2024-09

Threshold and Stability Results of Anew Mathematical Model for Infectious Diseases Having Effective Preventive Vaccine

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THRESHOLD AND STABILITY RESULTS OF A NEW MATHEMATICAL MODEL FOR INFECTIOUS DISEASES HAVING EFFECTIVE PREVENTIVE VACCINE

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SEPTEMBER, 2024

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Approval page of the project

I hereby certify that I have supervised, read and evaluated this project entitled ‘’ threshold and stability results of a new mathematical model for infectious diseases have effective preventive vaccine ‘’ by Debasu Lamesegn prepared under my guidance I recommend that the project is submitted for oral defense.

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Approval page

The project entitled ‘’ threshold and stability results of a new mathematical model for infectious diseases have effective preventive vaccine ‘’ by Debasu Lamesegn is approved for the degree of Master of Science in Mathematics.

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Acknowledgment

First and foremost, I would like to thank my great Almighty God and his Gracious MotherSaint Merry for being with me in all aspects of my life during my stay at everywhere.

My special and heart full gratitude and appreciation go to my advisor, **Dr. Tesfahun Berhane**. He gave many valuable suggestions and comments until the completion of the project. I greatly appreciate him not only for unlimited constructive advises in every aspect of my project work, but also with his professional and personal ethic, that should be an icon for others and your critical support and kind encouragement is really helpful my project work. These things made me strong to do so.

Finally, my special thanks go to my wife **Melikam Azimeraw** and my sincerely families, who are with me all the time, for their material, financial and moral supports to complete my project.

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List of symbols

N: Total population.

S: Susceptible class.

V: Vaccinated class.

E: Exposed class.

I: Infective class.

R: Recovered class.

b: birth rate or recruiment rate into the susceptible class.

$\beta_1, \beta_2, \beta_3$: transmission rates.

q: rate related to vaccination or another process.

v : vaccination efficacy or coverage.

μ: decay rate or mortality rate.

γ: rate of progression from expoed to infected.

η: additional removed rate from the exposed class.

ϕ:the region of the model

R_0: Basic reproduction number.

E^0: Disease free Equilibrium point.

E_1: Endemic Equilibrium point.

Acronyms

DFE: Disease free Equilibrium

EE: Endemic Equilibrium

SVEIR: Susceptible-Vaccinated-Exposed-Infective Recovered.

List of tables and figures

Abstract

In this project, we evaluate the impact of an effective preventive vaccine on the control of some infectious diseases by using the deterministic mathematical model. The model is based on the fact that the immunity acquired by a fully effective vaccination is permanent. Threshold R_0, defined as the basic reproduction number, is critical indicator in the extinction or spread of any disease in any population, and so it has a very important role for this project of the infectious disease that caused to an epidemic. In epidemic models, it is expected that the disease becomes extinct in the population if $R_0 < 1$. It is expected that the disease-free equilibrium point of the SVEIR model, and so the SVEIR model, is stable in the sense of local. And if $R_0 > 1$, then it is the existence of the local endemic equilibrium point. So the threshold value R_0 regarding to the SVEIR model is obtained and also discussed the numerical simulation of the model.

CHAPTER ONE

INTRODUCTION

1.1 Background of the project

It has been seen that epidemics have had major effects and leave deep remains on human lives throughout history. To prevent and control the spread of epidemic, the examination of its dynamics has an important role. In this context, mathematical modeling in epidemiology provides understanding and explanation of the underlying mechanisms that influenced the spread of disease, and it suggests control strategies. The COVID-19 pandemic, which emerged at the end of 2019 and is the most devastating epidemic of recent times, has seriously shaken humanity as a global threat. Modeling and analysis studies in mathematical epidemiology have focused on this ground in conjunction with this compelling and exhausting epidemic.

While dealing with mathematical modeling spread of disease, in order to formulate the transmissions of an epidemic, the population in a region is often divided into different compartments, and the models, which formulate the relations between these compartments, are called as compartmental models.

In mathematical epidemiology, the course of the disease in the population associates with whether the basic reproduction number is greater than 1, or not.

It can be made the comments:

- If $R_0 > 1$, then there is an increase in the speed of the spread.
- If $R_0 < 1$, then there is a decrease in the epidemic rate and the epidemic is under control.
- If $R_0 = 1$, then the speed of the spread is constant.

Thus, the value R_0 is very important since it can tell us whether the population is at risk about the disease. Therefore, calculating this value for any disease in any population is invaluable.

In order that the disease dies out in the population, it needs that $R_0 < 1$ and additionally the disease-free equilibrium point of the projected model is stable when $R_0 < 1$. In other words, the effort required to prevent an outbreak or to eliminate an infection in a population should be directed towards ensuring that the value R_0 is less than 1. In addition, it is expected that the disease-free equilibrium point of the model and so the model is stable in the sense of locally, when $R_0 < 1$.

1.2 Objectives of the project

1.2.1 General objective

The general objective of this project is to formulate and analyze the mathematical model on the control of infectious diseases of the SVEIR model.

1.2.2 Specific objectives

The specific objectives of the model are:-

- ✓ To formulate the SVEIR model for the infectious diseases.
- ✓ To determine the invariant region such as positivity and bounded ness of a solution in the region ϕ.
- ✓ To calculate the basic reproduction number, the disease free and endemic equilibrium point.
- ✓ To analyze the stabilities of the equilibrium points.
- ✓ To come up with the numerical solutions of the SVEIR model.

1.3 Methodology

We used a deterministic compartmental model and the SVEIR model is formulated by using a system of non-linear integro-differential equation which is well known to describe the epidemiology of infectious diseases.

In formulating the model:

- ❖ **Next generation matrix** is used to determine the basic reproduction number.
- ❖ To analyze the local stability behavior of DFE point we use **Jacobean matrix**.
- ❖ To analyze the global stability of DFE point we use **Castillo-Chavez theorem**.
- ❖ To analyze the local stability of EE point we use **Routh-Hurwitz criteria**.
- ❖ Mathematical software such as **python programs** is used in order to identify the impact of parameter gamma on the dynamics of the SVEIR model.

1.4 Organization of the project

This project is organized into five main chapters such as:

I. **Chapter one** presents about the introduction part of the project. This contains the background, objectives, methodology, organization, definitions of terms.

