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Research Article

SOME MATHEMATICAL MODELS AND APPLICATIONS USED IN EPIDEMICS

Arzu ÇİLLİ*[1], Kıvanç ERGEN[2], Ercüment AKAT[3]

[1]*Department of Physics, Yildiz Technical University, Esenler-İSTANBUL;* ORCID: 0000-0002-0596-3637
[2]*Department of Biophysics, Bülent Ecevit University, ZONGULDAK;* ORCID: 0000-0002-5655-5975
[3]*Department of Physics, Yeditepe University, İSTANBUL;* ORCID: 0000-0001-9267-1650

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ABSTRACT

Tuberculosis (TB), AIDS (Acquired Immune Deficiency Syndrome), measles, malaria and CCHF (Crimean-Congo Hemorrhagic Fever) are the main epidemic diseases that persist as major global health problems. Estimating the number of affected people from epidemic diseases is of importance to reduce/minimize the probable negative outcomes. Therefore applicable and appropriate mathematical modelling is very useful and necessary to analyse, forecast and prevent the evolution of the diseases. A variety of mathematical models are used to detect losses from many epidemic diseases seen in the world. Some of these are SI, SIS, SIR, MSIRS, etc. Among the models, we studied SI (Susceptible-Infective) and SIS (Susceptible-Infective-Susceptible) models to decide the best appropriate/fitting model and to predict the effects of these epidemic diseases in some countries, namely, Norway for TB, malaria for Nigeria, HIV/AIDS for Ghana, CCHF for Bulgaria and measles for Afghanistan. We showed the relative predictive power of each model and in general models were found to confirm the reliability and robustness. After the analysis of the numerical results, we concluded that the SI and SIS models are very good at predicting the number of infected individuals, sensitive to fluctuations in real data and can follow the trend of exact data. Moreover, they give results in a short time.
Keywords: Mathematical models, epidemic, diseases.

1. INTRODUCTION

An epidemic disease is a kind of illness that can propagate in a certain group by some types of interactions or infectious agents within a given geographic area or population group. It may also refer to the usual prevalence of a given disease with such area or group. Epidemic diseases have been an important problem for mankind. Although such diseases have impacts on every age of history of human being, they have a greater impact in certain periods. For example, The Black Death of 1347–1351, provides one of the tragic historical examples of an infection with a high rate of mortality, claiming an estimated 30–50% of the European population in only a five-year period [1]. Moreover, it cannot be denied that epidemic diseases have a negative impact on both business life and production. They may also lead to immigration for fear of life.

Scientists have always researched for the right methods to fight against epidemic diseases. Although some success has been obtained to some extent with antibiotics, vaccines and other

* Corresponding Author: e-mail: acilli@yildiz.edu.tr, tel: (212) 383 42 90

methods, still it has not been possible to remove these kinds of diseases completely. Bacteria causing tuberculosis and plague have gained antibiotic resistance and re-emerged in the course of time. Moreover, Lyme disease [3], Legionella [4], AIDS (Acquired Immune Deficiency Syndrome) [5], Hepatitis C [6], Severe Acute Respiratory Syndrome (SARS) [7] are the epidemic diseases appearing in recent years.

Fighting with such diseases primarily begins prior to epidemia. Taking appropriate precautions and foreseeing the impact of the diseases are of importance to reduce/ minimize the negative social and economic effects. For this reason, mathematical models are used and the SIR (Susceptible-Infected-Recovered) model is the one that is widely used to represent infectious diseases such as influenza, SARS, measles and mumps in which one shot epidemic waves can occur and the mortality is high or the recovery implies immunity [8]. Tuberculosis, HIV/AIDS and CCHF were also studied by the SIR model for Turkey [9]. In this project we aimed to predict the effects of some epidemic diseases in terms of the number of infected people by using mathematical models such as SI (Susceptible-Infected) and SIS (Susceptible-Infected-Susceptible).

In this respect Tuberculosis, Malaria, AIDS, CCHF and Measles were studied as model diseases. Predictive powers of the models in general were found to confirm the necessary reliability and robustness.

