

ADDIS ABABA UNIVERSITY



**COLLEGE OF NATURAL AND COMPUTATIONAL SCIENCE
DEPARTMENT OF MATHEMATICS
MATHEMATICALMODELLING USING IMPROVED SIR
MODELS WITH THE ENVIRONMENTAL NOISE!**

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Dedication

I would like to dedicate this thesis to the department of mathematics, college of natural and computational science, Addis Ababa University in **SIR model with the environmental noise** requirements for the degree of Master of Science in mathematics. Therefore; I declare that this report done by me during my study has not been submitted to any other higher institutions for the award of any academic certificate. A thesis Work submitted to the School of Graduate Studies of Addis Ababa University in “SIR Model with the environmental noise” of the Requirements for the Degree of Master of differential equation. A thesis Work submitted to the School of Graduate Studies of Addis Ababa University in “SIR Model with the environmental noise” of the Requirements for the Degree of Master of differential equation.

This thesis is approved by board of examiners:

Chairman of the Graduate committee: _____sign_____date_____

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ABSTRACT

I develop the SIR models and investigate the stability of their equilibrium points in this paper. Through vaccination strategies and the use of this Pontragin Maximum Principle, we are able to control the spread of disease through numerical research and the theory of optimal control. It is discovered that the models' disease-free equilibrium is asymptotically unstable otherwise and asymptotically stable when the fundamental reproduction number is less than one. Additionally, it was discovered that in cases when the fundamental reproduction number is greater than one, the endemic equilibrium is asymptotically stable; in other cases, it is asymptotically unstable. In order to predict and prevent epidemics, this work establishes the susceptible-infectious-recovered (SIR) compartment model for disease

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CHAPTER-ONE

1.INTRODUCTION

The study of the distribution and causes of health-related conditions, events, and diseases is known as epidemiology. The use of this thesis to prevent illness and address other health issues.

Epidemiological investigations, monitoring, and descriptive studies can be conducted using a variety of techniques to examine determinants.

- The impact of population dynamics, including births, deaths, and migrations, is disregarded during the time of infectious disease transmission.
- The SIR (susceptible-infected-removed) paradigm was created in the early 1900s by Ronald Rosswillium Hamer and associates.
- Diseases classified as infectious are those that are caused by microbiological agents that can spread from one organism to another or from person to person.
Examples of these illnesses are covid19, cholera, chickenpox, common cold, and others.
- However when disease spreads in a given population, it divides the population in to three variables.

S=susceptible

$S(t)$ =number of individuals that can get susceptible at the time t.

I= infective

$I(t)$ =the number of individuals that can get infected at the time t.

R=removed

$R(t)$ = the number of individuals who are immune or dead at the time t, then those three state variables are called SIR model.

$S(t)+I(t)+R(t)=N(t)=N$ for all $t \in [0, \infty)$. where N is total number of population.

The disease free-state indicates that $s(t)=N(t)=N, I(t)=0, R(t)=0$ for all $t \in [0, \infty)$

Determine the dynamics of the SIR model susceptible→infected→removed

We must identify

The rate at which the susceptible individuals get infected

The rate at which the infected people get recovered or die.

This study aims to find a optimal control strategies for the class of disease which confer permanent immunity to its victims after their infection period. When modeling infectious diseases, we have an infectious disease and based on this disease we build or formulate a model which translates mathematically the dynamics of the disease i.e we move from infectious disease to model. During the modeling process we often consider: mode and agent of transmission, immunity after infection etc.

Different models have been developed for infectious diseases and below are a list of some of the basic models for infectious diseases based mainly on if individuals become immune or susceptible after recovery from the disease

- Susceptible Infected (SI) model

This is used for diseases where an infected individual remains infected and infectious throughout his life. Example of such diseases is cytomegalovirus (CMV) and herpes

- Susceptible Infected Recovered (SIR) model:

An individual living the infected class is conferred permanent immunity after the infected individuals recover from the disease. Examples are Chickenpox and mumps

- Susceptible Infected Susceptible (SIS) model: Diseases here gives no immunity after infection. Infected go back to being susceptible when they recover from the disease. Examples are rhinoviruses, gonorrhea and chlamydia

- Susceptible Infected Recovered Susceptible (SIRS) model: Diseases modeled here confers temporary immunity to infect after recovery before they become susceptible again. An example is Seasonal flu

- Susceptible Exposed Infected Recovered Susceptible (SEIR) model: This is used for modeling diseases where Individuals experience a latent/incubation period when they are infected but not infectious then to being infectious and then to being recovered with permanent immunity. An example is Measles.

- Susceptible Exposed Infected Recovered Susceptible (SEIRS) model: This is the same as the SEIR model only that it confers temporary immunity after which recovered individual becomes susceptible again. Examples are Malaria and rotavirus.

To model the dynamics of infectious diseases such as chickenpox and mumps which leaves it's victims with Permanent immunity when recovered, we consider them before they become infected, when they are infected and after they are recovered. We do such using the SIR models:

The SIR models are one of the simplest and basic compartment models as many other models are derived from its basic form. The SIR model models the movement or flow of individuals between three compartments: Susceptible, Infected and Recovered/Removed. The models were formed by including the "Recovered/Removed" group to the more basic SI model which divides every compartment into two: Susceptible and Infected. Mathematically, the SIR model was proposed by W.O. Kermack and A.G. McKendrick in their 1927 paper titled "A contribution to mathematical theory of epidemics". For the SIR model, the rate at which people become infected is proportional to the number of people already infected with the disease, and the number of people who are susceptible. If there are lots of infected people, the chance of a susceptible coming in contact with someone who is already infected is high. Each member of the population in the SIR model typically progresses from the susceptible to infected/infectious to recovered/removed except if the disease is eradicated in time. This movement can be shown in the flow diagram

below in figure 1.1

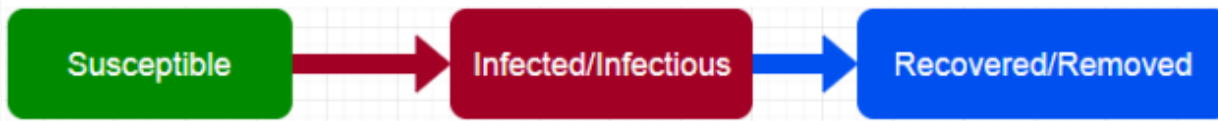


Figure 1.1: Flow diagram for a SIR Model.

where the boxes represents the different compartments and the arrows the transition between compartments. Since epidemics and infectious diseases have continued to plague man as they usual come into a population, infect a large portion of the population and leave scores dead. These days, a thorough understanding of these diseases is attained by epidemiological modeling and the use of mathematical equations to study the dynamics of these illnesses. Since infectious disorders such as chickenpox typically result in lifelong immunity, the SIR model is used to model them. When these infectious diseases are modeled, it's critical to determine how they will spread—typically by examining the model's stability at their equilibrium point, or the determinant of the spread—and perhaps identify the best course of action for mitigating or controlling the sickness.

1.1. Objective of the Study

The main objective of this study is to construct a reliable SIR model for analyzing the transmission disease some details. The other minor objectives of the model are as follows

Calculating the SIR model as shown in the fig 1.1 above by using the ODE

I introduce the three models such as S=fraction of total population are susceptible, I=fraction of total population are infected and R=fraction of total population are recovered, then the sum $S+I+R=1$.

