CHAPTER 1

INTRODUCTION

In this chapter, background of the study, definition of some basic terms, application of mathematical model, limitations of the study and overview of the thesis are explained.

1.1 Background of the Study

Mathematical models can be used to validate hypotheses made from experimental data, the designing and testing of these models has led to a testable experimental predictions. There are impressive cases in which mathematical models have provided an insight into biological systems, physical systems, decision making problems, space models, industrial problems, economical problems and so forth. The development of mathematical modeling is closely related to significant achievements in the field of computational mathematics. Real-world systems are complex and a number of inter related components are involved. In fact, infectious diseases causes mortality and suffering in many underdeveloped and developing countries, references go to some pioneers in the study of mathematical modeling of infectious diseases, in persons of Ronal Ross and Walliam Hammer, who in the beginin of twentieth century used the law of mass action to give an insight about the epidemic behaviour. The reed frost epidemic model was developed by Lowell Reed and Wade Hampton in the year 1927 to identify the relationship between the compartment of susceptible, infected and recovered individuals in a population. Throughout the history, communicable diseases play major effects on the development of mankind, since epidemic diseases some times causes deaths before it disappear and some times new diseases may appear and become endemic, some communicable disease such as cholora, tuberclosis and measles are threat in a modern life, diseases like chicken pox, usually has less symptoms and disappear on their own by their own accord (Diekmann et al., 2000).

Some diseases causes higher number of mortality within a short period of time, the occurance and problem cause by such diseases have become a great danger to many underdeveloped and developing countries where there are lack of technological and economical advancement. Anually people died in millions as a result of measles, respratory track infection, diarrhea and many more which can be easily control but left carelessly, some

diseases seem to stay permanently in some african countries, like maleria, cholora and sleeping sickness, the rate of problems which these diseases are causing interms of death and economic destruction has to be considered. Improvement of sanitation, effectiveness of antibiotics, as well as vaccination programs gave confidence that infectious diseases might be eliminate (Hallam & Gross, 2009).

The continuous emerging and spread of infectious diseases necessitate the issue of mathematical models which are considered as important tools of controlling the spread of diseases such as SIS, SIR, SEIR and so on. Models of infectious diseases can be identified as the description of the way infectious diseases spread into a population, according to the parameters and the initial conditions describing the environmental properties and the behavior of the disease (Vargas-de-le, 2011).

1.2 Definitions of Basic Terms

1.2.1 Mathematical Modelling

Can be defined as the process of applying mathematics to solve a real world problem with the view of making assumptions, predictions as well as interpretation of the solution from the mathematical models.

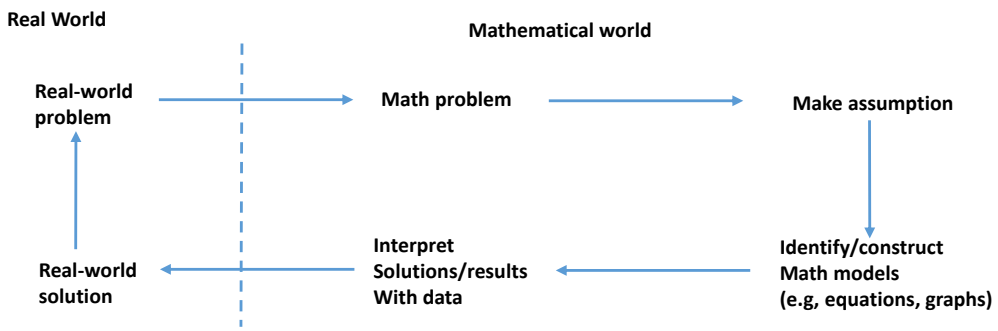

Figure: 1.1: Shows some stages of mathematical modelling

1.2.2 Some Approches of Mathematical Modelling

- Emperical Modelling: it involves using the data related to a problem in order to formulate or construct a mathematical relationship between the variables.
- Simulation Modelling: it consist the use of computer programs or technological tool in order to get a scenario base on a set of rules, the rules arise from an interpretation of how a process is supposed to progress or evolve.
- Deterministic Modelling: it involve the use of equation or set of equations to predict the value of aquantity or the out come of an event.
- Stochastic Modelling: is the extension of deterministic modelling in which the probabilities and randomness of an events happening are taking into consideration in formulating the equations of the model (Murray, 2002).

1.2.3 Infectious Diseases

Communicable or infectious diseases are caused as a result of virus, bacterium or parasite, or as a result of invation by a host organism generally micoorganisms which are invisible to the naked eye. It can easily comunicate from one person to another.

