	$-\frac{K_2(b\kappa + K_2)}{b\kappa\theta}$	-0.001
θ	$-\frac{K_2(b\kappa + K_2)}{b}$	-0.001
b	$-\frac{b}{b\kappa + K_2}$	0.008

For each parameter involved R_0 , the sensitivity analysis is therefore calculated.

The sensitivity indices R_0 concerning each parameter used in Basic Reproduction Numbers (R_0) are determined in the manner described below:

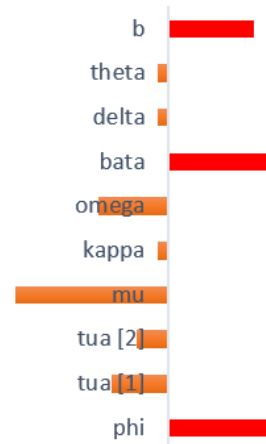


Figure 2. Chart of Sensitivity Analysis

Numerical Simulation

To authenticate the theoretical calculations of the model (2.9), the numerical simulations of the model are carried out by differential transformation method, using a set of estimated limit standards specified as shown in Table (2)

Table 3 and figure 2 show that the value of the basic reproduction number increases when the parameters with positive sensitivity values grow while the other parameters remain constant, which raises the endemicity of the disease in the population. It is increasingly challenging to maintain a disease-free environment due to the increase in basic reproduction numbers. The dynamic spread of epidemic diseases is less affected by parameters with negative sensitivity levels. Effective transmission rate β and recruitment π are the most sensitive parameters in this work. Medical professionals must focus on positive index parameters, particularly those that have a strong impact on the fundamental reproduction number (R_0) i.e. Effective transmission rate β and recruitment π in order to have stable free disease environment.

Figures 3a-3d illustrate the impact of incorporating awareness into the model. These figures demonstrate a significant increase in the number of susceptible individuals, accompanied by a corresponding decrease in the number of exposed individuals, all due to the increased awareness. The introduction of awareness into the model effectively reduces the populations in the exposed, infected, treated, and infected classes to zero. This outcome highlights the crucial role of awareness in disease control, as it not only curtails the spread of the infection but also aids in transitioning individuals into the susceptible class, ultimately preventing further transmission.

Figure 4 highlights the significant influence of disease awareness on the dynamics of susceptible individuals. The graph clearly illustrates that as awareness increases, there is a notable rise in the number of susceptible individuals, growing substantially from an initial value of 1,500 to 6,500. This increase can be attributed to the heightened understanding and adoption of preventive measures among the population, driven by awareness campaigns. By encouraging behavioral changes that reduce exposure to the disease, awareness not only limits the spread of infection but also shifts individuals from potentially exposed or infected categories back into the susceptible group.

