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SIR modeling of a disease spread with a detectable and undetectable infectious syndrome

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Abstract. **T**his paper proposes a model for the analysis of an infectious disease spread using a renewed deterministic model of Susceptible-Infected-Recovered (SIR). The SIR is based on compartments or partitions. In this case, the contaminated (infected) class is divided into two sub-compartments: detectable and undetectable. Numerical simulations are carried out to test the obtained theoretical results, and presentations follow graphically.

Keywords. SIR model, mathematical model, differential model, nonlinear system

1. Introduction

A mathematical model entails a representation of a physical or a real-life situation using mathematical ideas, concepts, expressions, and languages. The most important form of representation is a mathematical model of reality. Essentially, everything in the physical or biological universe is subject to analysis by mathematical models, whether natural or involving technology and human interference [1-4]. Epidemiology includes a systematic study and a review of the circumstances of health and disease incidence, trends, and determinants in established populations [5-7]. Mathematical models are among the main instruments used in the study of infectious disease dynamics. Some researchers have developed mathematical models to explain how diseases are spread within compartments of human or species subpopulations. Here, individuals are divided into compartments according to the features and functions of the disease being modeled [8]. A lot of researchers have used mathematical methods to explain the dynamics of a disease's transmission. In epidemiology, infection incidence force is clearly defined as the rate at which individuals are infected per unit when they come into contact with a susceptible person

during their infection time. A compartmental form of a model is a conceptual system that replicates how individuals communicate within a community in various compartments [9-12].

One of the known basic compartmental models is the classical SIR model, and several models are modified versions of this classical form [13, 14]. In the SIR model, S denotes the number of individuals (people) that are prone to the disease; whenever a susceptible and an infectious individual enters infectious contact, then, the susceptible individual contracts the disease and moves into the infectious compartment termed I, which denotes the number of infected species. These are people infected and able to infect susceptible members. Here, R refers to the number of individuals who are excluded (and immune), healed from the disease or deceased for one reason or the other. The number of deaths is assumed to be negligible compared with the total population. This compartment can also be deemed "safe" or "recovered." This model is fairly predictive for infectious disease transmission and where recovery offers enduring tolerance, such as measles, mumps, and rubella [4, 6].

2. Model formulation and derivation

In this section, the transmission dynamics are obtained on a compartmental basis, where the population is divided into four categories viz: susceptible $S = S(t)$, those who are neither infected nor immune, $I_d = I_d(t)$, denotes the population size of infective and detectable individuals, $I_u = I_u(t)$, denotes the population size of infective but undetectable individuals, and $R = R(t)$ denotes the population size of recovered individuals. It is assumed that there is recruitment to the susceptible class, natural death is accounted for at all levels, infective is either detectable or undetectable, while recovery is only from the detectable class.

For parameter description, Λ denote the recruitment rate into the susceptible compartment, μ is the natural death rate, r is the recovery rate for individuals in the infected detected class, while c_1 and c_2 are the effective contact rates infected and detected and infected but undetected classes, respectively.
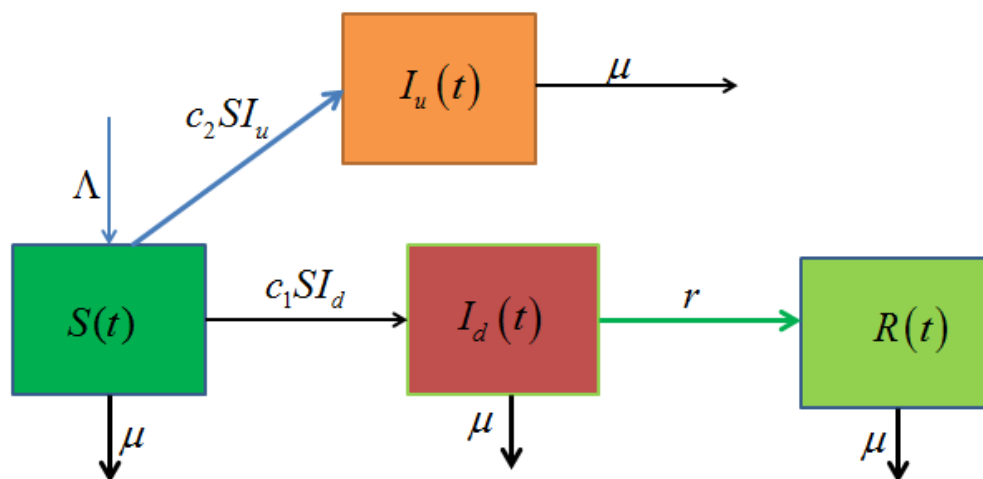