II. **Chapter two** contains some of the literature's review that is done before this project.

III. **Chapter three** contains the mathematical model formulation, qualitative analysis.

IV. **Chapter four** contains the numerical simulations with discussion. Finally,

V. **Chapter five** contains conclusion and recommendation of the model.

1.5 Definition of terms

Here, we introduce the following definitions that are necessary for the project:

- **Epidemiology** is the subject that studies the patterns of health, illness and associated factors at the population level.
- An infection is said to be **epidemic** in a population when that infection is maintained in the population without the need for external inputs.
- The **DFE point** is a point at which **no disease** is present in the population.
- The **EE** is a rapid spread of infectious disease to a large number of population within a short period of time.
- **Stability** of an equilibrium point x_0 means that if the system is slightly perturbed from (to) x_0 ,it will either return to x_0 (stable) or move away from x_0 (unstable).
- A person is said to be **Susceptible** if he is not yet infected by the disease but likely to get the disease in the future**.**
- An individual who enabling the **immune** system to create **antibodies** that **fight off** the infectious disease is known as **vaccinated.**
- A person is said to be **exposed** to a disease when the virus enters into the person's body and the effects of the disease cannot be identified.
- A person is said to be **infected** if it has the disease in its body and is able to transfer the disease to other susceptible persons**.**
- People who have **immune** to a disease are known as **Recovered.**

1.6 The Basic Reproduction Number

In modeling the spread of the disease, the basic reproduction number of the disease is a great

importance. It tells us whether or not the disease will persist or will be eradicated. The basic reproduction number denoted by R_0 and defined as the average number of secondary infections produced by a single infected individual in a completely susceptible population. In many infectious models, when $R_0 < 1$ this means the disease will be eradicated, it doesn't allow for disease persistence in the population. However,$R_0 > 1$ which means that the disease can invade the population. The reproduction number is very useful in the determining stability of disease free equilibrium. Over time the number of newly infected will decrease and the population can become disease free.

1.7 The Next Generation matrix

In epidemiology, the next generation matrix is a method used to derive the basic reproduction number, for a compartmental model of the spread of infectious diseases. The basic reproduction number R_0 is arguably the most important quantity in the infectious disease epidemiologically.

Let $X = (x_1, x_2, \dots\dots x_n)^T$, with each $x_i \geq 0 \quad for\ \forall i = 1,2,\dots,n$, be the number of individuals in each compartment. For clarity we sort the compartments so that the **first *m*** compartments **correspond to infected** individuals. The distinction between **infected** and **uninfected** compartments must be determined from the epidemiological interpretation of the model and cannot be deduced from the structure of the equations alone, as we shall discuss below. The basic reproduction number cannot be determined from the structure of the mathematical model alone, but depends on the definition of infected and uninfected compartments.

In order to compute R_0, it is important to distinguish new infections from all other changes in the population.

- Let K_i be the rate of appearance of new infections in compartment i.
- Let Q_i be incorporates the remaining transitional terms, namely births, deaths, disease progression and recovery.

It is assumed that each function (K_i , Q_i) is continuously with respect to X and differentiable at least twice with respect to each variable or X. The transmission model consists of the non-negative initial conditions together with the following system of equation. $\frac{dx_i}{dt} = K_i - Q_i$, $i = 1,2,\dots,n$.

Lemma 1.1: If $x_0$is a DFE point, then the derivatives $DK(x_0)$ and $DQ(x_0)$ are partitioned as $DK(x_0)=\begin{pmatrix}0 & k\\ 0 & 0\end{pmatrix}$, $DQ(x_0)=\begin{pmatrix}q & 0\\ J_3 & J_4\end{pmatrix}$. Where, K and Q are the m × m matrices defined by $K = (\frac{\partial k(x_0)}{\partial x_i})$ and $Q = (\frac{\partial q(x_0)}{\partial x_i})$ with $1 \leq i \leq m$. K is non-negative and Q is a non-singular m-matrix.

1.8 Stability of the equilibrium point

For most dynamical systems the equilibrium point of a system of nonlinear integro- differential equation plays an important role in the analysis of the model, we give the definition of an equilibrium point and describe the analysis of the equilibrium point below.

Notice: - Let p is said to be an equilibrium point of a continuous map $f: R^n \to R^n$ such that $f(p) = 0$.The linear part of f at p, denoted by $Df(p)$, is the matrix of partial derivatives at p. For $y \in R^n$, we write $f(y) = (f_1(y), f_2(y), \dots, f_n(y))^t$, the functions, f_i for $\forall i = 1,2,\dots,n$ are called the component functions of f. We define $Df(p) = \begin{pmatrix} \frac{\partial f_1(p)}{\partial y_1} & \frac{\partial f_1(p)}{\partial y_2} & \frac{\partial f_1(p)}{\partial y_3} & \cdots & \frac{\partial f_1(p)}{\partial y_n} \\ & \vdots & & \vdots & \vdots \\ \frac{\partial f_n(p)}{\partial y_1} & \frac{\partial f_n(p)}{\partial y_2} & \frac{\partial f_n(p)}{\partial y_3} & \cdots & \frac{\partial f_n(p)}{\partial y_n} \end{pmatrix}$

Called the **Jacobean matrix**.

1.8.1 Routh-Hurwitz Criterion

Theorem 1.1:-[18] (Routh-Hurwitz criterion) given the polynomial,$p(\lambda) = \lambda^n + \alpha_1\lambda^{n-1} + \cdots + \alpha_{n-1}\lambda + \alpha_n$ where the coefficients α_i are all constants, for $\forall i = 1, 2, 3 \dots n$. Defines the n Hurwitz matrices using the coefficients α_i of the characteristic polynomial as:

$H_1 = (\alpha_1)$, $H_2 = \begin{pmatrix}\alpha_1 & a_3\\ 0 & \alpha_2\end{pmatrix}$ and $H_3 = \begin{pmatrix}\alpha_1 & a_3 & 0\\ 0 & \alpha_2 & \alpha_4\\ 0 & 1 & \alpha_3\end{pmatrix}$

Where $\alpha_j = 0$ if $j > n$. All the roots of the polynomial $p(\lambda)$ are negative if and only if the determinants of all Hurwitz matrices are positive: $detH_j > 0,\ for\ \forall j = 1,2,\dots,n.$

For polynomials of degree $n = 2, 3, 4$ and 5 the Routh-Hurwitz criteria are summarized below.

