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MATHEMATICAL MODELING AND ANALYSIS OF AN SIR EPIDEMIC MODEL WITH THERAPY: EXISTENCE, POSITIVITY, AND STABILITY STUDY

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Abstract

The paper has introduced a modified SIR epidemic model that includes therapeutic intervention and demographic effects to examine the dynamics of the disease in the closed population. The model breaks down the population into the following compartments; susceptible, infected and recovered, with recruitment, natural death, and rate of therapy. The mathematical theory is mathematically analyzed to be well-posed. The existence and uniqueness of solutions are proved through standard Lipschitz conditions in which the system is said to evolve continuously out of any admissible initial condition. Solutions are proved to be positive, and this is necessary to make population compartments biologically meaningful. The model has a positively invariant region, and this indicates that total population is also bounded as time goes by. A basic reproduction number, $\mathcal{R}_0$, is calculated, which is a threshold value that is used to identify disease outbreak or extinction. Local stability is also studied using the Jacobian matrix whereby the disease-free equilibrium is determined. Moreover, global stability of the disease-free equilibrium is exercised by applying the Lyapunov functions methods and it proves that the disease dies when $\mathcal{R}_0 < 1$. The theoretical findings give basic insights on the epidemic behavior subjected to therapeutic and demographic influence. On the whole, this paper provides a solid mathematical model of infection dynamics and guarantees biologically plausible predictors and conditions when a disease.

INTRODUCTION

1.1 Infectious Disease Modeling

Mathematical modeling Infectious disease Infectious disease modeling is a mathematical method that is employed to learn how diseases are spread among populations. It gives a methodical structure to explain the distribution of diseases, their maintenance, or eventual fade out. These types of models can assist researchers to study the patterns of epidemics, predict the main epidemiological parameters, and the effectiveness of intervention measures [1-3]. Deterministic and stochastic models are mainly used based on the nature of the disease and availability of data. Mathematical models are a way of converting biological assumptions into equations and thereby predict disease outcomes in various scenarios, which makes it possible to obtain predictions and results of

diseases under varying conditions [4]. They are common in the planning and policymaking of health among the people. Modeling is also useful in the estimation of reproduction numbers, threshold conditions and equilibrium states. As the amount of computation power has increased, simulation based models have become valuable instruments in epidemiology studies. On the whole, the process of infectious disease modeling is the interface between mathematics, biology and public health to assist in making evidence-based decisions.

1.2 Tuberculosis

Tuberculosis (TB) is a chronic infectious disorder caused by a bacteria named as Mycobacterium tuberculosis which predominantly attacks the lungs but can also attack any other organ. It still occupies the place of the most common cause of infectious disease-related mortality on the planet, especially in underdeveloped countries, since the disease has claimed many lives [5,6]. TB is an air-borne-infectious disease that occurs when people with this disease sneeze or cough. The disease can be in the latent and active form and thus its management becomes complicated and demanding. It is also a serious problem based on socioeconomic factors, malnutrition, and the inadequate access of healthcare. It is needed to decrease the transmission and mortality through early diagnosis and efficient treatment of the problem involved in the issue of AIDS spread and disease contraction [7,8]. TB is still a major public health danger despite control programs that have taken place globally. Treatment and management are also complicated by drug-resistant strains. The mathematical modeling of TB is important in understanding the dynamic of this disease to develop effective control measures and minimize disease burden.

1.3 SIR Model

One of the simplest compartmental models in the field of epidemiology is the Susceptible-Infected-Recovered (SIR) model [9,10]. It separates a population into three categories: vulnerable individuals with a possibility of getting the disease, those with it who are capable of spreading it and recovered people with immunity to the disease through which they contract it but cannot spread it further [11]. This system of ordinary differential equations regulates the movement of individuals between these compartments in this model. It gives the information about how diseases are transmitted and their epidemics [12]. Among the critical parameters of the SIR model is the basic reproduction number that is essential to determine whether an infection will go or fizzle. The model presupposes the homogeneous mixing of population and the constant parameters. It is an extremely simple model that captures critical dynamics of an epidemic. Variations of SIR model may incorporate vital dynamics, vaccination or latency times. It is a basis of more sophisticated epidemiological models.