- to properly analyze the theoretical explanations,
- to more clearly display the mathematical analysis,
- to express the value of vaccines in boosting herd immunity.
- Find the model's basic reproduction number.
- Identify the model's equilibrium and stability points.
- Prevent the spread of illness.
- Understanding the disease dynamics.
- Predicting epidemic out comes

The main goals of studying how infectious diseases spread over time and place are to better understand the mechanisms of transmission and the characteristics that are crucial to their spread in order to make predictions and assess control measures.

1.2, Statement of the problem

The SIR model (susceptible-infected-recovered) was created by David and Long (2001) to simulate the long-term spread of an infectious illness in a particular population. It is suggested in this work to address some of the aspects, though, that this model is unable to account for. These elements are

The impact of birth and deaths from unrelated causes were not taken into account.

The infected people who pass away from the illness were not taken into account.

But in this thesis work, I study the constant birth and death rates

The population's overall health and nutritional level, which could positively influence the probability of epidemics happening, were not taken into account.

1.3 Structure of the thesis

The plan of this study analyzes the following points:

The first chapter contains a general introduction of a SIR model, the second chapter contains a brief history and the review of literature on the SIR model and mathematical tools used.

The third chapter contains the formulation of the SIR model i.e changing the SIR model in ordinary differential equations; determine the point where the maximum infection (I_{max}) occurred.

Calculate the change of the total population before and after taking the vaccination and the stability, equilibrium points and the reproductive number (R_0) of the SIR model and chapter 4 contains conclusions and reference

CHAPTER-TWO

2, LITERATURE REVIEW AND MATHEMATICAL TOOLS

2.1, Literature review

Applications of the mathematical modeling to the spread of disease (epidemic has long history and was initiated by Daniel Bernoulli who worked on the effect of cow pox Inoculation on the spread of small pox in 1760.

Mathematics has been used to understand & predict the spread of disease relating the important health question to the basic infection parameters.

Meghan(1998) developed a simple mathematical model for the number of the people infected with an infection disease such as chicken pox in a closed population. His study showed that if the parameter governing the spread of disease is positive, then the disease will spread throughout population and eradication is not possible. On the other hand if the parameter is negative, the chicken pox dies out in the population.

Kermack and Mckendrick(1927) proposed SIR model to explain the rapid rise and fall in the number of infected patients observed in epidemics such as cholera and Bubonic plague in a London.

2.2. The existence of SIR model:

2.2.1. The basic SIR model

The basic SIR model is provided as:

$$\frac{dS(t)}{dt} = -\beta S(t)I(t), \text{ at the time } t=0, \text{ then } S(0)=S_0>0.$$

$$\frac{dI(t)}{dt} = \beta S(t)I(t) - \gamma I(t), \text{ at } t=0, \text{ then } I(0)=I_0>0$$

$$\frac{dR(t)}{dt} = \gamma I(t), t=0, \text{ then } R(0)=R_0 \text{ where}$$

$S(t)$ = number of susceptible individuals at time t .

$I(t)$ = number of infected individuals at time t .

$R(t)$ = number of recovered individuals at time t .

$N(t)$ = total population at time t .

β = infectious rate of the disease.

γ = recovery rate of the disease.

R_0 = reproductive ratio of the disease

This model classifies individuals in a given population into three state variables susceptible, infective and recovered. However, in this model, an individual potentially moves from susceptible individuals to the infective individuals when he/she contacts an infected person.

For instance, the contact for common cold may be walking within a few feet of an infected person that has recently coughed

. Infectious individuals spread the disease to the susceptible and remain in the infectious pool for some period of time before moving into recovered people.

2.3. Mathematical tools.

We discuss the two main types of models and mathematical tools used for the analysis of the **SIR** models.

The tools such as equilibrium points, linearization, stability analysis, control and the basic reproductive number (R_0).

2.3.1. Differential equations

When modeling in epidemiology, the dynamical system is represented mathematically by differential equation.

Definition:-an equation that contains one or more derivatives of the dependent (unknown) variables with respect to one or more independent variables.

Examples; a, $dy=y^2+x$

$$b, u(x)+u(y)=xy$$

$$c, xy''+y'=0.$$

In this application the functions usually represents the physical quantities, the derivatives the rate of changes. A solution of the differential equation is a set of functional expressions for the variables that reduce the differential equation to an identity. There are two mainly types of the differential equations.

A. Ordinary differential equation (ODE).

Definition: if the unknown function in the differential equation depends only a single (one) variable, then it is an ordinary differential equation (ODE).

An equation containing an unknown function of one real or complex variable t and its derivatives of some given function of t .

Example; $y''+ty'+e^t y=\sin(t)$ is 2nd order ordinary differential equation, linear and non-homogenous. Where “ y ” is unknown dependent variable & “ t ” is independent variable.

B. The Partial differential equations (PDE).

A partial differential equation (PDE) is an equation that contains unknown multi variable functions and their Partial derivatives.

Examples:- $F(x,y,u(x,y),U_x(x,y),U_y(x,y))=F(x,y,u,U_x,U_y)=0$ is partial differential equation in two independent variables of the first order.

Types of Models:

Modeling according to (mar) is the process of producing from physical system.

A model is the representation of the construction and working of the dynamical system of interest.

The main purpose of model is to predict the effect of changes to the system. Basically there are two main types of the models.

I, Deterministic model

The initial circumstances and parametric settings examine the model's output, or result.

For well-defined linear models, a unique output is generated into a unique input, and for non-linear models, numerous outputs are available.

The input & output variables are fixed values

ii, Stochastic models

It is usually called statistical model because the randomness is present. Conversely to the deterministic model, the stochastic model's variable states are not described by unique values i.e at least one of the impute or output variables is probabilistic.

Definition: for the stability analysis we need the concept of the basic reproduction number denoted by (R_0), equilibrium point, linearization & stability.

Equilibrium: Equilibrium for the differential equation is constant solution to the differential equation.

In an epidemic model it is appoint of zero change in the two compartments at the given time t, dS and dI are constants, so

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

$$\frac{dI}{dt} = \beta S(t)I(t) - \delta I(t), \text{ but } dS=dI=0, \text{ then } dS=dI, \text{ there is no change.}$$

Clearly we can see that at $(S,I)=(0,0)$ and

$(S,I) = (1,0)$, The compartments have not changed at the equilibrium points.

Representing the equilibrium points as:

(S^*,I^*) we can observe that $(S^*,I^*)=(0,0)$ occurs after the epidemic

Linearization and stability of the equilibrium:

The process where one can approximate the non-linear differential equations by linear differential equations. In general anon-linear differential equation cannot be solved, but through linearization the resulting linear equation can be solved.