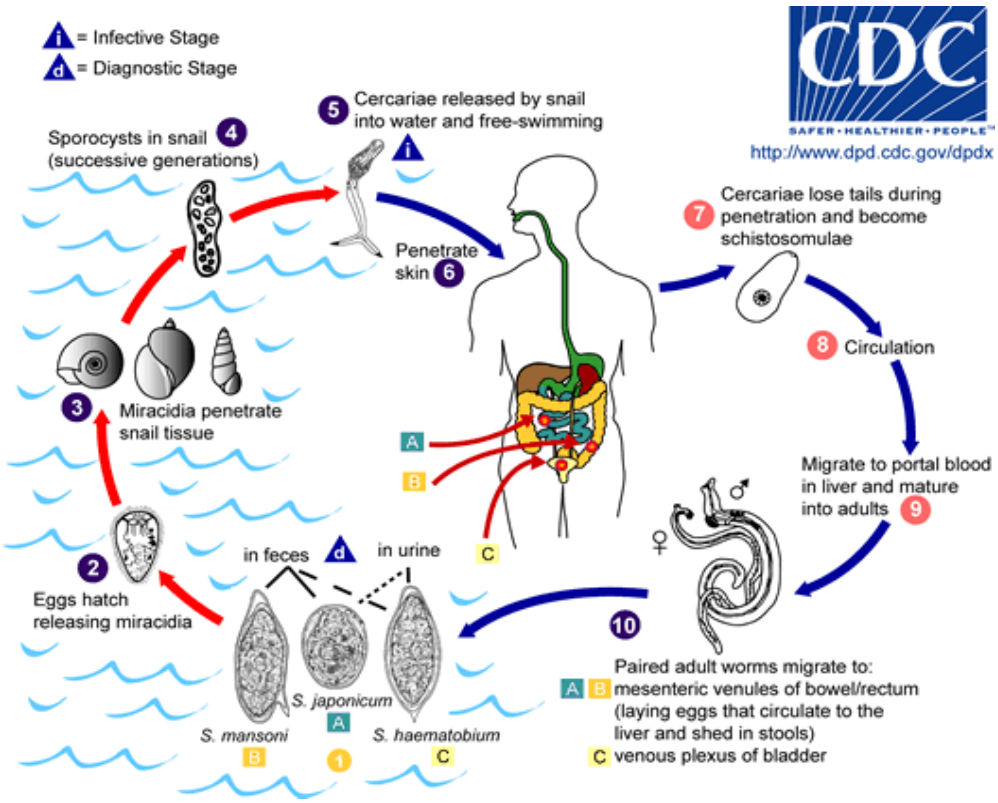

Figure: 1.2 Shows different stages of infection

1.3 Models

i) Exponential Growth

In a simplified conditions, such as a constant environment in which the population are fixed, the population size with respect to time depend on the difference between individual birth rate (B_0) and death rate (D_0), and given by:

$$\frac{dN}{dt} = (B_0 - D_0)N \tag{1.1}$$

where:

$B_0 =$ represents the birth rates of individuals at a time t .

$D_0 =$ represent the death rate of an individuals in a given time period, and

$N =$ the present population size.

The difference interm of birth and death rates $(B_0 - D_0)$ is called k, the rate of natural increase. It is the maximum number of individuals added to the population per unit time. Solving the differential equation (1.1) results to a formula that estimate a population size

$$N = N_0 e^{kt} \tag{1.2}$$

This equation gives the analysis that if birth and death rates are fixed, the population size grow exponentially. when transforming the equation into a natural logarithms, the exponential curve becomes linear, in which the slope of that line can be shown to be k

$$In(N) = In(N_0) + In(e)kt \tag{1.3}$$

and

$$k = [In(N) - In(N_0)\,]/t \tag{1.4}$$

where $In(e) = 1$. The population growth rate k, is a basic measure in population analysis, and it can also be used as a basis which compare between different populations and species.

ii) Logistic Growth

Equation (1.1) can be modified so that birth and death rates are not constant in a time t, but decreases or increases respectively as the population size increases :

$$\frac{dN}{dt} = N[(B_0 - r_b N) - (B_0 + r_d N)] \tag{1.5}$$

where r_b and r_d are the density-dependent birth and death rate constants. equation (1.5) predicts that a population stop growing when birth rate equals death rate,

$$B_0 - r_b N = D_0 + r_d N \tag{1.6}$$

And (1.6) is simplified to an equation showing the size at which the population is at steady state

$$N = \frac{(B_0 - D_0)}{(r_b + r_d)} \quad , \tag{1.7}$$

When the population is at steady state N is the carrying capacity of the environment, or C. This can be simplified:

$$C = \frac{k}{(r_b + r_d)} \tag{1.8}$$

Since $B_0 - D_0 = k$. If this new form of carrying capacity is combine with (1.5) it results to a familiar form of the logistic growth equation:

$$\frac{dN}{dt} = kN\left[\frac{(C-N)}{C}\right]. \tag{1.9}$$

iii) Taylor Series:

A Taylor series is a series expansion of a function about a point. A one dimensional Taylor series expansion of a real function $f(x)$ about a point $x = b$ is given by

$$f(x) = f(b) + (x-b)f'(x) + (x-b)^2 \frac{f''(a)}{2!} + (x-b)^3 \frac{f^{(3)}(b)}{3!} + \cdots$$

$$+(x-b)^k \frac{f^{(k)}(b)}{k!} + \cdots \tag{1.10}$$

iv) Exponential Decay:

A quantity is subject to exponential decay if it only decreases at a rate that is proportional to its value. This process can be described by the following equation, where *N* is the quantity and y is a positive number called the decay constant:

$$\frac{dN}{dt} = -yN. \tag{1.11}$$

The solution to this equation is:

$$N(t) = N_0 e^{-yt} \tag{1.12}$$

Here $N(t)$ is the quantity at time t, and $N_0 = N(0)$ is the initial quantity (Wiens, 2010).

v) Delay Model:

In general let consider a population change

$$\frac{dN}{dt} = f(N) \tag{1.13}$$

where $f(N)$ is a nonlinear function of N.

The main problems with single population models like (1.13) is that, the birth rate is considered to act at instant whereas there may be a time delay to take control of the time to reach maturity. We can also incorporate such delays by considering delay differential equation models of this form

$$\frac{dN}{dt} = f(N(t), N(t-T)), \tag{1.14}$$

with $T > 0$, the delay, is a parameter (Harko et al., 2014).

vi) SIR Model:

Kermack and Mckendrick in 1927 formulated a deterministic model for epidemic outbreak known as (SIR) Susceptible-Infected-Recovered model, or Kermack-Mckendrick epidemic model and is also called as a proposed special case of epidemic model.