2. MATERIAL AND METHODS

2.1. Epidemiological Models: SI and SIS

The mathematical epidemiological model that is probably the most widely used for theorizing about and emulating epidemics is the SIS model [10]. In this model which is implemented by an iterative calculation and is effective for epidemic diseases, the simplest version without demographic factors is defined as follows: It is assumed that in a closed society taken as the system there are no deaths, no births in the population, no migration into or out of the population and infected people are not re-infected after they have recovered. Of course these assumptions are valid for a limited interval of time. In SI model, over the course of the epidemic almost everyone eventually becomes infected. In the SIS model, each individual belongs to either the set of susceptible (S) or the set of infected people (I). Thus, the model can be shown as **S→I→S**, that is, a person is either susceptible or infected. In other words, a person does not gain immunity. After being infected, he/she can be susceptible again (i.e. after getting recovered). When a susceptible individual and an infected individual interact (by some manner), the former may be infected at a rate of infection, denoted by a constant β which can be positive or negative depending on the values for two successive years, as can be seen in Eq (7). In this way, susceptibility is the same for each individual. Having accepted these rules the following equations are obtained [10]:

Here we consider the SI and SIS models where the total population;

$$S(t) + I(t) = N \tag{1}$$

is a constant and is assumed not to change with time for our closed system.

For the SI model;

$$\frac{dS}{dt} = \left(-\frac{\beta}{N} \right) S(t) I(t) \tag{2}$$

$$\frac{dI}{dt} = \left(\frac{\beta}{N} \right) S(t) I(t) \tag{3}$$

For the SIS model;

$$\frac{dS}{dt} = \left(-\frac{\beta}{N}\right) S(t) I(t) + \gamma I(t) \tag{4}$$

$$\frac{dI}{dt} = \left(\frac{\beta}{N}\right) S(t) I(t) - \gamma I(t) \tag{5}$$

In Eq.[2] the prod uct *S*(*t*)*I*(*t*) represents the possible encounters between the susceptible and infected people. The larger the term $S(t)$ and/or $I(t)$, the larger the number of encounters between the susceptible and the infected people and therefore the greater the risk of spreading the disease.

By using Eq.[4] and Eq.[5], firstly γ is found as follows:

$$\gamma = \frac{\left(\frac{dR}{dt}\right)}{I(t)} \tag{6}$$

where *R* represents the recovered people. Since there are two groups, namely *S* and *I*, there is no *R* in the SI model, however, there are three groups, *S*, *I* and *R* in the SIR model. For Eq's. [2-6], we accept the number of people leaving the susceptible group is equal to incoming people to the infected group (I). In the meantime infected people can recover and this average recovering ratio is symbolized by γ, while $\frac{1}{\gamma}$ denotes the average infectious period. As time t approaches infinity, *S* and *R* approach '0' and '*N*', respectively. For solving the differential Eq.[2] and Eq.[3], the Euler Method is used. A susceptible individual may get in contact with an infected individual with probability β within a short time interval Δt. With high probability $1-\beta\Delta t$, the susceptible individual stays in the susceptible state throughout the interval Δt and this interval Δt can be identified with a discrete simulation time step.

2.2. Euler Method

Euler equations are given by discretization of the differential Eq's [2-5] and Eq's [4-5]; for SI and SIS respectively;

For the SI Model;

$$S_{n+1} = S_n - \left(\frac{\beta}{N}\right) S_n I_n \Delta t \tag{7}$$

$$I_{n+1} = I_n \left[1 + \left(\frac{\beta}{N}\right) S_n \Delta t\right] \tag{8}$$

For the SIS Model;

$$S_{n+1} = S_n - \left(\frac{\beta}{N}\right) S_n I_n \Delta t + \gamma I_n \tag{9}$$

$$I_{n+1} = I_n \left[1 + \left(\frac{\beta}{N}\right) S_n \Delta t\right] - \gamma I_n \tag{10}$$

Population in the next step can easily be determined in very short time intervals. To solve these equations, firstly the ratios β and γ (used in SIS model) had to be known. An approximate prediction on infected and healthy people can be made by knowing these β and γ ratios for a fixed number of populations in defined time intervals [10, 11, and 2].