To linearize S and I to be close to the equilibrium points (S^*,I^*) and take $X_1=S-S^*$ and $X_2=I-I^*$

$$dX_1=dS-dS^*, \Rightarrow dX_1=dS \text{ and}$$

$$dX_2= dI-dI^*, \Rightarrow dX_2=dI, \text{ there is no changes in equilibrium points}$$

i.e $S^*=I^*=0$ (because S^* and I^*) are constants. This means

$dx_1 = dS = -\beta S(t)I(t)$ and

$dx_2 = dI = \beta S(t)I(t) - \delta I(t)$, then by using the Taylor's series we assume that

$\frac{dS}{dt} = f(S, I)$ and $\frac{dI}{dt} = g(S, I)$ And expand along the equilibrium points (S^*, I^*) to give

$\frac{dS}{dt} = f(S^*, I^*) + (S - S^*) \frac{\partial f}{\partial S} + (I - I^*) \frac{\partial f}{\partial I} + \text{higher order term}$ and

$\frac{dI}{dt} = g(S^*, I^*) + (S - S^*) \frac{\partial g}{\partial S} + (I - I^*) \frac{\partial g}{\partial I} + \text{higher order term}$

But from the above $X_1 = S - S^*$ and $X_2 = I - I^*$ and the higher order terms being approximated to zeros

$f(S^*, I^*) = g(S^*, I^*) = 0$, since (S^*, I^*) are equilibrium points and

$\frac{dS}{dt} = \frac{dI}{dt} \Rightarrow dS = dI = 0$, then the equation becomes

$dS = (S - S^*) \frac{\partial f}{\partial S} + (I - I^*) \frac{\partial f}{\partial I} \Rightarrow dS = X_1 \frac{\partial f}{\partial S} + X_2 \frac{\partial f}{\partial I}$ and

$dI = X_1 \frac{\partial g}{\partial S} + X_2 \frac{\partial g}{\partial I}$ in matrix form these represented as follows;

$$\begin{pmatrix} dS \\ dI \end{pmatrix} = \begin{pmatrix} \frac{\partial f}{\partial S} & \frac{\partial f}{\partial I} \\ \frac{\partial g}{\partial S} & \frac{\partial g}{\partial I} \end{pmatrix} \begin{pmatrix} X_1 \\ X_2 \end{pmatrix} \text{-----} (1)$$

$dX = \dot{X} = JX$ Where J is the Jacobean matrix for X_1 and X_2 , since $dX_1 = dS$ and $dX_2 = dI$, then the Jacobin form of the equation (1) is the same as

$$J = \begin{pmatrix} -\beta I & -\beta S \\ \beta I & \beta I - \delta \end{pmatrix} (S^*, I^*) \text{ at the equilibrium points we have}$$

$$J = \begin{pmatrix} -\beta I^* & -\beta S^* \\ \beta I^* & \beta S^* - \delta \end{pmatrix}$$

And so disease free equilibrium we have $S(t) = 1$, $I(t) = 0$ and $R(t) = 0$, since $S(t) + I(t) + R(t) = N$ (the total population)

$$J(S^*, I^*) = \begin{pmatrix} -\beta I^* & -\beta S^* \\ \beta I^* & \beta S^* - \delta \end{pmatrix}$$

$$J(1, 0) = \begin{pmatrix} -\beta(0) & -\beta(1) \\ \beta(0) & \beta(1) - \delta \end{pmatrix} = \begin{pmatrix} 0 & -\beta \\ 0 & \beta - \delta \end{pmatrix}$$

Then to find the Eigen values of the Jacobean at the equilibrium points we have the formula

$$\begin{aligned} \det(J - \lambda I) = 0 &\Leftrightarrow \begin{vmatrix} 0 & -\beta \\ 0 & \beta - \delta \end{vmatrix} - \begin{vmatrix} \lambda & 0 \\ 0 & \lambda \end{vmatrix} = \begin{vmatrix} \lambda & -\beta \\ 0 & \beta - \delta - \lambda \end{vmatrix} = 0 \\ &\Leftrightarrow (-\lambda)(\beta - \delta - \lambda) + \beta(0) = 0 \\ &\Leftrightarrow \lambda(\beta - \delta - \lambda) = 0 \end{aligned}$$

$$\Leftrightarrow \lambda=0 \text{ and } \beta - \delta - \lambda = 0 \Rightarrow \lambda = \beta - \delta$$

Therefore the Eigen values are $\lambda=0$ and $\lambda = \beta - \delta$

The Eigen value of $\lambda = \beta - \delta$ is interest, then the behavior of the model is as follows:

- ✓ Stable if $\lambda = \beta - \delta < 0$ i.e $R_0 < 1$ (the infectious disease will vanish and hence there will be no epidemic)
- ✓ Unstable if $\lambda = \beta - \delta > 0$ i.e $R_0 > 1$ (an epidemic)
- ✓ The infectious disease will be die out time and can be easily controlled if the basic reproduction number is less than one i.e $R_0 < 1$.

Proposition; The solution to the linearized system near an equilibrium point are closed approximation to the solutions of the actual system provided that the linearized system is neither a center nor a system with a zero eigenvalue.

2.4 Notation and Elementary Discussions

Assuming equal birth and natural death rates, let's examine a population N that is large enough to remain constant since during the spread of disease the total population is constant. Newborns and individuals of all ages are also vulnerable. For any $t \in [0, \infty)$, there are only three compartments in this model: Susceptible $S(t)$, Infected $I(t)$, and Recovered $R(t)$. We make the assumption that

every member of the population is contagious, vulnerable, or immune to the disease for the rest of their lives.

The procedure is exemplified by:

$$S(t) \rightarrow I(t) \rightarrow R(t) \text{-----(1)}$$

Where $S(t)$ =number of susceptible individuals at the time t

$I(t)$ =number of infected individuals at the time t

$R(t)$ = number of recovered individuals at time t

The number of people who become infected per unit of time in epidemiology is called incidence rate. In the SIR model, incidence rate, as well as treatment rate plays an important role while analyzing the transmission of diseases births and deaths are not included in the SIR model because an epidemic spreads rather quickly in this model.

The data from infected individuals, patients who were discharged, and patients who were discharged during

the period of isolation and control were used to build the model (Harko et al., 2014). The SIR model does not distinguish between individuals who have recovered and those who have passed away; all are retained in compartment $R(t)$. This model makes the assumption that there are no important dynamics and that the population as a whole stays constant. These are the definitions of the three compartments.

Susceptible: The susceptible refers to a group of people who are not yet infected but may be infected with the infection rate of virus or any other virus at any time. Total number of susceptible people at time t is denoted by $S(t)$.

Infective: The infective refers to a group of people who have been infected and have infectivity. Infected individuals can spread the disease to susceptible individuals. After the recovery they enter the recovered compartment. Total number of infective people at time t is denoted by $I(t)$.

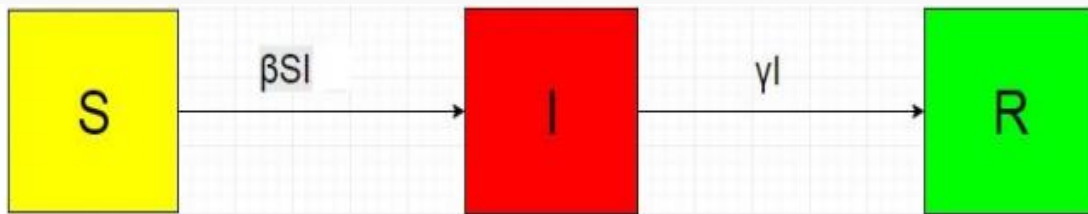
Removal: The removed refers to a group of people who have been removed from the infected people, such as died, isolated or recovered and are immunized to the infectious disease.

Let $R(t)$ is the number of recovered/removed individuals who are removed from the population by recovery, immunization, hospitalization, death or by any other means. In our model, the removed group consists of both recovered individuals, as well as the deaths caused by viral & microbiological agents.