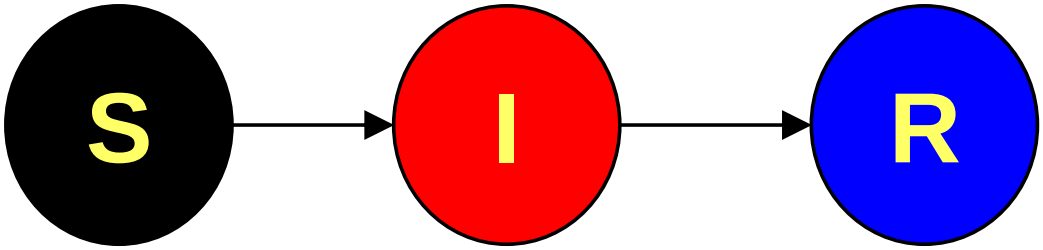

Figure*:* 1.3 Flowchart of (SIR) Susceptible-Infected-Recovered model

The model consist systems of nonlinear ordinary differential equation with mathematical representation as

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

$$\frac{dI}{dt} = kS(t)I(t) - \gamma I(t) \qquad (1.15)$$

$$\frac{dR}{dt} = \gamma I(t)$$

respectively, with the constants γ as the mean recovery rate and k as infection rate or can be regarded as rates of transition (probabilities) with the range $0 \leq k \leq 1$ and $0 \leq \gamma \leq 1$, in which a fixed population that consist of only three classes of compartments is considered.

(a) The function $S(t)$ represents the compartment of the susceptible individuals at time t when the disease is latent.

(b) The function $I(t)$ represents an infective compartment of individuals who have already been infected with the disease at a time t.

(c) The function $R(t)$ represents the compartment of individuals that are dead or recovered from the disease at a time t.

While the initial conditions

$$S_0 = S(0) \geq 0, I_0 = I(0) \geq 0, R_0 = R(0) \geq 0,$$

Satisfies the intuition

$$S_0 + I_0 + R_0 = N \text{ (Murray, 2002).}$$

vi)The Threshold Quantity:

The threshold quantity or basic reproduction number denoted as

$$R_o = \frac{kS_o}{\gamma}$$

determines whether the epidemic is present or not. If $R_o < 1$ there is no infection, but if $R_o > 1$ the epidemic is present. Also R_o as in the case of Kermack-Mckendrick epidemic model, can be regarded as secondary infection number caused as a result of single infective into a susceptible population of size N (Brauer & Castillo-Chavez, 2012).

vii)Equilibrium Point:

Equilibrium occurs in the model of infectious diseases when neither of the disease levels is changing, i.e. when all of the derivatives are equal to 0.

$$\frac{dS}{dt} = 0, \qquad \frac{dI}{dt} = 0 \quad \text{and} \quad \frac{dR}{dt} = 0.$$

The stability of the equilibrium point can be determined by linearizing the system of non-linear differential equations, while the other point requires a more sophisticated method.
The Jacobian matrix of the SIR model is

$$J(S,I) = \begin{bmatrix} \frac{\partial f}{\partial S} & \frac{\partial f}{\partial I} \\ \frac{\partial g}{\partial S} & \frac{\partial g}{\partial I} \end{bmatrix}$$

A state of a system which does not change is the equilibrium point of the system. If the equations of a system is refresented by a differential equation, then the equilibria of the system can be estimated by setting all derivatives to zero.

An equilibrium point of a system is considered as locally asymptotically **stable**, if the system always returns to the equilibrium point after small disturbances. If the system moves far away from the equilibrium point after small disturbances, then the equilibrium is **unstable** (Van Den Driessche & Watmough, 2002).

1.4 Application of Mathematical Model

Mathematical models are used to validate hypotheses made from experimental data and testing of these models has led to testable experimental predictions. There are impressive cases in which mathematical models provid an insight into biological systems, physical systems, decision making problems, space models, industrial problems, economical problems and so forth. The development of mathematical modeling is closely related to significant achievements in the area of computational mathematics.

1.5 Scope and Limmitation of the Study

The scope of this study is to discuss the role of the threshold quantity on local stability of SIR model with equal birth and death rates. The reed frost epidemic model was developed by Lowell Reed and Wade Hampton to identify the relationship between the compartment of susceptible, infected and recovered individuals in a population. Throughout the history, communicable diseases play major effects on the development of mankind, since epidemic diseases some times causes deaths before it disappear and new diseases may appear and become endemic. some communicable disease such as cholora, tuberclosis and measles are threat in a modern life, diseases like chicken pox, usually have less symptoms and disappear

on their own by their own accord. Looking at a limitations of mathematical model, an important inherent limitation of a model is created by what is left out. Problems arise when key aspects of the real-world system are inadequately treated in a model or are ignored to avoid complications, which may lead to incomplete models. Other limitations of a mathematical model are that they may assume the future will be like the past, input data may be uncertain or the usefulness of a model may be limited by its original purpose.

1.6 Overview

chapter one, presents the background of the study, definition of some basic terms, application of mathematical model as well as scope and limitations of the study.

Chapter two presents the literature related to the topic. In which some models such as the simple SIR model, the threshold quantity of simple SIR model, the SIRS model, the threshold quantity of SIRS, the relation between γ the recovery rate and β the average length of infection, the equilibrium analysis of SIRS model and the SIR model with induced vaccination are also discussed.

Chapter three, introduces the SIR model with birth and death rates equal, the steady states of the model and the role of threshold quantity on the local stability of the model.