1.4 SIR Model and Tuberculosis

Using SIR in a model of tuberculosis can assist researchers to examine the process of TB transmission and the maintenance of TB in groups of people [13, 14]. Even though TB has complicated phases like the latent infection, the SIR model offers a simplified form of transmission. In that regard, vulnerable people are the people at risk, infected people are the cases of active TB and recovered are the people who were treated successfully, or people who are immune. Based on the epidemiological data, the model can be used to estimate the transmission rates and the recovery rates. Through the evaluation of equilibrium states, scholars are able to tell whether TB will continue on an endemic basis or eradicated. The SIR model can also be used to test the intervention measures, including the treatment programs and awareness campaigns. The model has threshold conditions of disease eradication as the result of mathematical analysis. Though in more detailed models latent compartments might be included, the SIR structure provides a base of knowledge [15]. Therefore, it is an effective point of beginning to study the dynamics of TB.

2 SIR Model Structure

The mathematical model given is a SIR (Susceptible–Infected–Recovered) model, which is a deterministic model used to model the transmission dynamics of an infectious disease in the given population. The overall population is separated into three categories such as the susceptible (S), infected (I), and recovered (R). The population of the susceptibles is recruited at rate

Π, and removed by infection (at rate proportional to the product of susceptible and infected individuals) and removed by nature at rate δ. The population of the infected evolves as uninfected infections develop and succumb to the infection at rate $(\rho + \theta)$ and by natural elimination at rate δ. The recovered population grows with the people who were already infected recovering and it declines with natural removals at rate, δR. The model is based on homogeneous mixing, each person having equal chance of mixing, and offers a framework of understanding disease progression, equilibrium points, and the effect of intervention measures, in the long run. Examining this system of different equations allows getting an idea of the process of infection propagation and control measures efficacy.

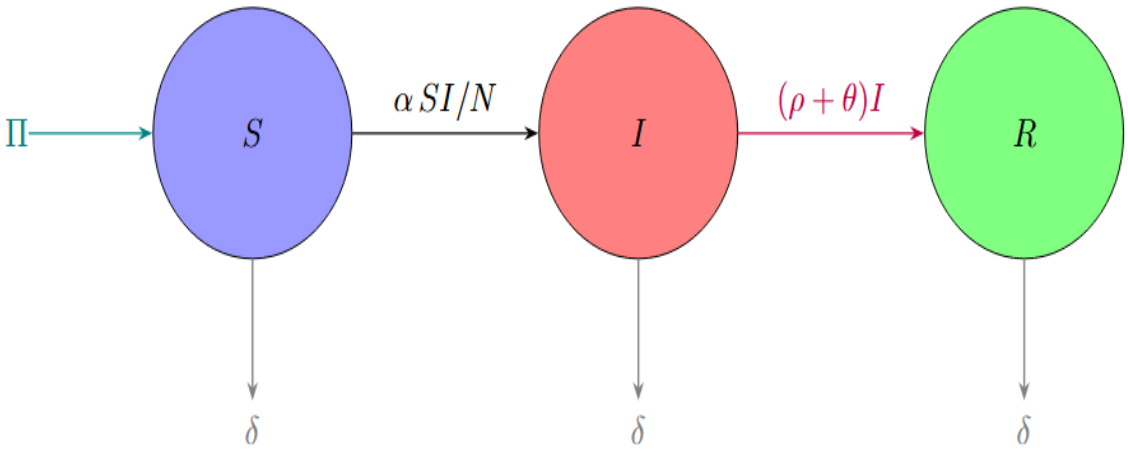

Figure 1: Flow Diagram of the SIR Epidemic Model with Therapy and Demography.

2.1 Model Equations Derived from Flow Diagram

Based on the transitions shown in the flow chart, the model is governed by the following system of differential equations:

$$\begin{aligned} \frac{dS}{dt} &= \Pi - \alpha\frac{SI}{N} - \delta S, \\ \frac{dI}{dt} &= \alpha\frac{SI}{N} - (\rho + \theta + \delta)I, \\ \frac{dR}{dt} &= (\rho + \theta)I - \delta R. \end{aligned} \quad (1)$$

With total population

$$N = S(t) + I(t) + R(t). \quad (2)$$

Table 1: Description of Model 1 Parameters

Symbol	Meaning	Unit
α	Transmission rate	per person per time
ρ	Natural recovery rate	per time
θ	Therapy rate	per time
δ	Natural death rate	per time
Π	Recruitment rate	persons per time
N	Total population size	persons