CHAPTER 3

3. FORMULATING SIR MODEL

The SIR model is an epidemiological model that computes the theoretical number of people infected with a contagious illness within a closed population over time (Kermack & Mackendrick, 1927). In SIR model, let $\beta > 0$ is the transmission rate, and $\gamma > 0$ is the recovery rate of the disease, and these parameters are determined depending on the fraction of the infected population, $I(t)$ changes over time. Therefore, an infected individual able to transmit the disease with $\beta N(t)$ others in per unit time and the fraction of contacts by an infected with a susceptible is $\frac{S(t)}{N(t)}$. The number of new infection in unit time is $\beta N(t) \frac{S(t)}{N(t)}$ that gives the rate of new infections as $\beta N(t) \frac{S(t)}{N(t)} I(t) = \beta S(t) I(t)$. Therefore, in the $S(t)$ compartment, $\beta S(t) I(t)$ individuals will be decreased; whereas in the $I(t)$ compartment, $\beta S(t) I(t)$ individuals will be increased, and $\gamma I(t)$ individuals will be decreased due to recovery. In the $R(t)$ compartment, $\gamma I(t)$ recovery individuals will be increased as shown in figure below.



Now, we have to know how the above variable changes with time.

The SIR model can be written using ordinary differential equations as:

$$\frac{dS(t)}{dt} = -\beta S(t) I(t) \text{ ----- (2)}$$

$$\frac{dI(t)}{dt} = \beta S(t) I(t) - \gamma I(t) \text{ ----- (3)}$$

$$\frac{dR(t)}{dt} = \gamma I(t) \text{ ----- (4)}$$

Where β symbolizes the contact between the susceptible and infected and also β is proportionality constant, γ is the recovery rate.

Obviously $\frac{d}{dt} (S+I+R)=0$, since the total population including birth and death of particular disease is fixed.

$\frac{\gamma}{\beta}$ is relative removal rate and $\left(\frac{\beta}{\gamma}\right)$ is the number of constants per infection and is called reproductive number which is denoted by $R_0 = \left[\frac{\beta}{\gamma}\right]$.

Equation (2) indicates that, $\frac{dS(t)}{dt} = -\beta S(t)I(t)$, then implies $\frac{dS(t)}{dt} < 0$, in the elapse of time, the people in S(t) Compartment will be decreased. $\frac{dI(t)}{dt} = \beta S(t)I(t) - \gamma I(t)$, then

I(t) initially increases exponentially, then moves to a plateau, and finally shrinks to zero if the disease is abolished completely after a finite time interval .

At, t = 0 the initial conditions of the model are.

$$S(0) = S_0 > 0, I(0) = I_0 > 0, R(0) = 0, I_0 \ll S_0 \text{ ----- (5)}$$

In the equilibrium disease is free during the SIR model, $S(t) = S_0, I(t) = 0, \text{ and } R(t) = 0$.

The time-dependent SIR model is much better to track the disease spread, control, and predict the future trend. Equations (2), (3), and (4) represent first-order non-linear differential equations of the SIR model. Epidemic is controlled if $S_0 < r$ where $r = \frac{\gamma}{\beta}$, then adding equation (2),(3)&(4) we get:

$$\frac{dS(t)}{dt} + \frac{dI(t)}{dt} + \frac{dR(t)}{dt} = 0, \text{ ----- (6)}$$

,then taking the integration from these differential equation we get the total population size in the SIR model as,

$$S(t) + I(t) + R(t) = N(t) = N \text{ (at fixed N) ----- (7)}$$

A susceptible is considered susceptible-infectious-susceptible (SIS) if they get sick and subsequently recover without immunity, such as with the common cold; that is, if $R(t) = 0$, meaning that there is no recovery or death happen due to disease we get, $S(t) + I(t) = N$, for all $t \in [0, \infty)$.

Theorem 1: In SIR model, S(t) is susceptible, and I(t) is infected at an arbitrary time t.

At t = 0 the initial conditions are, $S(0) = S_0 > 0$, and $I(0) = I_0 > 0$, then,

i), $I(t)_{\max} = I_0 + S_0 - r + r \ln\left(\frac{r}{S_0}\right)$ where $r = \frac{\gamma}{\beta}$ is the relative removal rate & in the model r is independent of any time.

ii, $S(t) = \exp\left[\ln S_0 - \beta(I_0 + S_0 - r + r \ln\left(\frac{r}{S_0}\right))t\right]$ at maximum I(t)

iii, $R(t) = \gamma(I_0 + S_0 - r + r \ln\left(\frac{r}{S_0}\right))t$ for I(t)max.

. Proof: At the arbitrary time t=0 in SIR model , S(t) is susceptible and I(t) is infected the initial conditions are, $S(0) = S_0 > 0$ and $I(0) = I_0 > 0$. Then dividing (3) by (2) we get

$$\frac{dI(t)dt}{dt dS(t)} = \frac{\gamma I(t) - \beta S(t)I(t)}{\beta S(t)I(t)} = \frac{\gamma - \beta S(t)}{\beta S(t)} = \frac{r}{\beta S(t)} - 1 \text{ then,}$$

$$dI(t) = \frac{r dS(t)}{S(t)} - dS(t) \text{ ----- (8)}$$

Then, integrating the equation (8) we get

$$\int dI(t) = \int \frac{r dS(t)}{S(t)} - \int dS(t), \text{ then } I(t) = r \ln(s(t)) - S(t) + A1. \text{ Therefore}$$

$$\mathbf{I(t)=r \ln s(t)-s(t)+A1} \text{-----(9)}$$

Using initial conditions in (9) we get

$I_0=r \ln s_0-s_0+A1$, then $A1=I_0+S_0-r \ln s_0$, substitute in the equation (9) we get.

$I(t)=r \ln(s(t)-S(t)+I_0+S_0-r \ln s_0$, the infected individuals at the time $t=0$ becomes

$$=I_0+S_0-S(t)+r \ln \frac{s(t)}{s_0} \text{ and } I(t) \text{ will be maximum if, } \frac{dI(t)}{dt} = 0, \text{ then (3) becomes}$$

$$\frac{dI(t)}{dt} = \beta S(t)I(t) - \gamma I(t)$$

$$\Rightarrow \frac{dI(t)}{dt} = 0, \text{ then}$$

$$\Rightarrow \beta S(t)I(t) - \gamma I(t) = 0$$

$$\Rightarrow (\beta S(t) - \gamma) I(t) = 0$$

$$\Rightarrow (\beta S(t) - \gamma) = 0, \text{ since } I(t) \text{ is maximum}$$

$$\Rightarrow \beta S(t) = \gamma, \mathbf{S(t) = \frac{\gamma}{\beta} = r}$$

$$\therefore \mathbf{I(t)_{max} = I_0 + S_0 - r + r \ln \frac{r}{s_0}} \text{-----(10)}$$

ii, Epidemics end at the limiting number of susceptible individuals, then substituting equation(10) in to equation(2) we get :