CHAPTER 2

RELATED RESEARCH

Chapter two presents the literature related to the topic, the simple SIR model, the threshold quantity of simple SIR model, the SIRS model, the threshold quantity of SIRS, the relation between γ the recovery rate and β the average length of infection, the equilibrium analysıs of SIRS model and the SIR model with induced vaccination are also discussed.

2.1 Review of Some Related Literature

Communicable diseases has been questioned and studied in years. In fact, infectious diseases causes mortality and suffering in many underdeveloped and developing countries. Improvement of sanitation, effectiveness of antibiotics, as well as vaccination programs gave confidence that infectious diseases might be eliminated (Diekmann et al., 2000).

The continuous emerging and spread of infectious diseases brings about the issue of mathematical models which are considered as important tools of controlling the spread of diseases such as SIS, SIR, SEIR and so on. Models of infectious diseases can be identified as the description of the way infectious diseases spread into a population, according to the parameters and the initial conditions describing the environmental properties and the behavior of the disease.

2.2 The Simple SIR Model

Kermack and Mckendrick (1927) formulated a deterministic model for epidemic outbreak known as (SIR) Susceptible-Infected-Recovered model, or Kermack-Mckendrick epidemic model and is also called as a proposed special case of epidemic model, figure below represents a simple S-I-R model.

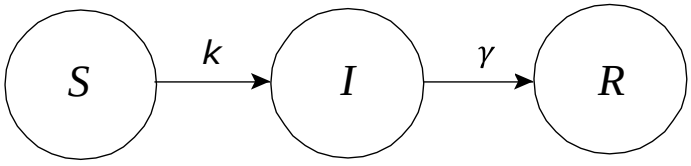

Figure: 2.1 Represents a simple S-I-R model

The model consist systems of nonlinear ordinary differential equation with mathematical representation as

$$\frac{dS}{dt} = -kS(t)I(t) \tag{2.1}$$

$$\frac{dI}{dt} = kS(t)I(t) - \gamma I(t) \tag{2.2}$$

$$\frac{dR}{dt} = \gamma I(t) \tag{2.3}$$

respectively, with the constants γ as the mean recovery rate and k as infection rate or can be regarded as rates of transition (probabilities) with the range $0 \leq k \leq 1$ and $0 \leq \gamma \leq 1$, in which a fixed population that consist of only three classes of compartments is considered.

(a) The function $S(t)$ represents the compartment of the susceptible individuals at time t when the disease is latent.
(b) The function $I(t)$ represents an infective compartment of individuals who have already been infected with the disease at a time t.
(c) The function $R(t)$ represents the compartment of individuals that are dead or recovered from the disease at a time t.

While the initial conditions

$$S_0 = S(0) \geq 0, I_0 = I(0) \geq 0, R_0 = R(0) \geq 0,$$

satisfies an intuition

$$S_0 + I_0 + R_0 = N.$$

Adding (2.1)-(2.3) of the above equations gave an important conclusion in the formulation of epidemic model, that is

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$$

Implies,

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

where N represents total of population size and S, I, R are all bounded by N(Murray, 2002).

2.3 The Threshold Quantity of Simple SIR Model

The threshold quantity or basic reproduction number denoted as

$$R_o = \frac{kS_o}{\gamma}$$

determines whether the epidemic is present or not. If $R_o < 1$ there is no infection, but if $R_o > 1$ the epidemic is present. Also R_o as in the case of Kermack-Mckendrick epidemic model, can be regarded as secondary infection number caused as a result of single infective into a susceptible population of size N (Brauer & Castillo-Chavez, 2012).

The epidemiologist conclude that, many infectious diseases are more complicated compared with the suggestion of simple SIR model. Rigorous observations and statistical methods almost tackled the complexity in behavior, biological and environmental properties of the disease. Also compartment is added to a model as the better way to overcome or mimic the disease (Ozcaglar et al., 2012).

2.4 The SIRS Model

Kermack and Mckendrick's epidemic model is an SIR (Susceptible Infected Recovered) model, without some vital dynamics (births and deaths). But the figure below represents the modified case in which a recovered individuals return back to the susceptible class,

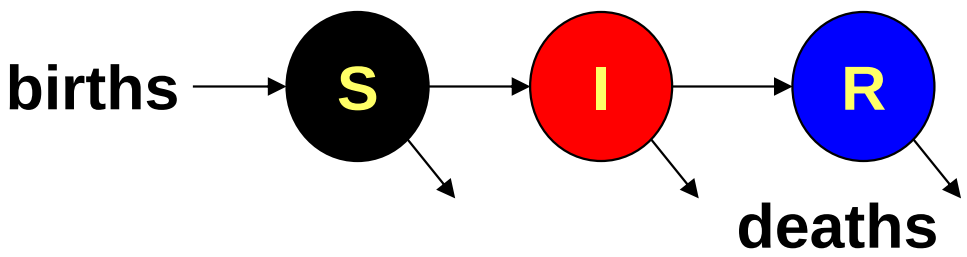

Figure: 2.2 Flowchart of SIRS model

The systems of nonlinear ordinary differential equation representing this situation is given by,

$$\frac{dS}{dt} = -kSI + \alpha(N - S) \tag{2.4}$$

$$\frac{dI}{dt} = kSI - (\gamma + \alpha)I \tag{2.5}$$

$$\frac{dR}{dt} = \gamma I - \alpha R \tag{2.6}$$

with the initial conditions

$$N_1 = S(0) \geq 0, N_2 = I(0) \geq 0, N_3 = R(0) \geq 0,$$

satisfying the equation

$$N_1 + N_2 + N_3 = N \text{ (Harko, Lobo, \& Mak, 2014).}$$

2.5 The Threshold Quantity of SIRS

The threshold quantity or basic reproduction number denoted as

$$R_o = \frac{k}{\gamma+\alpha} \tag{2.7}$$

determines whether the endemic is present or not. If $R_o = \frac{k}{\gamma+\alpha} < 1$ the disease is stable meaning there is no infection, but if $R_o = \frac{k}{\gamma+\alpha} > 1$ the disease is unstable meaning the endemic is present.