- ✓ If $n = 2$: $\alpha_i > 0$, $\forall i = 1, 2$.
- ✓ If $n = 3$: $\alpha_i > 0$, $\forall i = 1, 2, 3$ and $\alpha_1\alpha_2 > \alpha_3$.
- ✓ If $n = 4$: $\alpha_i > 0$, $\forall i = 1,2,3,4$ and $\alpha_1\alpha_2\alpha_3 > {\alpha_3}^2 + {\alpha_1}^2\alpha_4$.
- ✓ If $n = 5$: $\alpha_i > 0$, $\forall i = 1, 2, 3, 4, 5$, and $\alpha_1\alpha_2\alpha_3 > {\alpha_3}^2 + {\alpha_1}^2\alpha_4$, and $(\alpha_1\alpha_4 - \alpha_3)(\alpha_1\alpha_2\alpha_3 - {\alpha_3}^2 - {\alpha_1}^2\alpha_4) > \alpha_5(\alpha_1\alpha_2 - \alpha_3)^2 + {\alpha_5}^2\alpha_1$.

1.8.2 Castillo Chavez theorem

Theorem 1.2 :-([3]) (**Castillo Chavez theorem**) Assume that the model equation can be rewritten in the form $\frac{dX}{dt} = F(X, I)$ and $\frac{dI}{dt} = G(X, I)$, $G(X, 0) = 0$

Where X is a non-infected individual and I is infected individual, assume that $G(X, 0) = 0$ and let $E^0 = (X^*, 0)$ be an equilibrium point of the model equations.

If the following conditions are satisfied:

i. For $\frac{dX}{dt} = F(X, 0)$, the steady state X^* is globally asymptotically stable .

ii. $G(X, I) = AI - \hat{G}(X, I)$, $\hat{G}(X, I) \geq 0 \; for \; \forall (X, I) \in \gamma$.

Where, is a Matzler matrix (the off diagonal elements of A are non- negative) and ϕ is the region and also $\hat{G}(X, I)$ is the column matrix .

Then the steady state $E^0 = (X^*, 0)$ is globally asymptotically stable for the model provided that $R_0 < 1$.

CHAPTER TWO

LITERATURE REVIEW

In this chapter, some of these models are reviewed particularly those having the close relation to the objectives of this project.

Guihua & Zhen [6] (2005), formulated a $SEIR$ epidemic model in which the infectious force in the latent (exposed), infected and recovered period is studied. It is assumed that susceptible and exposed individuals have constant immigration rates. The model exhibits a unique endemic state if the fraction p of infectious immigrants is positive. If the basic reproduction number R_0 is greater than 1, sufficient conditions for the global stability of the endemic equilibrium are obtained by the compound matrix theory.

Kermack and McKendrick [9] (1927), this is an SIR model and there are many compartmental models provided basic principles for the spread of a disease in a population. Then, a lot of authors have tackled with various details to carry further forward this model. Adding a vaccination compartment is just one of these details. Immunization with vaccines is among the most effective methods of protection from infectious diseases which are common in the society and which have high contamination properties. Until today, many studies including the epidemic models with vaccination have been introduced.

O. Diekmann, etal. [11] (1990), used several values of the reproduction ratio and generation interval to model the potential spread of the pandemic influenza A (H1N1) across a network of 52 major cities using a simulation from stochastic Susceptible – Exposed – Infected – Recovered (SEIR) model, whiles also attempting to predict the effect of vaccination against the pandemic. The result of their simulation showed that in the absence of vaccination an attack rate (cumulative incidence of infection in a group of people observed over a period of time during an epidemic) of influenza A (H1N1) may reach 46 percent (%) when considering a completely susceptible population with an R_0 of 1.5 and a generation interval of 2 days, They then concluded that a mass vaccination program of a disease with a basic reproduction ratio of 1.5, resulting in 50% of the population being vaccinated, begun 6 months after the start of the pandemic could possibly reduce the total number of cases by 91%, while resulting in a reduction of approximately 44% for a virus with R_0 = 2.2. Also a multi wave pandemic is possible and may be curtailed using different immunization strategies.

Bolarin, [3] (2014), Based his study on the dynamical analysis of a new model for measles infection. His study used $SEIR$ model modified by adding vaccinated compartment. His model determined the required vaccination coverage and dosage that will guarantee eradication of measles disease with in a population.

Moneim [10] (2005), studied two classes of epidemic models. These models are the standard SIR and $SEIR$ models with time-varying periodic contact rate. The importance of the latent period was his target. When the latent period can be ignored and when it must be taken into account are the main points of his simulation. The comparison of the simulation results of his two models shows that the latent period is affecting the pattern of the dynamics of the disease. His paper addressed how model predictions are affected by the assumed form of the seasonally varying transmission rate and whether or not a latent class is included. Moreover, for some infectious diseases, using latent period leads to appearance or disappearance of some periodic solutions for the same parameter set. A key parameter for his models was the basic reproductive number R_0. He simulated his models for a set of values of parameters insuring that $R_0 > 1$, which represent the endemic case.

Rost [15] (2008), came up with a new $SEIR$ model with distributed infinite delay. The author stated that the infectivity depends on the age of infection. The basic reproduction number R_0, which is a threshold quantity for the stability of equilibrium, is calculated. If $R_0 < 1$, then the disease-free equilibrium is globally asymptotically stable and this is the only equilibrium. On the contrary, if $R_0 > 1$, then an endemic equilibrium appears which is locally asymptotically stable. Applying a permanence theorem for infinite dimensional systems, he obtains that the disease is always present when $R_0 > 1$.

Batista, M. [2] (2020), used an SIR model to predict the magnitude of the COVID- 19 epidemic in Pakistan and compared the numbers with the reported cases on the national database. They predicted that 90% of the population will have become infected with the virus if policy interventions seeking to curb this infection are not adopted aggressively.