Figure 1: Model compartmental diagram

By considering Figure 1 via the application of conservation principle, the following dynamics represent a set of a system of differential equations that models the situation, where the prime notation denotes derivative with respect to time:

$$\begin{cases} S' = \Lambda - \mu S - c_1 S I_d - c_2 S I_u \\ I'_d = c_1 S I_d - \mu I_d - r I_d \\ I'_u = c_2 S I_u - \mu I_u \\ R' = r I_d - \mu R \\ N = S + I_d + I_u + R \end{cases} \qquad (1)$$

subject to the following initial conditions:

$$\left(S(o), I_d(o), I_u(o), R(o) \right) = \left(S^0, I_d^0, I_u^0, R^0 \right). \qquad (2)$$

The model disease free equilibrium is given as:

$$_M DFE = \left(S^*, I_d^*, I_u^*, R^* \right) = \left(\frac{\Lambda}{\mu}, 0, 0, 0 \right)$$

Theorem 2.1: The basic variables in the SEIRD model (1.2) are positive at all time, $t > 0$. This implies that the solution set of the system in (1.2) at any time, $t > 0$, maintain non-negativity condition(s).

3. Gradient Solution and Numerical Simulations

In this section, values for the model parameters are used for the corresponding numerical simulations, and interpretations. Table 1, and Figure 2-5 suffice. However, other numerical approaches can be adopted [15-18].

Table 1: Model Parameters and Variables

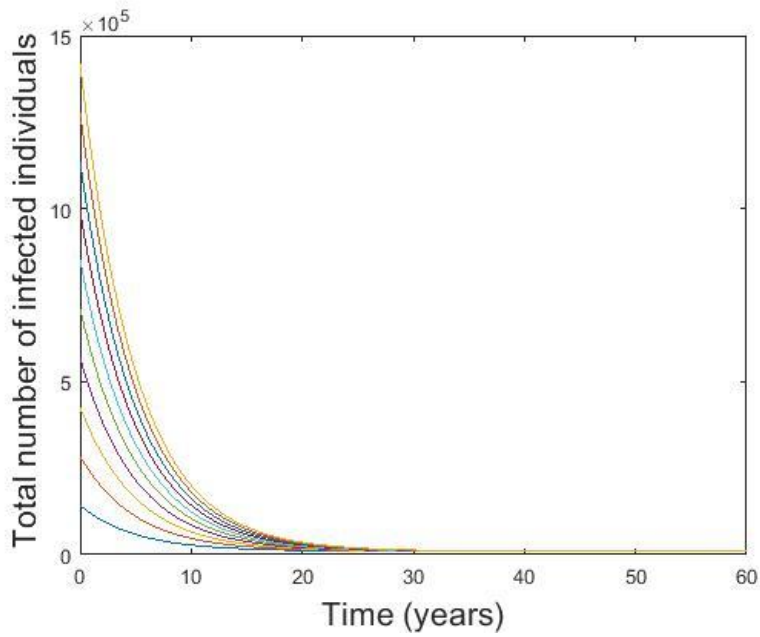| Variables	Meaning	Value	Parameters	Value
S	Susceptible	Initial estimate	c_1	$0.1, 0.2, 0.3$
I_d	Infected and detected	Initial estimate	c_2	$0.2, 0.3, 0.4$
I_u	Infected undetected	Initial estimate	μ	0.2
R	Recovered	Initial estimate	π	2000
			r	0.5