Note that the model with the parameter α, which represent the births and deaths is called a model of an endemic disease, while a model without a parameter α, is called a model of an epidemic disease (Adda & Bichara, 2011).

2.6 Relation Between γ The Recovery Rate and β The Average Length if Infection

Suppose that $S_o = S(0)$ is the number of individuals examined to have contacted the disease at time t.

Let $S(t)$ be the number of individuals who remain sick after a time t. consider γ as per capital rate of recovery, then the rate at which $S(t)$ changes is

$$\frac{dS}{dt} = -\gamma S(t) \tag{2.8}$$

Using the computation, $\sum_t tf(t)$ with $f(t)$ representing the proportion of scores in t values, to determine the average infection length of the disease.

Let [0, ∞) be divided into sub-intervals by

$$0 = t_o < t_1 < t_2 < t_3 < \cdots$$

Where,

$$t_{n+1} - t_n = \Delta t \quad \text{For all n} \geq 0.$$

Number of those recovered between t_n and t_{n+1} is

$$S(t_n) - S(t_{n+1})$$

with the approximate infection length t_n.

The proportion of cured susceptible individuals is

$$\frac{S(t_n) - S(t_{n+1})}{S_o},$$

which implies the infection mean value k is approximately,

$$\beta \approx \sum_{n=0}^{\infty} t_n \left(\frac{S(t_n) - S(t_{n+1})}{S_o}\right)$$

$$= \frac{1}{S_o}\sum_{n=0}^{\infty} t_n \left(\frac{S(t_n)-S(t_{n+1})}{\Delta t}\right)\Delta t \tag{2.9}$$

Note that as $\Delta t \longrightarrow 0$,

the proportion $\frac{S(t_n)-S(t_{n+1})}{S_o}$ approaches $-\frac{dS}{dt}$

and equation (2.8) approaches

$$\frac{1}{S_o}\int_0^{\infty} t\left(-\frac{dS(t)}{dt}\right)dt = -\frac{1}{S_o}\int_0^{\infty} t\, dS(t) \tag{2.10}$$

Which implies,

$$\beta = -\frac{1}{S_o}\int_0^{\infty} t\, dS(t) \tag{2.11}$$

Using equation (2.8) and applying integration by part in equation (2.11), results to

$$\beta = \frac{1}{\gamma} \tag{2.12}$$

Equation (2.12) gave the required result, meaning that the recovery rate γ is related to the average length of infection β (Rhodes & Anderson, 2008).

The idea of equilibrium and stability points of the epidemic outbreak, make it possible for the epidemiologists to carry out some analysis on the epidemic outbreak.

2.7 The Equilibrium Analysis of SIRS

At equilibrium equation (2.4) to (2.6) are all equal to zero, which implies

$$-kSI + \alpha(N - S) = 0 \tag{2.13}$$

$$kSI - (\gamma + \alpha)I = 0 \tag{2.14}$$

$$\gamma I - \alpha R = 0 \tag{2.15}$$

The incident rate $H = kSI$ is the transition rate of individuals from the susceptible class to the class of infected individuals. The threshold number $R_o = \frac{k}{\gamma+\alpha}$, determines the rate at which individual is infected with the disease.

From equation (2.5)

$$\frac{dI}{dt} = kSI - (\gamma + \alpha)I$$

$$= \frac{k}{\gamma + \alpha}(\gamma + \alpha)SI - (\gamma + \alpha)I$$

$$= R_o(\gamma + \alpha)SI - (\gamma + \alpha)I$$

$$= [R_oS - 1](\gamma + \alpha)I$$

Here $R_o > 0$, which implies $\frac{dI}{dt} > 0$, meaning that there will be an epidemic outbreak with the significant number of individuals infected with the disease, and the free equilibrium state of the disease is unstable. Also for $R_o < 0$, implies, $\frac{dI}{dt} < 0$, meaning that there will be no proper outbreak of epidemic in the population.

From equation (2.14)

$$(kS - (\gamma + \alpha))I = 0,$$

This implies, either

$$I = 0 \text{ or } kS - (\gamma + \alpha) = 0$$

Solving for $I = 0$ in equation (2.7) and (2.9), results to

$$R = 0 \text{ and } S = N,$$

meaning that the free equilibrium of the disease is

$$E_o = [N, 0, 0] \tag{2.16}$$

Also solving

$$kS - (\gamma + \alpha) = 0,$$

implies

$$S = \frac{\gamma+\alpha}{k} (2.7.5)$$

Substituting equation (2.7.5) in (2.7.1), implies,

$$-k\frac{\gamma + \alpha}{k} I + \alpha\left(N - \frac{\gamma + \alpha}{k}\right) = 0$$

$$(\gamma + \alpha)I = \frac{(\gamma + \alpha)}{k} - \alpha N$$

And

$$I = \frac{\alpha(\gamma+\alpha-kN)}{k(\gamma+\alpha)} \tag{2.17}$$

Substituting equation (2.17) in (2.15), implies,

$$\gamma\left[\frac{\alpha(\gamma + \alpha - kN)}{k(\gamma + \alpha)}\right] - \alpha R = 0$$

$$R = \frac{\gamma(\gamma+\alpha-kN)}{k(\gamma+\alpha)} \tag{2.18}$$

Thus the secnd equilibrium point of the epidemic is

$$E_1 = \left[\frac{\gamma+\alpha}{k}, \frac{\alpha(\gamma+\alpha-kN)}{k(\gamma+\alpha)}, \frac{\gamma(\gamma+\alpha-kN)}{k(\gamma+\alpha)}\right] \quad (2.19)$$

Equation (2.19) gave the required result, by showing the equilibrium point of the SIR model with the equal birth and death rates (Momoh, 2012).

