A study on mathematical models describing diseases

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Abstract. To describe the different types of diseases, especially infectious diseases, we can use mathematical modeling. Mathematical models can be used todays to describe a variety of diseases. In this paper, we intend to express the different mathematical models used for various diseases.

Motivation or purpose: In mathematical modeling of diseases, the main purpose is to study the spread of disease, and the understanding of the type of infection can help reduce disease transmission and disruption of the disease chain.

Method: According to the study of the results obtained from the differential equations, we can describe the behavior of diseases.

Results: Using mathematical modeling, we can analysis the disease accurately and show how effective the use of drugs, social spacing, and etc. how appropriate to control disease.

Conclusion: With more insight on the different types of mathematical models describing diseases, we can better understand the choice of mathematical model related to specific disease and thus better analysis.

Keywords: mathematical models, disease, differential equations.

AMS Mathematical Subjects Classification [2010]: 34A34, 34H05

1. Introduction

Diseases have always had a significant impact on human life. One of the diseases affected by human societies is plague that has been known as the "Black Death" in the 14th century. The disease began in Europe around 1967, and almost 25 % of the population died from illness [1]. Another example of the epidemic is an epidemic of smallpox in U.S.A. between 1507 and 1900. The spread of the disease killed about one - third of the native population of an island, and in 1520, half of the population of Mexico was destroyed by the disease [2]. Another disease that is responsible for causing a human acquired immune defect and strongly influences the mortality pattern in developed and developing countries affects HIV. At present, corona virus or covid-19 has become a serious threat to human societies. The items raised is some examples of diseases that can affect the population of a community. For this reason, the spread of diseases and how they control over recent years has been very significant, and mathematical models are an important tool to describe diseases, so in this paper we want to introduce different models of them. In fact the mathematical models and computer simulation perform mathematical analysis on the disease, it shows whether that the disease is spread rapidly and widely, remains in the current state or is lost in future. Various mathematical models have been used to explain and interpret the diseases in the form of differential equations, which are discussed in this paper.

2. SIR model

One of the models developed for contagious diseases is called the SIR model. In this model, at first a fixed initial population is considered as N. The population is divided into three sub - categories that are not necessarily identical. A group of people who have been infected with the disease that show with I (Infected), another group is people who have not been infected, but they 're prone to get infected that show with S (Susceptible) and the third group that is going to be good after disease that show with R (Recovered).

In this model, members of S are entered into the set with transmission rates α, Also, members of I are entered into a set of R with a rate γ that indicates the average time period of the disease.

S → I → R

In order to compute the arbitrary moment t values s(t), I(t) and R(t), which represent the number of members of the set S, I and R, we need to solve the following equations that are in the form of differential equations:

$$\frac{dS}{dt} = -\alpha SI$$

$$\frac{dI}{dt} = \alpha SI - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

In this model, it is assumed that the rate of risk for all population is equal to α, as well as per unit time each member of S is equal to the set I. In this regard, there is a reproduction threshold that is called λ, which consists of: $\lambda = \frac{S\alpha}{\gamma}$. In the proposed model, when $\lambda < 1$ the sickness is not infectious, and if it is $\lambda > 1$, the disease will infect everyone with time over time, and when $\lambda = 1$ the system is in equilibrium, the system is in equilibrium, but it is on the verge of the outbreak [3].

3. SI model

This model is similar to the SIR model, except that in this model it is assumed that the epidemic is incurable [4].

S → I

The differential equations of the model are given to describe S(t) and I(t) in this model as follows:

$$\frac{dS}{dt} = -\alpha SI$$

$$\frac{dI}{dt} = \alpha SI$$

With initial conditions satisfying $S(0) + I(0) = N$.

4. SIRS model

In this section, another case is developed for the epidemic, which is very similar to the SIR model, except that the members of R set are joining the S set after a while. This model is called SIRS model. The purpose of this section is constructing a mathematical model of a generalized epidemic SIRS (Susceptible, Infective, Recovered and Susceptible) model of the term [5].

$$S \longrightarrow I \longrightarrow R \longrightarrow S$$

The differential equations of the model to compute the values S(t), I(t) and R(t) are as follows:

$$\frac{dS}{dt} = -\alpha SI + \sigma R$$

$$\frac{dI}{dt} = \alpha SI - \gamma I$$

$$\frac{dR}{dt} = \gamma I - \sigma R.$$

5. SEIR model

In this case, the new phenomenon that is discussed is the latency of the disease. Sometimes the disease factor is placed without any signs in the patient's body, which is known as the incubation period.

Healthy people who are prone to illness (S), people with disease hidden in their body (E), sick people who can shift the disease to others (I) and those who are covered or quarantined (R). So for population N we have:

$$S(t) + E(t) + I(t) + R(t) = N$$

$$S \longrightarrow E \longrightarrow I \longrightarrow R$$

To describe the disease transmission in a certain population, suppose that e be the rate at which the exposed individuals become infectious, g is the rate at which infectious individuals recover and a denotes the death rate due to the disease. Let b be the natural birth rate and d denotes the natural death rate. These parameters are assumed constant in a finite horizon of interest. The rate of transmission is described by the number of contacts between susceptible and infectious individuals. If c is the incidence coefficient of horizontal transmission,
such rate is $cS(t)I(t)$. According to the proposed parameters, the model is as follows:

$$\frac{dS}{dt} = bN(t) - dS(t) - cS(t)I(t)$$

$$\frac{dE}{dt} = cS(t)I(t) - (e + d)E(t)$$

$$\frac{dI}{dt} = eE(t) - (g + a + d)I(t)$$

$$\frac{dR}{dt} = gI(t) - dR(t)$$

For more information on the model, we can refer to [6].

2. Main Results

Understanding how infectious diseases spread in a community can lead us to reduce disease transmission and this understanding is possible by a mathematical model. In this paper, different mathematical models are presented to describe the diseases. As proposed by the mathematical model, we can describe an epidemic as a result of the model's analysis of how disease is developed in society, home quarantine, social spacing and how to use medication to control disease. On the other hand, due to the effectiveness of disease behavior, for example to get infected with disease or once infected with a disease, it is necessary the model type is properly chosen so that the analysis is correct to predict the behavior of the model.

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