Figure 2: Shows the simulation result when $c_1 = 0.1$ and $c_2 = 0.2$

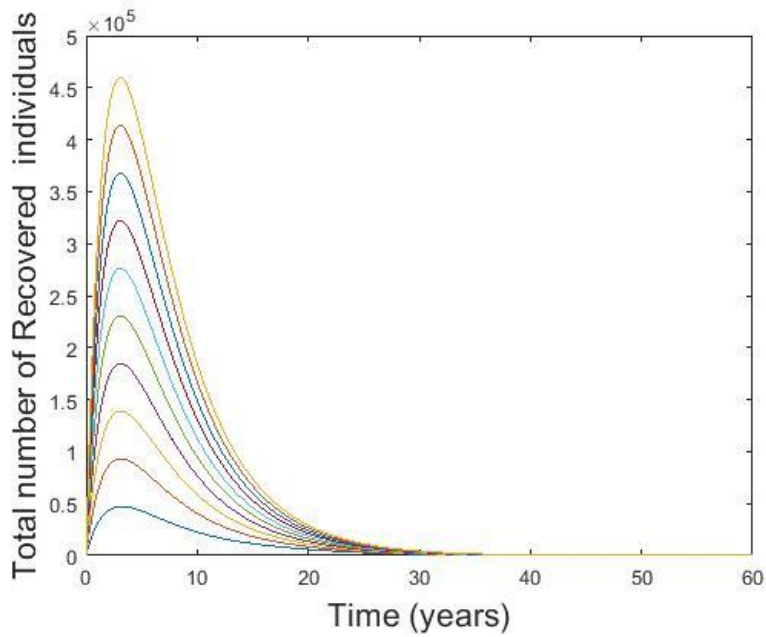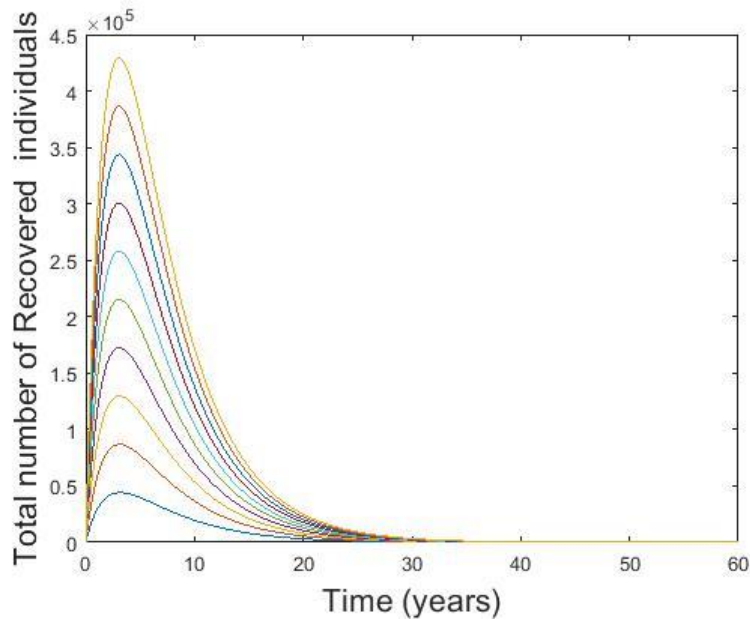**Figure 3:** Shows the simulation result when $c_1 = 0.2$ and $c_2 = 0.3$

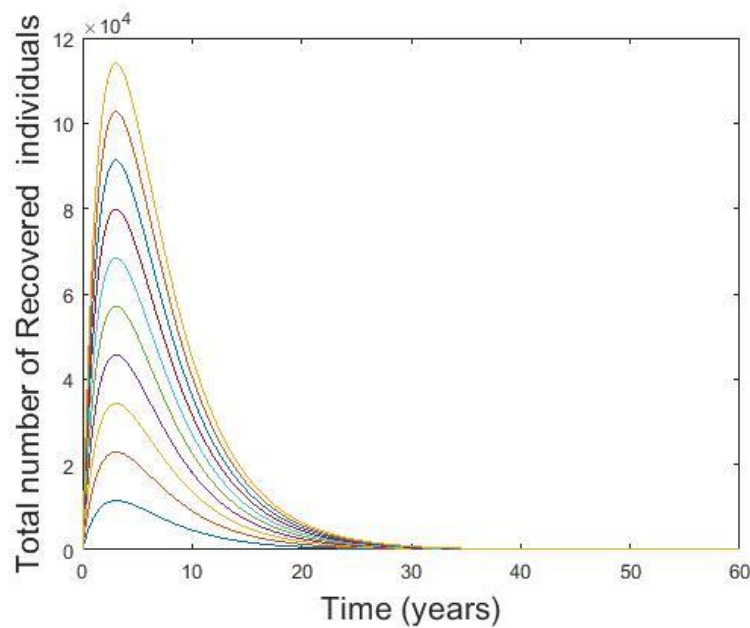**Figure 4:** Shows the simulation result when $c_1 = 0.3$ and $c_2 = 0.4$

Figure 5: Shows the simulation result when $c_1 = 0.3$ and $c_2 = 0.4$

In Table 1, the hypothetical values for the model parameters and variables are presented. Figure 2-5 shows the graphical views of the gradient plots of infected individuals with fixed and varied contact rates. Figure 2, 3, and 4 shows the recovery class when $c_1 = 0.1$ and c_2 0.3, when c1= 0.2 and c2=0.3, and when c1= 0.3 and c2= 0.3, respectively.

The important features of the model is that it allows disease transmission by individuals in the infected undetected and detected classes I_u and I_d respectively. From the recovery class it is obvious that when the contact rate is increased, the total number of recovery persons also increased.

4. Conclusion

In this paper, we have examined a deterministic model of SIR with a nonlinear infection flow terms. The proposed model is a renewed version of the classical SIR model which would be of great application with respect to disease transmission and compartmental interactions. Infectious classes that were detectable and undetectable were considered. This work can be extended to include exposed and vaccinated classes. Numerical simulations are hypothetically conducted to verify the theoretically obtained results, and graphical presentations follow.

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