Table 2: State Variables of the Model 1

Variable	Description	Interpretation
$S(t)$	Susceptible individuals	Population at risk of infection
$I(t)$	Infected individuals	Currently infectious population
$R(t)$	Recovered individuals	Immune or removed population

2.2 Basic Reproduction Number

In epidemiology, the basic reproduction number, denoted by $\mathcal{R}_0$ is a basic measure that quantifies the average number of secondary infections of one infected person in a completely susceptible population. It gives a limit on whether an infectious disease will be propagated or eliminated. When $\mathcal{R}_0$ is more than 1, there is a possibility of the infection spreading and leading to an epidemic and if the $\mathcal{R}_0$ is less than 1 then the disease will ultimately vanish. The effective reproduction number, R_t considers the change in susceptibility and interventions as time progresses such that, $\mathcal{R}_0$ relies on the rate of transmission, contact rate and infectiousness duration. The calculation of $\mathcal{R}_0$ enables governmental bodies in the field of health to determine the level of control measures. It is also useful in determining the vaccination coverage that is required to produce herd immunity. In this way, reproduction number can be considered as one of the main instruments used to predict the evolution of the disease and make appropriate interventions.

For the proposed model (1), $\mathcal{R}_0$ can be determined using the next generation matrix method [16-18]

$$\frac{dI}{dt} = \alpha \frac{SI}{N} - (\rho + \theta + \delta)I, \quad (3)$$

at the beginning of an outbreak

$$S \approx N.$$

Thus

$$\frac{dI}{dt} = (\alpha - (\rho + \theta + \delta))I. \quad (4)$$

The infection grows if

$$\alpha > \rho + \theta + \delta. \quad (5)$$

Dividing by $(\rho + \theta + \delta)$ gives

$$\mathcal{R}_0 = \frac{\alpha}{\rho + \theta + \delta}. \quad (6)$$

Interpretation

- If $\mathcal{R}_0 < 1$, the infection dies out.
- If $\mathcal{R}_0 = 1$, the disease persists at equilibrium.
- If $\mathcal{R}_0 > 1$, the infection spreads.

Epidemiological Significance

The reproduction number provides essential insight into disease control. Reducing transmission (α) through interventions or increasing recovery through treatment (ρ and θ) decreases $\mathcal{R}_0$. Increasing therapy rate is especially effective because it shortens infectious duration. Public health strategies therefore aim to reduce $\mathcal{R}_0$ below unity to eliminate disease transmission.

Threshold Theorem

The disease-free equilibrium is locally asymptotically stable if $\mathcal{R}_0 < 1$ and unstable if $\mathcal{R}_0 > 1$. Hence $\mathcal{R}_0$ acts as the fundamental threshold parameter governing disease invasion or eradication.

3 Mathematical Analysis of the Model

The mathematical analysis of infectious disease models needs a strict interpretation of solution behavior of the system of differential equations. The existence and uniqueness is what assures that, given initial conditions, a system will have a well-defined and unique solution over time, which is important to reliable predictions. Positivity of solutions is what guarantees that all state variables, including susceptible, infected, and recovered populations, will always be non-negative, as is the biological fact of the population sizes. The idea of an invariant region determines a portion of the phase space that is limited in extent as well as has an area in which all the trajectories of the system have to stay to guarantee that the model itself acts in a consistent way and on realistic scales. Combining these properties gives a mathematical basis to stability analysis of equilibria, the long run behavior of the disease, and effectiveness of intervention strategies. The model has gained a biological meaning by defining these basic properties and is mathematically sound.

3.1 Existence and Uniqueness of Solutions

Consider the system

$$\frac{dS}{dt} = \Pi - \alpha\frac{SI}{N} - \delta S, \quad (7)$$

$$\frac{dI}{dt} = \alpha\frac{SI}{N} - (\rho + \theta + \delta)I, \quad (8)$$

$$\frac{dR}{dt} = (\rho + \theta)I - \delta R, \quad (9)$$

with initial conditions

$$S(0) \geq 0, \quad I(0) \geq 0, \quad R(0) \geq 0.$$

Define the vector function

$$F(S, I, R) = \begin{pmatrix} \Pi - \alpha\frac{SI}{N} - \delta S \\ \alpha\frac{SI}{N} - (\rho + \theta + \delta)I \\ (\rho + \theta)I - \delta R \end{pmatrix}. \quad (10)$$