Hong et al. [13] (2020), Used SEIR compartments by considering limited parameters, from January 22, 2020 to March 3, 2020 and Prediction SEIR forecasted by using SEIR model. They also looked at the feelings, current disease trends and economic and political impacts. It also proposed SEIR model by incorporating the intrinsic impact of hidden exposed and

infectious cases on the entire procedure of epidemic, which is difficult for traditional statistics analysis.

Giordano et al.[5] (2020), is proposed a new epidemic model in the case of Italy that discriminates between infected individuals depending on whether they have been diagnosed and on the severity of their symptoms. For the very dangerous COVID-19, an exposed individual is infectious and can transmit the virus to susceptible people rapidly. An infected person is infectious but may be sent to hospitals quickly and separated from the susceptible people, making them unlikely to transmit the virus to susceptible people. In the case of Ethiopia, a limited number of mathematical models on COVID-19 outbreak have been studied with real data.

Mathematical models are extremely important in improving our understanding of population dynamics of infectious diseases. Models are a crucial tool to help with controlling and preventing the spread of the infectious disease based on scientific evidence. In this project we have introduced a new compartmental model called as $SVEIR$ model by considering the disease control strategy called vaccination. In this study we developed a mathematical model for control of infectious disease in the epidemiology. We used $SVEIR$ model to determine the basic reproduction number, and also analysis local and global stability of disease free, existence of endemic, local stability of endemic equilibrium point of the SVEIR model and the numerical simulation of the model with discussion.

CHAPTER THREE

MATHEMATICAL MODEL FORMULATION AND ANALYSIS

3.1 Mathematical model formulation

Mathematical model can be used as a mechanism or tool that help explain, describe, predict finding and understanding of biological Phenomena, within appropriate assumptions according to biological landscapes to change mathematical language. The model formulation process clarifies assumptions, variable, and parameters; moreover, models provide conceptual results such as thresholds, basic reproduction number and stabilities. Modeling can be used to estimate key parameters by fitting data; Models can be used in comparing diseases of different types or at different times or in different populations.

In this project, we are going to formulate the model equations of $SVEIR$ model based on the deterministic approach and develop expressions for the equilibrium points. The main interest was to study these models to understand the long-time behavior of the dynamics of infectious diseases, thus, whether the disease would die out eventually or would persist as well as to determine the stabilities of local and global of the disease free and local of the endemic equilibrium points. The model subdivides the human population into five (5) compartments depending on the epidemiological status of individuals. The compartments are susceptible S, Vaccinated V, Exposed E, infected I and the recovered R.

In this model the equation is a deterministic and compartmental. Compartmentalize refers a group of persons with similar status or with respect to the same disease. Mathematical model is formulated to describe the transmission dynamics of infectious diseases, hence the model is formulated and control using non-linear integro-differential equations. While building such models, it must be assumed that the population size in a compartment is differentiable with respect to time and that the epidemic process is deterministic. The progression of infectious diseases with in the total population can be simplified to five non-linear integro-differential equations. These five equations represent five different groups of people: the susceptible, the vaccinated, the exposed, the infective, and the recovered.

The variables we used in the $SVEIR$ model can be described as follow:

- ✓ $\mathbf{S}(\mathbf{t})$: Susceptible individual at time $\mathbf{t}$.
- ✓ $\mathbf{V}(\mathbf{t})$: Vaccinated individual at time $\mathbf{t}$.

- ✓ **E(t)**: Exposed individual at time **t**.
- ✓ **I(t)**: Infectious individual at time **t**.
- ✓ **R(t)**: Recovered individual at time **t**.
- ✓ **N(t)**: Total population at time **t**.

The parameters of the model and their descriptions:

- All newborn individuals entering to the susceptible class with a constant rate b.
- The effective contact rate between infectious individuals and susceptible is β_1.
- The effective contact rate between infectious and vaccination who's vaccinated at time $t - \tau$ and vaccine effect has not yet started is β_2.
- The effective contact rate between infectious and susceptible who's vaccinated at time $t - \tau$ and vaccine effect has started, but the protection by the vaccine <1 is β3.
- The rate of vaccinated individuals within susceptible group is q.
- Natural death rate in each compartment is μ.
- The death rate derived from pathogen causing to outbreak is δ.
- The rate at which exposed individuals become infectious is γ.
- The transition rate from the infectious individuals to the Recover is α.
- The transition rate from exposed individuals to the Recover is η.

📖 The body's immune system through vaccination is often applied before encountering with microorganisms.

📖 The protective effect does not occur immediately after the vaccine is administered.

- If the vaccine begins h time after vaccination then the protection of an individual who vaccinated at time t begins at time t + h. So $q \int_0^h e^{-\mu\tau} S(t-\tau)d\tau$ is the number of individuals who have been vaccinated at time $t - \tau$ and their protection effect of vaccine has not yet started since the time threshold h does not completed, at time t.
- The vaccine does not yet form any effect, a vaccinated individual who have not yet any protection enters to compartment E if exposing to the infectious agent with a sufficiently effective contact with infectious individuals. This transition is expressed with the term $q\,\beta_2 I(t) \int_0^h e^{-\mu\tau} S(t-\tau)d\tau$ in the model.

📖 Another fact that no vaccine has a 100% protective effect. In some individuals, the body's