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

$$= -\beta S(t)(I_0 + S_0 - r + r \ln \frac{r}{s_0})$$

$$\Rightarrow \frac{dS(t)}{S(t)} = -\beta (I_0 + S_0 - r + r \ln \frac{r}{s_0}) dt, \text{ then integrating both sides become}$$

$$\int \frac{dS(t)}{S(t)} = -\beta \int (I_0 + S_0 - r + r \ln \frac{r}{s_0})$$

$$\Leftrightarrow \ln S(t) = -\beta (I_0 + S_0 - r + r \ln \frac{r}{s_0}) t + A2, \text{ then by the initial conditions}$$

$$S(0) = S_0 > 0, \text{ then at } t=0 \mathbf{A2 = \ln S_0}$$

$$\Rightarrow \ln s(t) = -\beta (I_0 + S_0 - r + r \ln(r/s_0)) t + \ln S_0$$

$$e^{\ln s(t)} = e^{-\beta (I_0 + S_0 - r + r \ln(\frac{r}{s_0}) t + \ln S_0)}, \text{ by taking both sides "e" both sides}$$

$$S(t) = \exp \left[\ln s_0 - \beta \left(I_0 + S_0 - r + \frac{r \ln r}{s_0} \right) t \right], I(t)_{max}$$

iii, In equation (4), $\frac{dR(t)}{dt} = \gamma I(t)$ and in equation (10)

$I_{max} = I_0 + S_0 - r + r \ln\left(\frac{r}{S_0}\right)$, then

$$\frac{dR(t)}{dt} = \gamma(I_0 + S_0 - r \ln\left(\frac{r}{S_0}\right)), \text{ then substituting equation (10) in equation (4)}$$

$$\Rightarrow dR(t) = \gamma(I_0 + S_0 - r \ln(r/S_0)) dt \text{-----(11)}$$

then integrating both sides of the equation becomes

$$\int dR(t) = \gamma \int (I_0 + S_0 - r \ln\left(\frac{r}{S_0}\right)) dt$$

$$\Rightarrow R(t) = \gamma(I_0 + S_0 - r \ln(r/S_0))t + A_3 \text{-----(12)}$$

, then using the initial condition $R(0)=0$, at $t=0$ we get $R(0) = \gamma(I_0 + S_0 - r \ln(r/S_0)) \times 0 + A_3$

$$\Leftrightarrow R(0) = A_3, \text{ the } A_3 = 0$$

$$\therefore R(t) = \gamma(I_0 + S_0 - r \ln(r/S_0))t \text{-----(13)}$$

, the recovery becomes max.

Theorem 2: In SIR model, $S(t)$ susceptible, and $R(t)$ is recovery/dead at an arbitrary time t .

At $t = 0$ the initial conditions are, $S(0) = S_0 > 0$, $R(0) = 0$, then,

i, $S(t) = e^{-\frac{R(t)}{r}} + \ln S_0$

ii, $R(t) = r \ln(S_0/S(t))$

iii, $t = \frac{1}{\gamma} \int_0^R \frac{dR}{N(t) - e^{-\frac{R(t)}{r} + \ln S_0} - R_{\infty}}$, where $r = \frac{\gamma}{\beta}$, the relative removal rate.

Proof: Dividing (4) by (2) we get, $\frac{dS(t)}{dR(t)} = -\frac{\beta S(t)I(t)}{\gamma I(t)} = -\frac{\beta S(t)}{\gamma}$

$$\frac{dS(t)}{dR(t)} = -\frac{\beta}{\gamma} S(t)$$

$$\Rightarrow \frac{dS(t)}{S(t)} = -\frac{\beta}{\gamma} dR(t) \text{-----(14)}$$

, then integrating we obtain

$$\int \frac{dS(t)}{S(t)} = -\frac{\beta}{\gamma} \int dR(t)$$

$$\Rightarrow \ln S(t) = -\frac{1}{r} R(t) + A_4$$

$$\therefore \ln S(t) = -\frac{1}{r} R(t) + A_4 \text{-----(15),}$$

then at $t=0$ the initial conditions are $S(0) = S_0 > 0$ and $R(0) = 0$, then (15) gives $\ln(S_0) = -\frac{1}{r} R(0) + A_4$,

$$A_4 = \ln S_0$$

$$\ln S(t) = -\frac{1}{r} R(t) + \ln S_0 \Rightarrow e^{\ln S(t)} = e^{-\frac{R(t)}{r} + \ln S_0}, \text{ then } S(t) = e^{-\frac{R(t)}{r} + \ln S_0}$$

ii, from (i) $S(t) = e^{-\frac{R(t)}{r} + \ln S(0)} \Rightarrow R(t) = r \ln\left(\frac{S_0}{S(t)}\right)$ and gain we have,

$S(t) + I(t) + R(t) = N(t)$, by the definition of SIR model.

$$\Rightarrow \mathbf{I(t) = N(t) - S(t) - R(t)} \text{----- (16)}$$

by substituting (16) in (4) we get

$$\frac{dR(t)}{dt} = \gamma(N(t) - S(t) - R(t)) \text{----- (17)}$$

$$dR(t) = \gamma[N(t) - S(t) - R(t)]dt,$$

$\int_0^R dR(t) = \gamma(N(t) - S(t) - R(t))t$, then integrating becomes

$$t = \frac{1}{\gamma} \frac{\int_0^R dR(t)}{N(t) - S(t) - R(t)} = \frac{1}{\gamma} \frac{\int_0^R dR(t)}{N(t) - e^{-\frac{R(t)}{r} + \ln S_0}} \text{----- (18),}$$

then Equation (18) gives the time of recovery of the disease.

$$\text{Hence (17) gives, } \frac{dR(t)}{dt} = 0 \text{----- (19)}$$

, Integrating (19) we get,

$R(t) = \text{constant} = R_\infty$ since $t \rightarrow \infty$, then equation (18) becomes

$$t = \frac{1}{\gamma} \int_0^{R_\infty} \frac{dR}{N(t) - e^{-\frac{R(t)}{r} + \ln S_0 - R_\infty}} \text{----- (20)}$$

Theorem 3: In SIR model, $S(t)$ is susceptible, $I(t)$ infected, and $R(t)$ is recovery/dead at an arbitrary time t , then the disease is bounded $\forall t \geq 0$.

i, $S_0 \leq S(t) \leq N(t)$

ii), $I_0 \leq I(t) \leq N(t)$

iii, $0 \leq R(t) \leq N(t)$.

Proof: i) For $t = 0$, then $S(0) = S_0 > 0$ and for $0 < t < \infty$ we have, $S(t) = e^{-\frac{R(t)}{r} + \ln(S_0)} > 0$.

Almost all the individuals in the society are susceptible and some of the individuals in the society has a probability of infection by transmission disease then, $S(t) \leq N(t)$ for $t \rightarrow \infty$,

$$S(t) = S_\infty \leq N(t) \infty.$$

$$\therefore S_0 \leq S(t) = S_\infty \leq N(t)$$

ii) For $t = 0$, $I(0) = I_0 > 0$, and for $t > 0$ we have

$I(t) = I_0 + S_0 - r + r \ln r \leq 0$. Almost all the individuals may be infected, i.e., some of the individuals in the society can be infected by transmission disease or nobody can be infected, then

$I(t) \leq N(t)$ for $t \rightarrow \infty, I(t) = I_\infty \leq N(t)$. Hence, $I_0 \leq I(t) \leq N(t)$.

iii) For $t = 0, R(0) = 0$, i.e before the SIR model pandemic outbreak everybody in the society were disease free.

For $0 < t < \infty$ we have, $R(t) = rI(t) / s(t) \geq 0$.

Almost all the infected individuals can be recovered. Some of the infected individuals or all the members of the society can be recovered from disease.

On the other hand, some or all the disease infected individuals or persons may die.