We observe that F is continuously differentiable with respect to (S, I, R) for all $(S, I, R) \in \mathbb{R}^3_+$. Moreover, for any bounded region $\Omega \subset \mathbb{R}^3_+$, the partial derivatives of F are bounded. Specifically,

$$\left|\frac{\partial F_i}{\partial S}\right|, \left|\frac{\partial F_i}{\partial I}\right|, \left|\frac{\partial F_i}{\partial R}\right| \leq L < \infty, \quad i = 1,2,3$$

for some constant L. Hence F satisfies the Lipschitz condition in Ω.
By the Picard–Lindelöf theorem, this guarantees the existence and uniqueness of a solution $(S(t), I(t), R(t))$ passing through any initial point in the feasible region $\mathbb{R}^3_+$. Consequently, the model is well-posed and its solutions are uniquely determined by the initial conditions.

3.2 Positivity of Solutions

Theorem. If the initial conditions satisfy

$$S(0) > 0, \quad I(0) > 0, \quad R(0) > 0,$$

then the solutions remain positive for all $t > 0$.

Proof.

From the first equation of the model (1),

$$\frac{dS}{dt} \geq -\left(\alpha \frac{I}{N} + \delta\right) S. \tag{11}$$

This implies

$$S(t) \geq S(0) e^{-\int_0^t (\alpha I/N + \delta)\, ds} > 0. \tag{12}$$

Similarly, from the second equation of the model (1),

$$\frac{dI}{dt} \geq -(\rho + \theta + \delta) I \tag{13}$$

$$I(t) \geq I(0) e^{-(\rho+\theta+\delta)t} > 0. \tag{14}$$

In the end, from the third equation of the model (1),

$$\frac{dR}{dt} \geq -\delta R \tag{15}$$

$$R(t) \geq R(0) e^{-\delta t} > 0. \tag{16}$$

Hence all state variables remain nonnegative for all $t > 0$.

3.3 Invariant Region

Let

$$N(t) = S(t) + I(t) + R(t). \tag{17}$$

Adding the model (1) equations gives

$$\frac{dN}{dt} = \Pi - \delta N. \tag{18}$$

This linear differential equation has solution

$$N(t) = \frac{\Pi}{\delta} + \left(N(0) - \frac{\Pi}{\delta}\right) e^{-\delta t}. \tag{19}$$

Thus,

$$0 \le N(t) \le \frac{\Pi}{\delta} \quad \text{for all } t \ge 0.$$

Therefore the feasible region

$$\Omega = \left\{(S, I, R) \in \mathbb{R}^3_+ \ : \ S + I + R \le \frac{\Pi}{\delta}\right\} \tag{20}$$

is positively invariant.

Interpretation. The invariant region ensures that solutions remain biologically meaningful and bounded. The total population approaches the steady state value Π/δ, which represents the demographic equilibrium level determined by recruitment and natural mortality.

Conclusion of Mathematical Properties

The model satisfies three fundamental mathematical conditions:

- A unique solution exists for any admissible initial condition.
- All state variables remain nonnegative for all time.
- The total population remains bounded within a biologically feasible region.

These properties confirm that the model is mathematically well-posed and epidemiologically valid, making it suitable for theoretical analysis, numerical simulation, and public health interpretation.

4 Equilibria and Stability Analysis

Disease- Free Equilibrium (DFE) is a concept that is central in the analysis of infectious disease models, which denotes an equilibrium where no agent in the population is infected. The study of the local stability of the DFE can be used to identify whether tiny perturbations, like the incorporation of a handful of infected individuals will die out, or cause an outbreak. Local stability is usually determined by applying a linearization methodology and the basic reproduction number, $\mathcal{R}_0$. When the value of 0 is lower than 1, the DFE is locally asymptotically stable and this means that the disease has no way of invading the population, global stability of the DFE means that, at any initial level of infections, the system will eventually settle in the disease-free state. The approach of establishing global stability may require building suitable Lyapunov functions or analogy theorems. The analyses present heartening views on the planning of the public health because they reveal the circumstances under which an illness may be eliminated. The local and global stability of DFE need to be comprehended to provide effective control and intervention strategies.