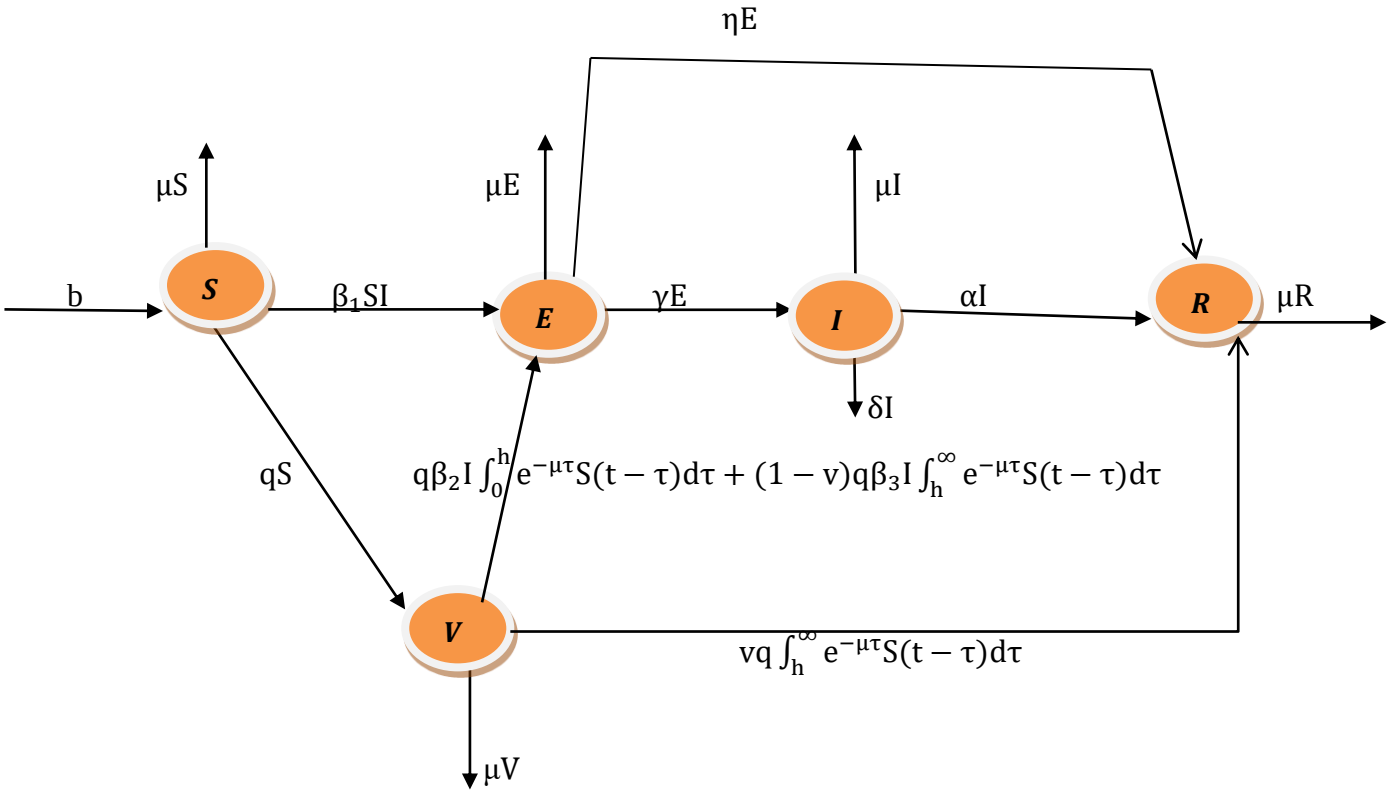
response to the vaccine may be weak because of various reasons. Therefore, the vaccine protection is lower for such individuals, and it can be seen that the protective efficacy in after vaccination is not fully formed. By considering this situation,

- The protection rate provided by the vaccine has been shown by ν in the model. As a result of effective contact between infectious individuals and the vaccinated individuals whose protection provided by the vaccine is less than 1, enter to latent compartment by exposing to the infectious agent. This transition is denoted by$(1-\nu)q\beta_3 I(t)\int_h^\infty e^{-\mu\tau}S(t-\tau)d\tau$.
- The individuals, whose protection level provided by the vaccine is 1 and so have full protection, include to the class R by gaining immunity. This transition is represented by the term $\nu q\int_h^\infty e^{-\mu\tau}S(t-\tau)d\tau$.

The following assumptions have been used in the formulation of the SVEIR model:

- All the parameters of the model are positive.
- Individuals are equally likely to be infected by the infectious individuals in acase of contact except those who are immune.
- All recruited human population is susceptible.
- Infectious individuals are detected early and isolated for immediate treatment.
- There is equal birth and death rates and all newborns are assuming to be susceptible.
- The population under study is uniform and mixes homogeneously.
- The natural death rates are assumed to be the same for all the compartments.
- Recovered individuals are permanently immune that means the recovered individuals have not a chance to be susceptible again.
- We assume that the vaccinated population, are accounted for if they were vaccinated before the disease started to spread. Thus, the vaccinated population would start in the recovered group.
- We assumed that if the infected person did not die from the disease, then He/she becomes immune upon recovery.
- We assume no one is vaccinated during the time the disease is spread, and proceed as in the previous section.

Figure 1:-The flow chart for the model of infectious diseases.



Based on figure 1, the classic model for micro parasite dynamics is the flow of hosts between the compartments of the model.

- ✓ The number of individuals' bS fractions entering to the susceptible class.
- ✓ A rate of β_1 and q are Leave from S and enter in to E and V, respectively.
- ✓ γE an individual's move from exposed to infectious.
- ✓ ηE an individual's move from exposed to recovered.
- ✓ αI an individual's move from infectious to recover.
- ✓ The natural death rate μ is subtracted from the individual population of all compartments.
- ✓ the death rate δI is subtracted from the infectious .
- ✓ The number of terms $q\beta_2 I \int_0^h e^{-\mu\tau} S(t-\tau)d\tau + (1-v)q\beta_3 I \int_h^\infty e^{-\mu\tau} S(t-\tau)d\tau$ is move from vaccinated to expose.
- ✓ The number of terms $vq \int_h^\infty e^{-\mu\tau} S(t-\tau)d\tau$ is move from vaccinated to recover.