Both recovered and death individuals are removed from the $R(t)$ compartment.,

$R(t) \leq N(t)$. For $t \rightarrow \infty$ we have,

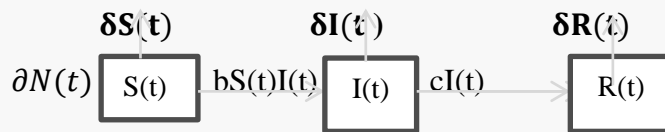
$R(t) = R_\infty \leq N(t)$. Hence, $0 \leq R(t) \leq N(t)$.

3.1, SIR Model with death

At the particular time t , population in the world is constant so that, the birth rate is equal to death rate. Let the birth rate be, $\partial > 0$ and also the death rate be, $\delta > 0$; consequently, $a = \delta$.

Let the new born babies are quite healthy but susceptible, i.e., $B(t) = \partial N(t)$ susceptible individuals will in total populations. Suppose b is the contact rate, in the $S(t)$ compartment at this time, $bS(t)I(t)$ will be decreased and similarly the individuals of $I(t)$ compartment, $bS(t)I(t)$ will be increased. Take c is the recovery rate of disease, in the $I(t)$ compartment, $cI(t)$ individuals will be reduced. In the $S(t), I(t)$ and $R(t)$ compartments the amount of death are $\delta S(t), \delta I(t)$, and $\delta R(t)$ respectively.

Then equations of SIR model can be written as:



Flow chart of SIR model considering birth & death

$$\frac{dS(t)}{dt} = \partial N(t) - bS(t)I(t) - \delta S(t) \text{ ----- (21)}$$

$$\frac{dI(t)}{dt} = bS(t)I(t) - cI(t) - \delta I(t) \text{ ----- (22)}$$

$$\frac{dR(t)}{dt} = cI(t) - \delta R(t) \text{ ----- (23)}$$

Where $S(0) \geq 0, I(0) \geq 0$ and $R(0) \geq 0$, the flow chart of SIR model by considering both death & birth.

3.2, Vaccination and herd immunity

When susceptible people receive vaccinations, they are taken out of the susceptible group. Even if a vaccination has a 100% success rate. It is exceedingly expensive to vaccinate a whole community, and not everyone can receive the vaccine for the disease that is being transmitted.

Can an epidemic be stopped by immunizing a small portion of the susceptible class, we wonder? Our thesis of the SIR model makes it clear that the answer is in fact true, and that the mechanism is known as herd immunity.

Everyone who has taken the immunization to the full prescribed dosage becomes immune to that particular disease. Herd immunity is the state in which a sufficient number of people of a population are immune to stop the spread of an infectious illness. The immune population is uniformly distributed across the community, and social mixing occurs in a homogenous manner.

A larger proportion of individuals receive vaccinations to achieve herd immunity. Following increasing vaccination, the individuals transfer from the $S(t)$ compartment to the $R(t)$ compartment, where they will not die. If p represents the percentage of the whole population (N) that has received vaccinations, then $(1-p)$ represents the percentage of people who have not received vaccinations, with $0 < p < 1$. The immunized class will proceed straight to the recovered class, avoiding the vulnerable class.

On the other hand, the unvaccinated individuals will go into the susceptible class.

Therefore, the total population that are vaccinated is

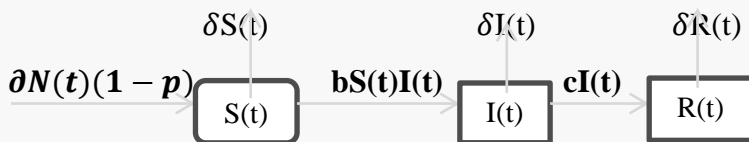
$\partial N(t)p$, which will be added in the recovery compartment $R(t)$. On the other hand, the unvaccinated Populations is $\partial N(t)(1-p)$, which still remain in the susceptible compartment $S(t)$.

After, Vaccination the equations of SIR model can be written as:

$$\frac{dS(t)}{dt} = \partial N(t)(1-p) - bS(t)I(t) - \delta S(t) \text{ ----- (24)}$$

$$\frac{dI(t)}{dt} = bS(t)I(t) - cI(t) - \delta I(t) \text{ ----- (25)}$$

$$\frac{dR(t)}{dt} = cI(t) - \delta R(t) + \partial N(t)p \text{ ----- (26)}$$



The flow chart of vaccination including both death and birth.

Theorem4:In ‘‘SIR’’ model assume that $p=0.1, S(t)=2I(t)$ and $R(t)=0$, then $N(t)=S(t)+I(t)=3I(t)$, then $\delta = \frac{70c}{11}$.

Proof: Dividing equation (24) by equation (25) we get

$$\begin{aligned} \frac{dS(t)}{dI(t)} &= \frac{aN(t)(1-p) - bS(t)I(t) - \delta S(t)}{bS(t)I(t) - cI(t) - \delta I(t)} \\ &= \frac{\delta(1-p)(S(t)+I(t) - bS(t)I(t) - \delta I(t)}{bS(t)I(t) - cI(t) - \delta I(t)} \\ &= \frac{\delta(1-p)3I(t) - 2bI(t)I(t) - 2\delta I(t)}{2bs(t)I(t) - cI(t) - \delta I(t)} \\ &= \frac{3\delta - 3\delta p - 2bI(t) - 2\delta}{2bI(t) - c - \delta} \\ 2 &= \frac{\delta - 3\delta p - 2bI(t)}{2bI(t) - c - \delta} \Rightarrow 4bI(t) - 2c - 2\delta = \delta - 3\delta p - 2bI(t) \\ 6bI(t) - 2c &= 3\delta - 3\delta p \\ \Rightarrow I(t) &= \frac{3\delta + 2c - 3p\delta}{6b} \text{-----(1) and} \end{aligned}$$

Dividing equation (24) by (26) we get $I(t) = \frac{3\delta - 4c - 15\delta p}{2b}$ ----- (2)

then combine equation (1) and (2) we have $\delta = \frac{70}{9}c$, so the death rate is $\frac{70}{9}c$ times the infection rate i.e the infection rate(c)=11 and the death rate(δ) = 70.

3.3 Immunity Loss of Vaccine

In section 3.2 we have assumed that vaccine is 100% efficacy. In real field observation, no vaccine gives full protection to transmission disease of SIR model or other epidemic disease. Therefore, individuals who take vaccine are not fully immunized. Overtime the immunity due to vaccination shall decrease the transmission of disease in SIR model. For that situation, the vaccinated individual’s will be susceptible to infectious disease.

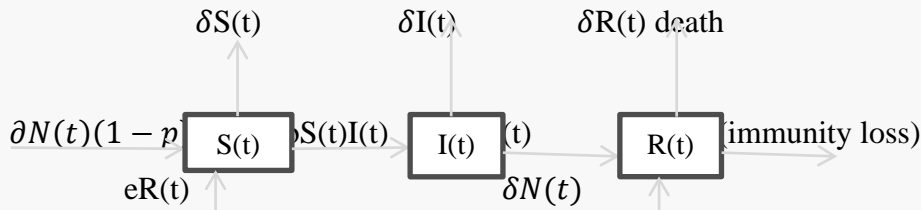
Let $e > 0$ be the rate of immunity loss, then in $R(t)$ compartment, $eR(t)$ people will be decreased due to loss of immunity, and these $eR(t)$ individuals will add in $S(t)$ compartment.