The role at which the vaccination program plays on the disease free equilibrium point and epidemic equilibrium point, is of considerable important, which can be easily seen in the process of controlling many epidemic outbreak, such as measles, polio and so on.

2.8 The SIR Model with Induced Vaccination

Now, another SIR model with induced vaccination is considered and presented as follows,

$$\frac{dS}{dt} = -kSI + \alpha(N - h - S) \quad (2.20)$$

$$\frac{dI}{dt} = kSI - (\gamma + \alpha)I \quad (2.21)$$

$$\frac{dR}{dt} = \gamma I - \alpha R \quad (2.22)$$

$$\frac{dV}{dt} = \alpha h - \alpha V \quad (2.23)$$

where S,I,R represent the compartments of susceptible, infected, recovered population and V represent the group of individuals that have been vaccinated, h is the vaccination rate, k represents the infection rate, α is the mortality rate and γ represents the recovery rate (Vargas et al., 2011).

CHAPTER 3

MODEL AND IT IS ANALYSIS

This chapter introduces the SIR model with birth and death rates equal, the steady states of the model and the role of threshold quantity on the local stability of the model.

3.1 Model

Kermack and Mckendrick's epidemic model is an SIR (Susceptible Infected Recovered) model, based on simple assumptions, without some vital dynamics (births and deaths). But in some infectious diseases new susceptible individuals arrive into the population, for this case deaths has to be included in the model. In modelling this case, the population is divided into three compartments that is S-I-R and a death rate α is considered equal to the birth rate, the figure below represents a modified susceptible-infected-recovered epidemic model in which the birth and death rates are considered to be equal.

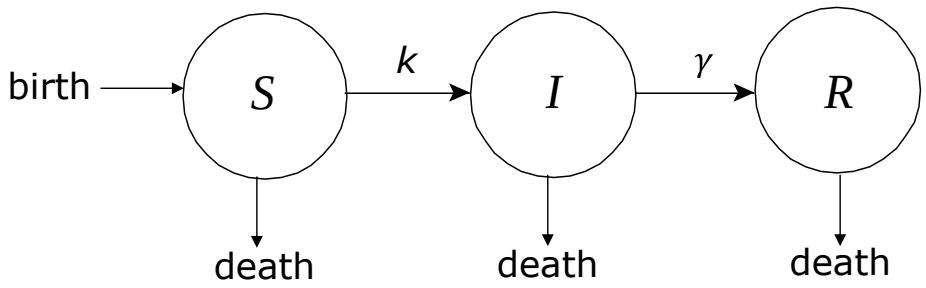

Figure: 3.1 Represents a flowchart of a modified susceptible-infected-recovered epidemic model in which the birth and death are considered to be equal.

In this compartmental model, t is an independent variable, and the rate at which individual is moving from one class to the other are mathematically expressed as derivatives, the system of nonlinear ordinary differential equation representing this situation is given by

$$\frac{dS(t)}{dt} = \alpha - kSI - \alpha S \tag{3.1}$$

$$\frac{dI(t)}{dt} = kSI - (\gamma + \alpha)I \tag{3.2}$$

$$\frac{dR(t)}{dt} = \gamma I - \alpha R \tag{3.3}$$

with the constants γ as the mean recovery rate and k as infection rate or can be regarded as the rates of transition (probabilities) with the range $(0 \leq k \leq 1)$ and $(0 \leq \gamma \leq 1)$, in which a fixed population that consist of only three compartments is considered.

(a) The function $S(t)$ is the fraction that represents the compartment of the susceptible individuals at time t, when the disease is at latent state.

(b) The function $I(t)$ is the fraction that represents an infective compartment of individuals who have already been infected with the disease at a time t.
(c) The function $R(t)$ is the fraction that represents the compartment of individuals that are dead or recovered from the disease at a time t.
The population density is fixed, so that

$$S(t) + I(t) + R(t) = 1$$

And

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$$

In line with previous researches like (Hallam & Gross, 2009) and (Brauer & Castillo-Chavez, 2012), this model is developed base on the following assumptions:

(i) The population is considered to be fixed.
(ii) The only way an individual can leave the susceptible class is to be infected and the only way an individual can leave the infected compartment is to recover from the disease. Once an individual recovered, the person possessed immunity.
(iii) Sex, social status and the race has no effect on the probability of being infected.
(iv) There is no inherited immunity from the disease.
(v) The degree of interactions between the members of the population is the same.
(vi) The birth and death rates are included.
(vii) The birth and death rates are equal so that the population is stationary.

3.2 The Equilibrium Analysis

At equilibrium equation (3.1) to (3.3) are all equal to zero, which implies

$$-kSI + \alpha(1 - S) = 0 \tag{3.4}$$

$$kSI - (\gamma + \alpha)I = 0 \tag{3.5}$$

$$\gamma I - \alpha R = 0 \tag{3.6}$$

solving for $I = 0$, $R = 0$ and $S = 1$ in equation (3.4) to (3.6), results to the first steady state that is a zero steady state, which is also called as the free- disease equilibrium point

$$E_o = [1,0,0] \tag{3.7}$$

Most of the interests are at non zero steady state, for which I, R are non-zero and S are not equal to 1, now let go about non zero steady state by considering a situation where there are infected individuals in a given population.