3. RESULTS

It is assumed that population is fixed in the SI and SIS models. β values were calculated for each disease using the related values of two previous consecutive years. The values for β and γ

are calculated using the real data for each model and the same values are used in the estimations. In this study each β for the mentioned calculation was used separately if the exact numbers were obtained, otherwise the same β was used for the following years as can be seen from the tables. Thus predicted results were given. This relatively weak model is unable to estimate the number of dead people so we cannot give the number of deaths. In all calculations, data were supplied by Global Tuberculosis Report 2013, 2014, World Health Statistics 2014, 2015 and World Malaria Report 2014 of World Health Organization (WHO).

3.1. Cases of Tuberculosis and Predictions in Norway

In this section, tuberculosis is considered as an epidemic disease. Norway was chosen as a developed country. Tuberculosis patients' estimation in Norway between 2014 and 2016 was given in Table 1. First, using the patients' population of the previous years, predictions of patients' population for the following years are obtained. These predictions and exact results are given in Table 1. Although it is seen that tuberculosis case estimation (Estimated Number) for 2013 in SIS model is greater than the real number of cases (Exact Number), it is closer to real number of cases when compared to SI model's estimation. In other words, exact number lies between the SIS and SI models' estimations. After the validation and verification we could have predicted the number of cases for 2014, 2015 and 2016, it can be said that estimated numbers are between the predicted values by the two models. Not all models are appropriate for all kinds of diseases. Hence, the SI model is not convenient for tuberculosis, as is seen from Table 1. However, the SIS model is quite appropriate for this disease.

Table 1. Number of Cases of Tuberculosis and Predictions in Norway*

***Population for Norway was taken as 5 million.

Year	Exact Number	SI			SIS			
		β	Estimated Number	Error (%)	γ	β	Estimated Number	Error (%)
2012	510	----	----	----	----	----	----	----
2013	550	78.45	514	6.5%	0.98	1.078	560	2%
2014	----	"	554	----	"	"	604	----
2015	----	"	559	----	"	"	663	----
2016	----	"	564	----	"	"	728	----

3.2. Cases of Malaria and Predictions in Nigeria

90% of all malaria deaths occur in sub-Saharan Africa where Nigeria is a country in that region [12]. Malaria cases were estimated for the year 2013 by the SI and the SIS models with 0.030 % and 0.056 % error respectively. Table 2 shows Malaria cases and predictions for Nigeria for the years 2014-2017. Here, the SI model gave a better estimation according to SIS model for the mentioned disease and estimated number by the SI model is greater than that of the SIS model. It is convenient to use both the SI and the SIS models in the estimation for malaria, because the values found are very near the real data, as is seen from Table 2.

3.3. Cases of HIV/AIDS and Predictions in Ghana

In Table 3, the prediction of the HIV/AIDS patients' population in Ghana was given by SI and SIS models between 2014 and 2017. Prediction for the cases in 2013 was made with a 0.004

% error by the SIS model. Real numbers of cases for 2012 and 2013 were given in Table 3 and it is seen that they are decreasing. Both SI and SIS models are capable of showing this trend. However, SIS model predictions for 2014 and beyond 2014 were smaller than those of the SI model. Predictions by SI and SIS were very close to each other and estimated numbers are also very close to exact numbers. Therefore, these models give us a chance to infer an excellent prediction from the data. For the case of HIV/AIDS both the SI and SIS models yield values near the real data.

Table 2. Number of Cases of Malaria and Predictions in Nigeria*

*Population for Nigeria taken as 173615345.

Year	Exact Number	SI		SIS		
		β	Estimated Number	γ	β	Estimated Number
2012	6938519	----	----	----	----	----
2013	12830911	0.884	12827039	0.973	1.897	12823678
2014	----	"	23335175	"	"	22887826
2015	----	"	41190876	"	"	38312326
2016	----	"	68964556	"	"	57674692

Table 3. Number of patients in Cases of HIV/AIDS and Predictions in Ghana*

*Population for Ghana taken as 26 million.