The system of equations in SIR model becomes:

$$\frac{dS(t)}{dt} = \partial N(t)(1 - p) - bS(t)I(t) - \delta S(t) + eR(t) \text{----- (27)}$$

$$\frac{dI(t)}{dt} = bS(t)I(t) - cI(t) - \delta I(t) \text{----- (28)}$$

$$\frac{dR(t)}{dt} = cI(t) - \delta R(t) + \delta N(t)p - eR(t) \text{----- (29)}$$



Flow chart of SIR Model after immunity loss of vaccine considering death and birth.

Example: In SIR model, if $p=0.5$ and $R(t)=0, N(t)=S(t)+I(t)=5I(t)$ and $S(t)=4I(t)$, then $e = \frac{84c+190\delta}{21}$,

further if $c=0.035, \delta = 0.007$, then $e = 0.203333 \dots$

Proof: Divide equation (27) by equation (28), we get

$$= \frac{\delta(1-p)(S(t) + I(t) - bS(t)I(t) - \delta S(t) + eR(t)}{bS(t)I(t) - cI(t) - eR(t)}$$

$$\frac{dI(t)}{dt} = \frac{-4\delta pI(t) + (\delta - \delta p)I(t) - 4bI(t)I(t) + e/4I(t)}{4bI(t)I(t) - cI(t) - \delta R(t)}$$

$$4 = \frac{-4\delta p + \delta - \delta p - 4bI(t) + \frac{e}{4}}{4bI(t) - c - \delta} = 16bI(t) - 4c - \delta = -5\delta p + \delta + \frac{e}{4} - 4bI(t)$$

$$20bI(t) = \frac{\delta}{4b} + \frac{c}{5b} + \frac{e}{80b} \dots \dots \dots (*) \text{ and}$$

Dividing equation (27) by equation (29), we have

$$\frac{dS(t)}{dR(t)} = \frac{\partial N(t)(1-p) - bS(t)I(t) - \delta S(t) + eR(t)}{cI(t) - \delta R(t) + \partial N(t) - eR(t)} = \frac{\delta(1-p)(s(t)+I(t)) - bS(t)I(t) - \delta S(t) + eR(t)}{cI(t) - \delta R(t) + \delta p(S(t)+I(t)) - e/4I(t)}$$

$$\Rightarrow 16 = \frac{-4\delta p + \delta - \delta p - 4bI(t) + e/4}{c - \frac{\delta}{4} + 5\delta p - e/4} = 16c - 4\delta + 80\delta p - 4e = -5\delta p + \delta - 4bI(t) + e/4$$

$I(t) = -75\delta/8b - 4c/b + 17e/16b \dots \dots \dots (**)$, then from the (*) and (**),

we have $\frac{\delta}{8b} + \frac{c}{5b} + \frac{e}{80b} = -\frac{75\delta}{8b} - \frac{4c}{b} + \frac{17e}{16b}$

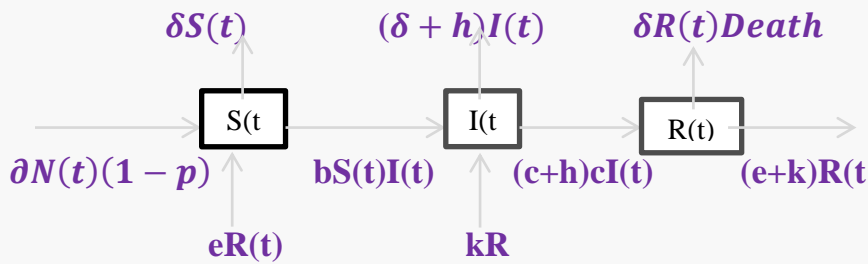
$$\Rightarrow e = \frac{760\delta + 336c}{84} = \frac{190\delta + 84c}{21}, \text{ if } \delta = 0.007 \text{ and } c = 0.035, \text{ then}$$

$$e = \frac{190 \times 0.007 + 84 \times 0.035}{21} = \mathbf{0.20333 \dots}$$

3.4 Re-infected of SIR model

In 3.3 above, no vaccination gives full protection to transmission disease of SIR model or other epidemic disease. Some people in the world are re-infected again by the infectious disease of SIR model.

Let $k > 0$ be the rate of re-infected individuals, then $kR(t)$ persons will be decreased from $R(t)$ compartment and $kR(t)$ individuals will add in the $I(t)$ compartment. And some of re-infected people may be die. Let $h > 0$ be the death of re-infected individuals with $h \neq \delta$ and $hI(t)$ will be reduced in the $I(t)$ compartment $hI(t)$ people added in $R(t)$ compartment. Figure shows flow chart of SIR model after re-infected the death and birth.



The system of equations of SIR model become

$$\frac{dS(t)}{dt} = \partial N(t)(1 - p) - bS(t)I(t) - \delta S(t) + eR(t) \text{ ----- (30)}$$

$$\frac{dI(t)}{dt} = bS(t)I(t) - cI(t) + kR(t) - (\delta + h)I(t) \text{ ----- (31)}$$

$$\frac{dR(t)}{dt} = (c+h)cI(t) + \partial N(t)p - (\delta + e + k)R(t) \text{ -----(32)}$$

3.5. STABILITY OF SIR MODEL

The stability of the SIR (Susceptible-Infected-Recovered) model indicates to the behavior of model's, equilibrium points, particularly the disease-free equilibrium (DFE) and the endemic-equilibrium (EE).

Stability analysis: Helps to determine how the system reacts to perturbations-whether the system returns to equilibrium or diverges away.

The key points of the stability of the SIR models are:-

I, Disease free equilibrium (DFE)

- Occurs when the infection disappears, with all individuals in the susceptible or recovered states.
- The stability refers to that if the infection is introduced at the low levels, it will die out over time.

II, Endemic equilibrium (EE)

- Represents the study state where the disease persists in the population.

Stability indicates that if the infection is present it will remain at the constant level.

To determine the stability points of the modified model, the Jacobean matrix of the system is obtained and evaluated at the equilibrium point.

The Eigen value analysis is checking the sign of Eigen values derived from the Jacobean matrix at the equilibrium points.

The eigenvalues of the Jacobean matrix is determined and is the stability points of the model.

Below is the summary of the Eigen values & how we determine the stability

- ✓ Both Eigen values are real & positive, and then the point is unstable i.e it diverges from the equilibrium points.
- ✓ Both Eigen values are real with opposite signs. The point is unstable and hence moves away from the equilibrium points.

Both Eigen values are real and negative, the point is stable and hence moves towards the equilibrium point

- ✓ Complex conjugate Eigen values with positive real part: The point is unstable and hence moves away from the equilibrium point

- ✓ Complex conjugate Eigen values with negative real part:
- ✓ The point is stable and hence moves towards the equilibrium point.
- ✓ Other cases are when we have repeated roots, a zero real part with an imaginary part or one real and one zero Eigen values.
- ✓ The Eigen values are determined using the relation:

$\det(J - \lambda I) = 0$. where I is the identity matrix, λ is a scalar and J is the Jacobin matrix at equilibrium

From the above equation we know that

$$\begin{aligned}\frac{dS(t)}{dt} &= \delta N(t) - bS(t)I(t) - \delta S(t) \\ \frac{dI(t)}{dt} &= bS(t)I(t) - cI(t) - \delta I(t) \\ \frac{dR(t)}{dt} &= cI(t) - \delta R(t)\end{aligned}$$

The equation of SIR model in the equilibrium point should be equal to zero.