From equation (3.6)

$$\gamma I - \alpha R = 0$$

The equation for the recovered individuals is

$$R = \frac{\gamma I}{\alpha} \tag{3.8}$$

Also from equation (3.5)

$$(kS - (\gamma + \alpha))I = 0$$

Implies,

$$kS - (\gamma + \alpha) = 0$$

since it is already known that, the class of infected individuals is not zero, which implies

$$S = \frac{\gamma+\alpha}{k} \tag{3.9}$$

from the fact that the sum of susceptible, infected and recovered individuals in a given population is equal to the total population, leads to

$$S(t) + I(t) + R(t) = 1 \tag{3.10}$$

Equation (3.10) gives

$$\frac{\gamma + \alpha}{k} + I + \frac{\gamma I}{\alpha} = 1$$

And

$$I = \frac{1-\frac{\gamma+\alpha}{k}}{1-\frac{\gamma}{\alpha}} \tag{3.11}$$

Thus the non-zero steady state which is the second steady state is

$$E_1 = \left[\frac{\gamma+\alpha}{k}, \frac{1-\frac{\gamma+\alpha}{k}}{1-\frac{\gamma}{\alpha}}, \frac{\gamma I}{\alpha}\right] \tag{3.12}$$

which is the endemic equilibrium point, for E_1 to be the real steady state, the values of S, I and R in equation (3.12) has to be greater than zero, at this second steady state, let consider

$$\frac{1 - \frac{\gamma + \alpha}{k}}{1 - \frac{\gamma}{\alpha}} > 0$$

Which means that

$$1 - \frac{\gamma + \alpha}{k} > 0$$

$$1 > \frac{\gamma + \alpha}{k}$$

$$\frac{k}{\gamma+\alpha} > 1 \tag{3.13}$$

Remark: the endemic equilibrium point of the disease exists only when $k > \gamma + \alpha$. i.e. the rate of infection must be bigger than the infected individuals for the disease to be endemic (Vargas et al., 2011).

3.3 The Threshold Quantity

The threshold quantity or basic reproduction number is regarded as the average number of secondary cases brought by infected individual in his entire life as infectious when introduced into a susceptible population and is denoted by

$$R_o = \frac{k}{\gamma+\alpha} \tag{3.14}$$

determines whether the endemic is present or not (Ozcaglar et al., 2012).

If $R_o = \frac{k}{\gamma+\alpha} < 1$ the disease is stable meaning there is no infection, but if $R_o = \frac{k}{\gamma+\alpha} > 1$ the disease is unstable meaning the endemic is present.

Also from equation (3.2)

$$\frac{dI}{dt} = kSI - (\gamma + \alpha)I$$

$$= \frac{k}{\gamma + \alpha}(\gamma + \alpha)SI - (\gamma + \alpha)I$$

$$= R_o(\gamma + \alpha)SI - (\gamma + \alpha)I$$

$$= [R_oS - 1](\gamma + \alpha)I \tag{3.15}$$

From equation (3.15) $R_o > 0$, implies $\frac{dI}{dt} > 0$, meaning that there will be an epidemic outbreak with the significant number of individuals infected with the disease, and the free equilibrium state of the disease is unstable. Also for $R_o < 0$, implies, $\frac{dI}{dt} < 0$, meaning that there will be no proper outbreak of epidemic in the population(Van Den Driessche & Watmough, 2002).

3.4 Stability Analysis

Now, let study the linear stability of the disease free-equilibrium and endemic disease equilibrium points. For simplicity, consider the total population density

$$S(t) + I(t) + R(t) = 1$$

Implies

$$R(t) = 1 - S(t) - I(t)$$

Therefore it is enough to use

$$\frac{dS}{dt} = \alpha - kSI - \alpha S = F(S, I) \tag{3.16}$$

$$\frac{dI}{dt} = kSI - (\gamma + \alpha)I = G(S, I) \tag{3.17}$$

Then, the jacobian matrix of the equation (3.16) and (3.17) is

$$J(S, I) = \begin{bmatrix} \frac{\partial F(S,I)}{\partial S} & \frac{\partial F(S,I)}{\partial I} \\ \frac{\partial G(S,I)}{\partial S} & \frac{\partial G(S,I)}{\partial I} \end{bmatrix}$$

Which implies

$$J(S,I) = \begin{bmatrix} -kI - \alpha & -kS \\ kI & kS - (\gamma + \alpha) \end{bmatrix}$$

The jacobian matrix at the first steady state (the disease free-equilibrium point) is evaluated as

$$J(1,0) = \begin{bmatrix} -\alpha & -k \\ 0 & k - (\gamma + \alpha) \end{bmatrix}$$

and the characteristic equation corresponding to the first steady state is also evaluated as

$$\begin{bmatrix} -\alpha - \lambda & -k \\ 0 & k - \alpha - \gamma - \lambda \end{bmatrix} = 0$$

which implies,

$$(-\alpha - \lambda)(k - \alpha - \gamma - \lambda) = 0$$

$$\lambda^2 + (2\alpha - k + \gamma)\lambda + (\alpha^2 - \alpha k + \alpha\gamma) = 0$$

$$= \frac{-(2\alpha - k + \gamma) \pm \sqrt{(2\alpha - k + \gamma)^2 - 4(\alpha^2 - \alpha k + \alpha\gamma)}}{2}$$

$$= \frac{-(2\alpha - k + \gamma) \pm \sqrt{(k - \gamma)^2}}{2}$$

$$= \frac{-(2\alpha - k + \gamma) \pm (k - \gamma)}{2}$$

which gives the eigenvalues $\lambda_1 = -\alpha$ and $\lambda_2 = k - \alpha - \gamma$.