3.1.1 Model equation

Based on the assumptions of the model for the transmission dynamics of Infective disease is given by the following deterministic system of non-linear integro-differential equations:

$$\begin{cases} \frac{dS}{dt} = b - \beta_1 S I - qS - \mu S & \ldots (3.1) \\ \frac{dV}{dt} = qS - q\beta_2 I \int_0^h e^{-\mu\tau} S(t-\tau)d\tau - vq \int_h^\infty e^{-\mu\tau} S(t-\tau)d\tau - (1-v)q\beta_3 I \int_h^\infty e^{-\mu\tau} S(t-\tau)d\tau - \mu V & \ldots (3.2) \\ \frac{dE}{dt} = \beta_1 S I + q\beta_2 I \int_0^h e^{-\mu\tau} S(t-\tau)d\tau + (1-v)q\beta_3 I \int_h^\infty e^{-\mu\tau} S(t-\tau)d\tau - \gamma E - \eta E - \mu E & \ldots (3.3) \\ \frac{dI}{dt} = \gamma E - \alpha I - \delta I - \mu I & \ldots (3.4) \\ \frac{dR}{dt} = vq \int_h^\infty e^{-\mu\tau} S(t-\tau)d\tau + \eta E + \alpha I - \mu R & \ldots \ldots (3.5) \end{cases}$$

The model is restricted to non-negative conditions for all the time given by:-$S_0 > 0, V_0 > 0, E_0 > 0, I_0 > 0$ and $R_0 > 0$. Here the total population N can be obtained from N= S+V +E +I + R

3.2 Invariant region

The system in the model describes a population. Since in epidemiology we are dealing with populations, the following two conditions are quite important:

I. the solution should be non-negative over time

II. The solution should be bounded.

Now, we show the positivity and bounded ness of the solutions.

3.2.1 Positivity and bounded ness of the solutions

Theorem 3.1:-if the model equation (3.1) to (3.5) and the initial conditions $(S_0, V_0, E_0, I_0, R_0)$ is non negative, then the equation (3.1) to (3.5) has a unique solution which is non negative and bounded in the region ϕ.

Proof: - Summing up the five equations (3.1) to (3.5) we obtain: $\frac{dN}{dt} = \frac{dS}{dt} + \frac{dV}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dR}{dt}$

$$= b - \mu(S + V + E + I + R) - \delta I$$

$$= b - \mu N - \delta I \quad \text{Since } N = S + V + E + I + R$$

$$N' = b - \mu N - \delta I$$

$$\delta I = b - \mu N - N' \geq 0$$

$$\Rightarrow N' \leq b - \mu N \quad \ldots (3.6)$$

$N' \leq b - \mu N$ Since the solution N is positive. Solving the differential inequality, we get the relation, $N' + \mu N \leq b$

This is the first order linear inequality, then multiplying both sides by the integrating factor $e^{\mu t}$

$$e^{\mu t}\frac{dN}{dt} + \mu e^{\mu t}N \leq be^{\mu t}$$

$$\Rightarrow \frac{d(Ne^{\mu t})}{dt} \leq be^{\mu t}$$

$$\Rightarrow \int d(Ne^{\mu t}) \leq b\int e^{\mu t}dt$$

$$\Rightarrow Ne^{\mu t} \leq \frac{b}{\mu}e^{\mu t} + c$$

$$\Rightarrow N \leq \frac{b}{\mu} + ce^{-\mu t} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (3.7)$$

Applying the initial condition when $t = 0$, we find the solution as: $N_0 - \frac{b}{\mu} \leq c$

Let we take $c = N_0 - \frac{b}{\mu}$ $\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (3.8)$

Now, we substitute (3.8) in to (3.7) we obtain: $N \leq \frac{b}{\mu} + \left(N_0 - \frac{b}{\mu}\right)e^{-\mu t}$

$\Rightarrow N$ is positive for all $t \geq 0$. By using positivity solution

$$0 \leq N \leq \frac{b}{\mu} + \left(N_0 - \frac{b}{\mu}\right)e^{-\mu t}$$

$$\Rightarrow 0 \leq \frac{b}{\mu} + \left(N_0 - \frac{b}{\mu}\right)e^{-\mu t}$$

$$\Rightarrow -\frac{b}{\mu}e^{\mu t} \leq N_0 - \frac{b}{\mu}$$

$$\Rightarrow N_0 \leq \frac{b}{\mu}$$

If $N_0 \leq \frac{b}{\mu}$, then $N \leq \frac{b}{\mu}$ for all $t \geq 0$. So the region ϕ is positively invariant for the model equations (3.1) to (3.5). Also, it is clearly seen that $N \leq \frac{b}{\mu}$ is bounded above.

3.3 Qualitative analysis of the model

3.3.1 Disease free equilibrium point

Disease free equilibrium point is defined as the steady state solution of the mathematical model indicating that there is **no disease** in the population. In this case we say that the population is disease free. If the DFE is stable, then it is expected that the population will be disease free over time. The DFE point is finding by setting the right hand sides of the model equations (3.1) to (3.5) equal to zero.

Let $E^0 = (S_0, V_0, E_0, I_0, R_0)$ represents the DFE point of the model. Hence in the absence of the disease we have $I_0 = E_0 = 0$. Then the DFE point (E^0) will be obtained as:

From the model equation (3.1) we have: $0 = b - \beta_1 S_0 I_0 - q S_0 - \mu S_0$,

$$S_0 = \frac{b}{q+\mu} \quad \text{Since,} \quad I_0 = 0$$

From the model equation (3.2) we have:

$$0 = \quad qS_0 - q\,\beta_2 I_0\, S_0 \int_0^h e^{-\mu\tau} d\tau \; - vq\, S_0 \int_h^\infty e^{-\mu\tau} d\tau - (1-v) q \beta_3 I_0\, S_0 \int_h^\infty e^{-\mu\tau} d\tau - \mu V_0$$

$$\Rightarrow V_0 = \frac{qS_0 - vq\, S_0 \int_h^\infty e^{-\mu\tau} d\tau}{\mu} = \frac{\mu qb - vqbe^{-\mu h}}{\mu^2(q+\mu)} \quad \text{Since, } S_0 = \frac{b}{q+\mu} \quad \text{and} \quad I_0 = 0$$

By computing the same steps from the model equation (3.5) we have:

$$0 = vq\, S_0 \int_h^\infty e^{-\mu\tau} d\tau + \eta E_0 + \alpha\, I_0 - \mu R_0$$

$$\Rightarrow R_0 = \frac{vq\, S_0 \int_h^\infty e^{-\mu\tau} d\tau}{\mu} = \frac{vq\, be^{-\mu h}}{\mu^2(q+\mu)} \qquad \text{Since, } S_0 = \frac{b}{q+\mu} \quad \text{and} \quad \int_h^\infty e^{-\mu\tau} d\tau = \frac{e^{-\mu h}}{\mu}$$

Therefore, the disease free equilibrium point (E^0) is given by

$$E^0 = \left(\frac{b}{q+\mu}, \frac{\mu qb - vqbe^{-\mu h}}{\mu^2(q+\mu)}, 0, 0, \frac{vq\, be^{-\mu h}}{\mu^2(q+\mu)}\right) \quad \text{And } N_0 = S_0 + V_0 + E_0 + I_0 + R_0 = \frac{b}{\mu}$$

The existence of the endemic equilibrium point depends on N_0 and will be presented later.