All equations in the system remain constant with time, and then we can find the equilibrium points of SIR model.

$$\frac{dS(t)}{dt} = \frac{dI(t)}{dt} = \frac{dR(t)}{dt} = 0, \text{ since the equation remains constant with the time}$$

$$\Rightarrow bS(t)I(t) - cI(t) - \delta I(t) = 0$$

$$\Rightarrow bS - c - \delta = 0, I(t) \neq 0, \text{ since } \mathbf{I_{max}} \text{ at } \frac{dI(t)}{dt} = 0, \text{ then } S(t) = (c + \delta) / b$$

$$\therefore S(t) \text{ is stable at the point of } \left\{ \frac{(c + \delta)}{b} \right\}. \text{ And also } \delta N(t) - bS(t)I(t) - \delta S(t) = 0$$

$$\delta N(t) = bS(t)I(t) + \delta S(t)$$

$$\delta N(t) = (bI + \delta)S(t)$$

$$N = \frac{(bI + \delta)S(t)}{\delta}, \text{ since } S = \frac{c + \delta}{b}, \text{ then } N = \frac{(bI + \delta) \left(\frac{c + \delta}{b} \right)}{\delta} \text{ so the total population is stable at the point}$$

$$N = \left(\frac{c + \delta}{\delta} \right) I(t) + \frac{c + \delta}{b} \text{ and } N - \left(\frac{c + \delta}{\delta} \right) I(t) \Rightarrow I(t) = \frac{\delta N}{c + \delta} - \frac{\delta}{b}, I(t) \text{ is stable at this point.}$$

3.6 Basic Reproduction number (Ro)

It is denoted by (Ro)

(Ro) is the average number of secondary cases caused by a single infected person in completely susceptible population.

In epidemiology, the basic reproduction number (Ro) is the expected number of cases directly generated by one method in a population where all the individuals are susceptible to infection. This number (Ro) is a measure of the potential for disease spread with in population. It is not biological constant for a pathogen, because it is affected by other factors, such as environmental conditions and the behavior of the infected population. There is no general method to calculate the basic reproduction number. It is widely varies depending on country, culture, calculation, stage of the outbreak. Different authors take different methods to determine (Ro) for controlling the disease.

If $R_0 < 1$, the DFE is stable and disease die out the infection is faded out in present in the population, there will be an epidemic if and only if $\frac{dI(t)}{dt} > 0$.

If $R_0 < 1$, disease free equilibrium of infectious disease will be locally asymptotically stable.

Then the number of infectious individuals decreases monotonically to zero and the disease will not spread. In this case, the introduced infected will recover or die without being able to replace themselves by new infections.

If $R_0 > 1$ ----- epidemic equilibrium is stable (EE)(measles)and each infected individual spreads the disease to more than one person indicating that the infection will spread through population.

$R_0 = 1$ it is endemic like cholera ,the infectious disease will be unstable and number of infected persons will increase and the disease will spread.

For $R_0 = 1$, there will be a sharp threshold between the disease dying out. It can be seen from the model equations that the infection term is $\beta S(t)I(t)$. For the entirely susceptible population we have that $S \approx 1$.

$$\frac{dI(t)}{dt} = \beta S(t)I(t) - \gamma I(t)$$

$$\text{Since } \frac{dI(t)}{dt} > 0 \Rightarrow \beta S(t)I(t) - \gamma I(t) > 0 \Rightarrow \beta I(t) - \gamma I(t) > 0 \Rightarrow \beta - \gamma > 0 \text{ since } I(t) > 0$$

$$\Rightarrow \beta > \gamma$$

$\Rightarrow \frac{\beta}{\gamma} > 1$, then I(t) will increase if $\frac{\beta}{\gamma} > 1$ & decrease if $\frac{\beta}{\gamma} < 1$. so $\frac{\beta}{\gamma}$ is the basic reproduction model(R_0).

There is an increase in I(t) if $R_0 = \frac{\beta}{\gamma} > 1$ & decrease I(t) if $R_0 = \frac{\beta}{\gamma} < 1$.

Calculating R_0

In the SIR model (R_0) can be derived from the model parameters specifically

$R_0 = \frac{\beta}{\gamma}$ where β is the transmission rate and γ is the recovery rate

Reducing β or increasing γ the spread of the disease can be controlled.

Example: consider the pandemic disease above equation numerically with $\beta = 0.127$ and $\gamma = 0.055$, then

$$R_0 = \frac{\beta}{\gamma} = \frac{0.127}{0.055} = 2.3090909 \dots$$

4. Conclusions

This thesis models a general class of transmissible diseases that, after a victim recovers, provide lifelong immunity (chicken pox, cow pox, and biological agents are examples of such diseases). It is regarded as an effective and adaptable technique for figuring out how diseases spread and carrying out public health interventions. It is noted that the SIR model offers a fundamental structure for examining the pandemic transmission illness.

This paper discusses vaccination, loss, re-infection, stability, and growth in herd immunity.

Basic reproduction is discussed in some details. We have also observed that if more people are vaccinated, more herd immunity will grow against highly infectious disease. Vaccination program will be success only if a large portion of the population receives the vaccines the transmission of disease. a large portion of the global population irrespective of nation, religion, region, poor, and rich, must bring under vaccination. The public health officials, social workers, governments and common people must encourage actively others for vaccinating all the people in the country

In the modeling process, the population is sub-divided into three classes:

Susceptible, Infected and Recovered (SIR).

The modeling produces two models: one with vital dynamics and the other without vital dynamics (without demography).

The basic reproduction number (R_0) for the two models were determined to be

The stability of equilibrium for the two models is carried out and

for the model without demography, it is observed that two equilibrium points exist : one before the epidemic (Disease Free Equilibrium ($S; I_-$) = (1; 0) and the other after the epidemic ($S_-; I_-$) = (0; 0).

The disease free equilibrium for the model without demography was asymptotically stable when the basic reproduction number is less than one i.e. $R_0 < 1$ and unstable otherwise. For the model with demography, two equilibrium were discussed : disease free equilibrium ($S; I_-$) = (1; 0) and endemic equilibrium ($S_-; I_-$) the disease free equilibrium is asymptotically stable for

$R_0 < 1$ and asymptotically unstable for $R_0 > 1$. For the endemic equilibrium point of the model with demography, it is asymptotically stable for $R_0 > 1$ and asymptotically unstable for $R_0 < 1$.

It is also presented in this thesis the optimal control in the form of vaccination subject to SIR epidemiological model. The model's control strategies, "vaccination"; is used to demonstrate the optimal

both the susceptible and infected individuals and increasing the recovered individuals.

4.1 Recommendations and Further Work

It is advised that control tactics be employed to eradicate illnesses in this class of SIR models based on the findings of this thesis. These preventative measures could include immunization (as in this thesis), therapies, and isolation (because the primary mode of transmission is through contact with infected individuals), isolation or any other tactic that can be used to manage or eradicate these illnesses from the general public. Additionally, it is advised that the SIR epidemiological model study conducted in this thesis be expanded upon. Using other epidemiological models in order to determine how to treat these infectious diseases.

The evaluation for the additionally, the SIR epidemic model might be extended to investigate the criteria for both asymptotic and global Included in stability.

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