Year	Exact Number	SI		SIS		
		β	Estimated Number	γ	β	Estimated Number
2012	241800	----	----	----	----	----
2013	225420	-0.07	224874	0.950	0.8905	225410
2014	----	"	209641	"	"	209140
2015	----	"	194966	"	"	194152
2016	----	"	181421	"	"	180338

3.4. Cases of CCHF and Predictions in Bulgaria

This model is mainly based on the data obtained 10 to 12 years ago. Here it is emphasized that the estimates found by the models exhibit anomalies when faced with extraordinary situations. The unusual increase in the diseases within the period 2007-2008 cannot be observed in the estimations. In Table 4, CCHF exact cases were given [13]. Awareness of being bitten by infected ticks can lead people to go to medical centres without spreading the disease and contaminate others. In CCHF (Crimean-Congo Hemorrhagic Fever), contamination occurs by way of blood and body fluids. Therefore it is much likely that medical personnel are at high risk compared with ordinary people. Inconsistency of these models' estimation can be attributed to this fact. Since in this model the estimations are carried out by the data belonging to a very early period, the model cannot be expected to be sensitive for the abrupt increase in the number of cases between 2007-2008 tabulated in Table 4.

Table 4. Number of patients of CCHF Cases and Predictions in Bulgaria*

*****Population for Bulgaria taken as 7683000.

Year	Exact Number	SI		SIS		
		β	Estimated Number	γ	β	Estimated Number
2005	14	----	----	----	----	----
2006	7	-0.5	7	0.857	0.357	7
2007	2	"	~3	"	"	~4
2008	13	"	1	"	"	1
2009	6	"	6	"	"	7
2010	----	"	3	"	"	3

3.5. Cases of Measles and Predictions in Afghanistan

Measles used to account for estimated 30000-35000 deaths each year in Afghanistan [14]. Therefore, to reduce measles-related mortality, the nationwide measles vaccination campaign was conducted throughout 2002 and measles immunization coverage among 1-year-old babies was 75% in 2013 [15]. Table shows the exact number [16] and estimated numbers between 2005-2010. Here, SIS model gave the exact value. Pretty close values have been obtained by both models. As can be seen from this table, the SI and SIS models are appropriate for the measles.

Table 5. Number of patients of Measles Cases and Predictions in Afghanistan*

*Population for Afghanistan taken as 31411743.

Year	Exact Number	SI		SIS		
		β	Estimated Number	γ	β	Estimated Number
2010	6420	----	----	----	----	----
2011	4856	-0.244	4854	0.994	0.750	4857
2012	----	"	3671	"	"	3674
2013	----	"	2776	"	"	2780
2014	----	"	2099	"	"	2107

4. CONCLUSION

It is quite difficult to find the data used in checking the validity of these models for the epidemics. For Turkiye it can be tested whether the models do work, by using the data obtained from the public health authorities. However, to investigate some foreign countries only the data from World Health Organization (WHO). But one cannot reach the data older than 2-3 years. Hence one cannot compare the estimated values with the recent data. Besides this the countries and the diseases mentioned in this study are randomly chosen among the recent data published.

In this framework, to minimize the negative effects of some epidemic diseases, mainly tuberculosis, Malaria, AIDS, Crimean-Congo Hemorrhagic Fever and Measles, their prospective prevalence was tried to predict by a mathematical modelling SI and SIS. Predictive power of the models in general was found to confirm the reliability and robustness.

Analyzing the numerical results we concluded that the framework of the SI and SIS models;

i- can predict the number of infected individuals well,
ii- are sensitive to fluctuations in real data,
iii- are able to predict the trend of the exact data and
iv- give good results in a short time.

Although the mathematical models used here are convenient for the monotonically increasing or decreasing cases, they might not be applicable for cases where abrupt jumps may occur.

If efficient precautions are not put into action, it is inevitable for many people to escape from being affected by epidemic diseases, namely social problems and deaths. Therefore, the data provided in this project are very important for the related institutions (Ministry of Health, hospitals etc.) to take precautions and face the situation in the future as far as prediction is concerned. The application of such studies gives hope to contribute positively to economies of countries in terms of planning the drugs, doctors, medical personnel etc. It will help to take precautions for prevention of the evolution of the diseases.

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