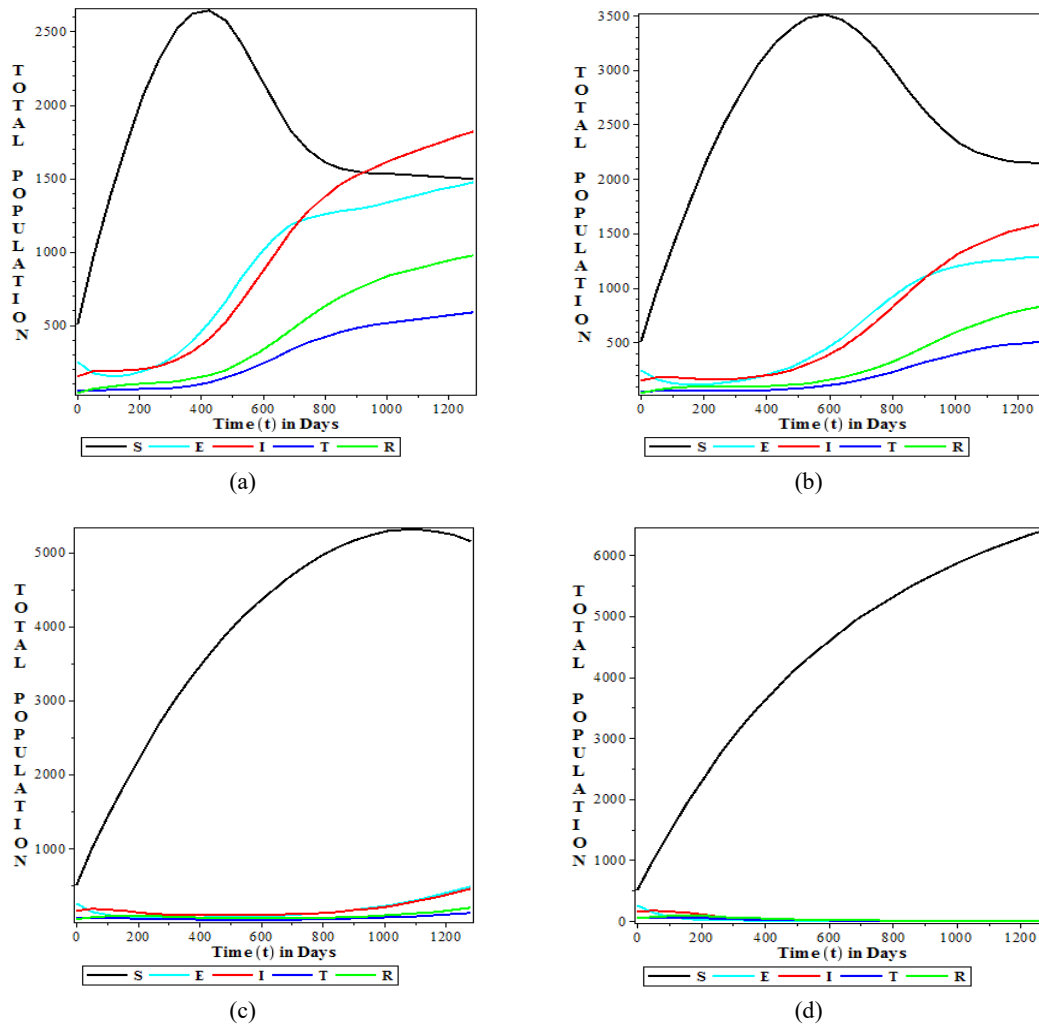


Figure 3 (a) Graph of the Total Population with $\omega = 0.0$ (b) Graph of the Total Population with $\omega = 0.3$ (c) Graph of the Total Population with $\omega = 0.6$ (d) Graph of the Total Population with $\omega = 1.0$.

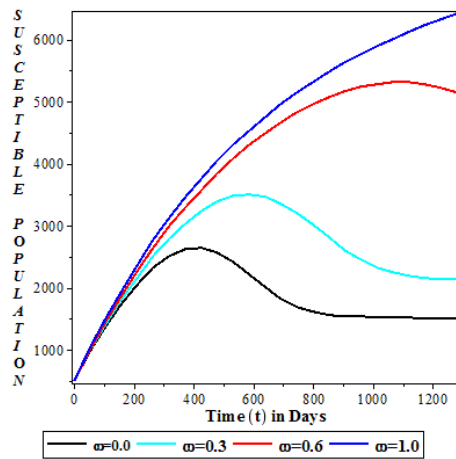


Figure 4. Graph of the Susceptible Population with $\omega = 0.0; 0.3; 0.6 \& 1.0$

Figure 5 demonstrates the profound impact of a high awareness rate on the elimination of SEITR (Susceptible - Exposed - Infected-Treated - Recovered) epidemic diseases. The figure reveals that when the awareness rate reaches a sufficiently high level, it effectively reduces the number of exposed individuals from an initial value of 1,400 to zero. This outcome underscores the critical role of awareness in curbing and potentially eradicating the spread of the disease. By promoting preventive behaviors, enhancing early detection, and encouraging treatment compliance