3.3.2 Basic reproduction number

For finding the basic reproduction number by using the next generation matrix of KQ^{-1} where K and Q are **transmission** and **transition** matrices, respectively. To calculate K and Q, we will only consider equations (3.3) and (3.4):

$$\begin{cases} \dfrac{dE}{dt} = \beta_1 S\, I + q\,\beta_2 I \displaystyle\int_0^h e^{-\mu\tau} S(t-\tau) d\tau + (1-V) q \beta_3\, I \int_h^\infty e^{-\mu\tau} S(t-\tau) d\tau - (\gamma + \eta + \mu) E \\ \dfrac{dI}{dt} = \gamma E - (\alpha + \delta + \mu) I \end{cases}$$

Let $X = \left(\frac{dE}{dt}, \frac{dI}{dt}\right)$ be a column vector and the nonlinear integro-differential equations of the first two compartments are rewritten as $K = (k_1, k_2)$ and $Q = (q_1, q_2)$

To calculate k as follows:

$$k = \begin{bmatrix} k_1 \\ k_2 \end{bmatrix} = \begin{bmatrix} \beta_1 S\, I + q\,\beta_2 I \displaystyle\int_0^h e^{-\mu\tau} S(t-\tau) d\tau + (1-v) q \beta_3\, I \int_h^\infty e^{-\mu\tau} S(t-\tau) d\tau \\ 0 \end{bmatrix}$$

And to calculate q as follows: $\mathrm{q} = \begin{bmatrix} q_1 \\ q_2 \end{bmatrix} = \begin{bmatrix} (\gamma + \eta + \mu)\mathrm{E} \\ (\alpha + \delta + \mu)\mathrm{I} - \gamma\mathrm{E} \end{bmatrix}$

We need to differentiate both matrices k and q with respect to E and I. The associated matrix is given by: $\mathrm{K} = \begin{bmatrix} \frac{\partial \mathrm{k}_1}{\partial \mathrm{E}} & \frac{\partial \mathrm{k}_1}{\partial \mathrm{I}} \\ \frac{\partial \mathrm{k}_2}{\partial \mathrm{E}} & \frac{\partial \mathrm{k}_2}{\partial \mathrm{I}} \end{bmatrix}$ And also similarly $\mathrm{Q} = \begin{bmatrix} \frac{\partial \mathrm{q}_1}{\partial \mathrm{E}} & \frac{\partial \mathrm{q}_1}{\partial \mathrm{I}} \\ \frac{\partial \mathrm{q}_2}{\partial \mathrm{E}} & \frac{\partial \mathrm{q}_2}{\partial \mathrm{I}} \end{bmatrix}$

In the absence of the disease, the two matrices become:

$\mathrm{K} = \begin{bmatrix} 0 & \beta_1 \mathrm{S}_0 + \mathrm{q}\,\beta_2\,\mathrm{S}_0 \int_0^{\mathrm{h}} \mathrm{e}^{-\mu\tau}\mathrm{d}\tau + (1-\mathrm{v})\mathrm{q}\beta_3 \mathrm{S}_0 \int_{\mathrm{h}}^{\infty} \mathrm{e}^{-\mu\tau}\mathrm{d}\tau \\ 0 & 0 \end{bmatrix}$ and $\mathrm{Q} = \begin{bmatrix} \gamma + \eta + \mu & 0 \\ -\gamma & \alpha + \delta + \mu \end{bmatrix}$

Next to find the inverse of Jacobean matrix Q which is given by:

$$\mathrm{Q}^{-1} = \begin{bmatrix} \frac{1}{\gamma + \eta + \mu} & 0 \\ \frac{\gamma}{(\gamma + \eta + \mu)(\alpha + \delta + \mu)} & \frac{1}{\alpha + \delta + \mu} \end{bmatrix}$$

We now compute the product of both matrices K and Q^{-1}

$$\mathrm{KQ}^{-1} = \begin{bmatrix} \frac{\gamma \mathrm{b}\left(\beta_1 + \mathrm{q}\,\beta_2 \left(\frac{1}{\mu} - \frac{\mathrm{e}^{-\mu\mathrm{h}}}{\mu}\right) + \frac{(1-\mathrm{v})\mathrm{e}^{-\mu\mathrm{h}}\mathrm{q}\beta_3}{\mu}\right)}{(\mathrm{q}+\mu)(\gamma + \eta + \mu)(\alpha + \delta + \mu)} & \frac{b\left(\beta_1 + \mathrm{q}\,\beta_2 \left(\frac{1}{\mu} - \frac{\mathrm{e}^{-\mu\mathrm{h}}}{\mu}\right) + \frac{(1-\mathrm{v})\mathrm{e}^{-\mu\mathrm{h}}\mathrm{q}\beta_3}{\mu}\right)}{\alpha + \delta + \mu} \\ 0 & 0 \end{bmatrix}$$

Where, $\int_0^{\mathrm{h}} \mathrm{e}^{-\mu\tau}\mathrm{d}\tau = \frac{1}{\mu} - \frac{\mathrm{e}^{-\mu\mathrm{h}}}{\mu}$, $\int_{\mathrm{h}}^{\infty} \mathrm{e}^{-\mu\tau}\mathrm{d}\tau = \frac{\mathrm{e}^{-\mu\mathrm{h}}}{\mu}$ *and* $\mathrm{S}_0 = \frac{\mathrm{b}}{\mathrm{q}+\mu}$

$$|\mathrm{KQ}^{-1} - \lambda\mathrm{I}| = \begin{vmatrix} \frac{\gamma \mathrm{b}\left(\beta_1 + \mathrm{q}\,\beta_2 \left(\frac{1}{\mu} - \frac{\mathrm{e}^{-\mu\mathrm{h}}}{\mu}\right) + \frac{(1-\mathrm{v})\mathrm{e}^{-\mu\mathrm{h}}\mathrm{q}\beta_3}{\mu}\right)}{(\mathrm{q}+\mu)(\gamma + \eta + \mu)(\alpha + \delta + \mu)} - \lambda & \frac{b\left(\beta_1 + \mathrm{q}\,\beta_2 \left(\frac{1}{\mu} - \frac{\mathrm{e}^{-\mu\mathrm{h}}}{\mu}\right) + \frac{(1-\mathrm{v})\mathrm{e}^{-\mu\mathrm{h}}\mathrm{q}\beta_3}{\mu}\right)}{\alpha + \delta + \mu} \\ 0 & -\lambda \end{vmatrix}$$