4.1 Disease-Free Equilibrium

The disease-free equilibrium (DFE) is obtained by setting $I = 0$ and $R = 0$ and solving

$$\frac{dS}{dt} = 0, \quad \frac{dR}{dt} = 0.$$

From the first equation of the model (1):

$$\Pi - \delta S = 0, \tag{21}$$

$$S^* = \frac{\Pi}{\delta}, \tag{22}$$

Thus the DFE is

$$E_0 = \left(\frac{\Pi}{\delta}, 0, 0\right). \tag{23}$$

4.2 Local Stability of Disease-Free Equilibrium

- If $\mathcal{R}_0 < 1$, DFE is locally asymptotically stable.
- If $\mathcal{R}_0 > 1$, DFE is unstable.

The Jacobian matrix of the model (1) is obtained as:

$$J = \begin{pmatrix} -\alpha I/N - \delta & -\alpha S/N & 0 \\ \alpha I/N & \alpha S/N - (\rho + \theta + \delta) & 0 \\ 0 & \rho + \theta & -\delta \end{pmatrix}. \tag{24}$$

Jacobian matrix at E_0 is obtained as:

$$J = \begin{pmatrix} -\delta & -\alpha & 0 \\ 0 & \alpha - (\rho + \theta + \delta) & 0 \\ 0 & \rho + \theta & -\delta \end{pmatrix}. \tag{25}$$

Evaluating at E_0 gives eigenvalues

$$\begin{aligned} \lambda_1 &= -\delta, \\ \lambda_2 &= -\delta, \\ \lambda_3 &= \alpha - (\rho + \theta + \delta). \end{aligned} \tag{26}$$

λ_3 can be simplified as:

$$\lambda_3 = \frac{1}{(\rho+\theta+\delta)}(\mathcal{R}_0 - 1). \tag{27}$$

λ_3 is negative when $\mathcal{R}_0 < 1$.

Thus, all eigenvalues have negative real parts. Which proves the local stability of DFE.

4.3 Global Stability of Disease-Free Equilibrium

Consider the Lyapunov function

$$V(t) = A_1 I. \tag{28}$$

Differentiating yields:

$$\frac{dV(t)}{dt} = A_1\left(\alpha\frac{SI}{N} - (\rho + \theta + \delta)I\right). \tag{29}$$

After simplification above equation is reduced as:

$$\frac{dV}{dt} = \frac{1}{(\rho+\theta+\delta)}\left(\frac{\alpha}{(\rho+\theta+\delta)} - 1\right). \tag{30}$$

Substituting value of $\mathcal{R}_0$ from equation number 6 into above equation, yields:

$$\frac{dV}{dt} = \frac{1}{(\rho+\theta+\delta)}(\mathcal{R}_0 - 1)I. \tag{31}$$

If $\mathcal{R}_0 < 1$, above equation can be written as:

$$\frac{dV}{dt} \leq \frac{1}{(\rho+\theta+\delta)}(\mathcal{R}_0 - 1)I. \quad (32)$$

Whenever $\mathcal{R}_0 < 1$, we obtain $\frac{dL(t)}{dt} < 0$, which shows that Z_0 is the only compact invariant subset of Ω. Hence, LaSalle's invariant principle [19] confirms that Z_0 is globally asymptotically stable in Ω.

5 Conclusion

This paper has formulated a SIR epidemic model with therapeutic intervention and demographic effects into an extended model. The model considers all the rates of the recruitment, natural death, infection, recovery, and therapy, which makes it a realistic model of studying the dynamics of the disease. We analyzed the model strictly and determined basic mathematical properties. Existence

and uniqueness of solutions were established by Lipschitz condition and Picard-Lindelof theorem, which is a well-posed model. We proved the positivity of solutions and the existence of a positively invariant region which ensures that population compartments are biologically meaningful and bounded in time. A threshold value was determined as the basic reproduction number of $\mathcal{R}_0$ and the disease-free equilibrium was determined. Both the local and the global stability of the disease-free equilibrium were determined, which indicated that the disease dies out whenever the value of $\mathcal{R}_0$ is less than one. These findings give some basic knowledge on the dynamics of the infectious disease when under the effect of therapy and demographic processes. In general, the research provides a solid mathematical basis to the study of the spread of infections and the management of the outbreaks of the disease. The framework can be extended in the future, with more compartments, control policies, or more complicated epidemiological conditions. The theoretical review reveals that the model is useful in determining how disease will behave and whether intervention strategies will be effective in a population.

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