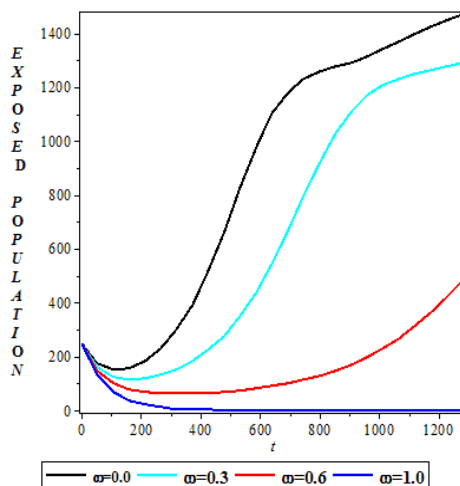


Figure 5. Graph of the Exposed Population with $\omega = 0.0; 0.3; 0.6 \& 1.0$

Figure 6 illustrates the dynamic effect of awareness on the threshold basic reproduction number (R_0), which is a critical measure of disease transmissibility. The figure reveals that in the absence of awareness $\omega = 0$, the basic reproduction number remains high at $R_{01} = 1.450$, indicating a strong potential for the disease to persist and spread within the population. However, as awareness increases when ($\omega = 0.2$), the basic reproduction number decreases significantly, reaching ($R_0 = 0.870$). This reduction is pivotal because it brings the value of (R_0) below the critical threshold of 1, signifying a shift from an endemic state to a declining disease trajectory. By lowering (R_0), awareness directly reduces the transmission potential of the disease, thereby decreasing its prevalence and minimizing its impact on the community.

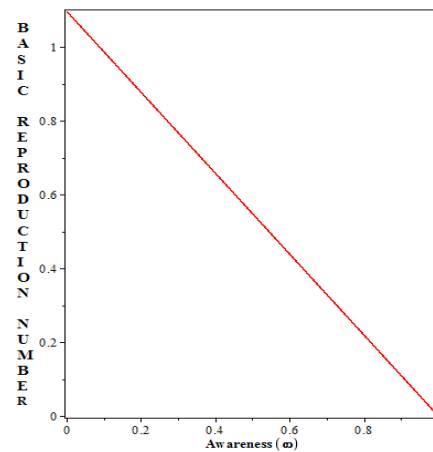


Figure 6. Graph of the Basic Reproduction Number Against Awareness (ω)

In conclusion, this research's qualitative study of the model indicates the model's well-posedness and the solutions' uniqueness. The next-generation matrix was used to calculate the basic reproduction number (R_0) and the stability of the model equilibrium.

Each model was shown to have two equilibrium points: a disease-free equilibrium that is locally asymptotically stable whenever $R_0 < 1$ and an unstable equilibrium that results in the existence of an endemic equilibrium when $R_0 > 1$. The parameters that fuel the spread of the disease were identified through sensitivity analysis of basic

reproduction number parameters; the results demonstrate that effective contact rate and recruitment into the population through birth or immigration are the parameters that increase the basic reproduction number, which will further the spread of the disease in the environment.

The awareness of the disease plays a vital role in the control of SEITR epidemic model; it was observed that the awareness of the disease reduces the number of infected individuals and the spread of the disease in the community.

Conclusions

This study has developed five nonlinear differential equations to investigate how awareness influences the dynamic spread of SEITR. To analyze the disease transmission dynamics and the impact of awareness on curtailment/eradication, numerical simulations were performed using the Maple program and differential transformation method. Additionally, a qualitative analysis of the model reveals that it is well-posed and has unique solution. The basic reproduction number R_0 and stability of the model's equilibrium were determined using the next-generation matrix.

The models revealed two equilibrium points : a stable disease-free equilibrium when $R_0 < 1$, and an unstable equilibrium leading to an endemic equilibrium when $R_0 > 1$. Sensitivity analysis of the basic reproduction number R_0 identified the key parameters driving disease spread : effective contact rate and population growth through birth or immigration. These parameters increase R_0 , fostering disease propagation in the environment.

Numerical simulations revealed that disease awareness plays a crucial role in controlling the SEITR epidemic model. The results showed that increased awareness significantly reduces the number of infected individuals and slows the spread of the disease in the community.

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