$\lambda_1 < 0$. Let consider λ_2, if $k - \alpha - \gamma < 0$ then $k < \alpha + \gamma$ or $\frac{k}{\gamma+\alpha} < 1$ or $R_o < 1$ as both the eigenvalues are negative then, the disease free-equilibrium point is locally asymptotically stable, meaning that there will be no outbreak of epidemic in the population but if $k > \alpha + \gamma$ the infected class exists.

The jacobian matrix at the second steady state (the disease endemic equilibrium point) is evaluated as

$$J\left(\frac{\gamma+\alpha}{k}, \frac{1-\frac{\gamma+\alpha}{k}}{1-\frac{\gamma}{\alpha}}\right) = \begin{bmatrix} -\left(\frac{\alpha(k-\alpha-\gamma)}{\alpha-\gamma}\right) - \alpha & \alpha-\gamma \\ \frac{\alpha(k-\alpha-\gamma)}{\alpha-\gamma} & 0 \end{bmatrix}$$

And the characteristic equation corresponding to the second steady state is also evaluated as

$$\begin{bmatrix} -\left(\frac{\alpha(k-\alpha-\gamma)}{\alpha-\gamma}\right) - \alpha - \lambda & \alpha-\gamma \\ \frac{\alpha(k-\alpha-\gamma)}{\alpha-\gamma} & -\lambda \end{bmatrix} = 0$$

$$-\lambda\left(-\left(\frac{\alpha(k-\alpha-\gamma)}{\alpha-\gamma}\right) - \alpha - \lambda\right)) - \alpha(k-\alpha-\gamma) = 0$$

$$\lambda^2 + \frac{\alpha k}{\alpha+\gamma}\lambda + \alpha(k-\alpha-\gamma) = 0$$

$$\lambda = \frac{1}{2}\left[-\frac{\alpha k}{\alpha+\gamma} \pm \sqrt{\left(\frac{\alpha k}{\alpha+\gamma}\right)^2 - 4\alpha(k-\alpha-\gamma)}\right]$$

Or

$$\lambda = \frac{1}{2}\left[-\alpha\, R_o \pm \sqrt{\alpha^2\, {R_o}^2 - 4\alpha(k-\alpha-\gamma)}\right]$$

If $\alpha^2 {R_o}^2 < 4\alpha(k - \alpha - \gamma)$ the eigenvalues are both complex with the real part $-\alpha R_o$ which is negative and if $\alpha^2 {R_o}^2 > 4\alpha(k - \alpha - \gamma)$ the real part is also negative, since the real part of each eigenvalue is negative, it is concluded that the endemic equilibrium point of the disease is stable (Chauhan et al., 2014).

CHAPTER 4

CONCLUSIONS

In this study, the SIR model with equal birth and death rates is considered. The analysis shows that the local stability of the SIR model is obtained by the threshold number. If the threshold number is less than one, there will be a disease-free steady state and is locally stable in a feasible region, meaning, the disease will die out from the population. But if the threshold number is greater than one, there will be a unique disease steady state which is locally stable in the interior of the feasible region and the disease is present in the population. The proof is based on the method of linearization. Materials are organized according to the mathematical theory not the biological applications.

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Approval of Director of Graduate School of Applied Sciences

Prof.Dr. İlkay SALİHOĞLU

We certify that, this thesis is satisfactory for the award of the degree of Masters of Science in Mathematics

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I hereby declare that all information in this document has been obtained and presented in accordance with academic rules and ethical conduct. I also declare that, as required by these rules and conduct, I have fully cited and referenced all material and results that are not original to this work.

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To my daughter Maryam...

ABSTRACT

In this study, the simple SIR epidemic model is modified, and the analysis shows that the local stability of the model is obtained by the threshold number. If the threshold number is less than one, there will be a disease-free steady state and is locally stable in a feasible region, meaning, the disease will die out from the population. But if the threshold number is greater than one, there will be a unique disease steady state which is locally stable in the interior of the feasible region and the disease is present in the population. The proof is based on the method of linearization. Materials are organized according to the mathematical theory not the biological applications.

***Keywords*:** Threshold quantity, local stability, epidemic disease, SIR model, endemic disease

ÖZET

Bu araştırmada, basit bir SIR epidemik model modifiye edilmiştir ve modelin yerel stabilitesi eşik sayısı tarafından elde edilen analiz gösterilmiştir. Eşik sayısı birden az ise, orada hastalık barındırmayan kararlı bir durum olabilir ve uygulanabilir bir bölgede yerel olarak kararlı olacak , yani, populasyon dışında ölecek şekilde kararlı durum olacaktır. Eşik sayısı birden büyük olursa, uygun bölgenin içinde bölgesel olarak istikrarlı olan kararlı olan tek hastalık olacak ve hastalık populasyonda mevcut bulunacaktır. İspat lineerleştirme yöntemine dayalıdır. Bu çalışma matematiksel teori üzerine kurulmuş olup bioloji uygulamaları içermemektir.

Anahtar Sözcükler: Eşik değeri, yerel stabiliti, epidemik hastalık, SIR model, endemik hastalık

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SIR Susceptibe Infected Recovered

SIRS Susceptibe Infected Recovered Susceptible