So the characteristics polynomial of KQ^{-1} appears with

$$-\lambda\left(\frac{\gamma \mathrm{b}\left(\beta_1 + \mathrm{q}\,\beta_2 \left(\frac{1}{\mu} - \frac{\mathrm{e}^{-\mu\mathrm{h}}}{\mu}\right) + \frac{(1-\mathrm{v})\mathrm{e}^{-\mu\mathrm{h}}\mathrm{q}\beta_3}{\mu}\right)}{(\mathrm{q}+\mu)(\gamma + \eta + \mu)(\alpha + \delta + \mu)} - \lambda\right) = 0$$

Thus, the Eigen values of the next generation matrixes are

$$\lambda_1 = 0 \qquad \textit{and}\ \lambda_2 = \frac{\gamma \mathrm{b}\left(\beta_1\mu + \mathrm{q}\,\beta_2 \left(1 - \mathrm{e}^{-\mu\mathrm{h}}\right) + (1-\mathrm{v})\mathrm{q}\beta_3\mathrm{e}^{-\mu\mathrm{h}}\right)}{(\mathrm{q}+\mu)\mu(\gamma + \eta + \mu)(\alpha + \delta + \mu)}$$

Here, the spectral radius of the next generation matrix is

$$\rho(\mathrm{K}Q^{-1}) = \max\{\lambda_1, \lambda_2\} = \frac{\gamma \mathrm{b}\left(\beta_1\mu + \mathrm{q}\,\beta_2 - \mathrm{q}\,\beta_2\mathrm{e}^{-\mu\mathrm{h}} + (1-\mathrm{v})\mathrm{q}\beta_3\mathrm{e}^{-\mu\mathrm{h}}\right)}{\mu(\mathrm{q}+\mu)(\gamma + \eta + \mu)(\alpha + \delta + \mu)}$$

Hence, the basic reproduction number of the model is given as (3.9) below:

$$R_0 = \frac{\gamma b(\beta_1\mu + q\beta_2(1-e^{-\mu h}) + (1-v)q\beta_3 e^{-\mu h})}{(q+\mu)\mu(\gamma+\eta+\mu)(\alpha+\delta+\mu)} \quad \ldots\ldots (3.9)$$

Hence, the effect of vaccine will always reduce the effect of the basic reproduction number R_0 .

3.3.3 Local stability of the disease free equilibrium point

Theorem 3.2: The disease-free equilibrium point is locally asymptotically stable when the basic reproduction number $R_0 < 1$ and unstable when $R_0 > 1$.

Proof: It is enough to show that Disease Free equilibrium point of the model (3.1) to (3.5) is stable if and only if all the trace and determinant of the Jacobean matrix at E^0 are negative and positive respectively. The Jacobean matrix evaluated at DFE point is given by:

$$J(E^0) = \begin{bmatrix} -q-\mu & 0 & 0 & \frac{-b\beta_1}{q+\mu} & 0 \\ J_1 & -\mu & 0 & J_2 & 0 \\ 0 & 0 & -\gamma-\eta-\mu & L & 0 \\ 0 & 0 & \gamma & -\alpha-\delta-\mu & 0 \\ J_3 & 0 & \eta & \alpha & -\mu \end{bmatrix}$$

Where, $J_1 = q - vq \int_h^{\infty} e^{-\mu\tau} d\tau$,

$$J_2 = -q\beta_2 S_0 \int_0^h e^{-\mu\tau} d\tau - vq S_0 \int_h^{\infty} e^{-\mu\tau} d\tau - (1-v)q\beta_3 S_0 \int_h^{\infty} e^{-\mu\tau} d\tau \ ,$$

$$L = \frac{b(\beta_1\mu + q\beta_2(1-e^{-\mu h}) + (1-v)q\beta_3 e^{-\mu h})}{\mu(q+\mu)} \quad \text{And} \quad J_3 = vqS_0 \int_h^{\infty} e^{-\mu\tau} d\tau$$

The sign of the Eigen values of the Jacobean matrix gives the information about the stability of the equilibrium that is if all the Eigen values of the Jacobean Matrix have negative real part, then the equilibrium point E^0 of the system is locally asymptotically stable, otherwise unstable. Therefore we need to show all the Eigen values of $J(E^0)$ are negative. As the second and fifth columns contain only the diagonal terms which form the two negative Eigen values are $\lambda_1 = -\mu$ *and* $\lambda_2 = -\mu$ .The other three Eigen values can be obtained from the sub-matrix $J_1(E^0)$ formed by excluding the second and fifth rows and columns of $J(E^0)$.

Then the reduced Jacobean matrix $J_1(E^0)$ becomes

$$J_1(E^0) = \begin{bmatrix} -(q+\mu) & 0 & \frac{-b\beta_1}{q+\mu} \\ 0 & -(\gamma+\eta+\mu) & L \\ 0 & \gamma & -(\alpha+\delta+\mu) \end{bmatrix}$$

where $L = \frac{\mathrm{b}(\beta_1\mu + q\beta_2(1-e^{-\mu h}) + (1-v)q\beta_3 e^{-\mu h})}{\mu(q+\mu)}$

Additionally in the reduced Jacobean matrix the first column contain only the diagonal terms which form the one negative Eigen value is $\lambda_3 = -(q+\mu)$ .Now we can find the characteristic equation of the reduced Jacobean matrix by using: $Det(\mathrm{J}_2(E^0) - \lambda I) = 0$

$$\Rightarrow \begin{vmatrix} -p_1 - \lambda & L \\ \gamma & -p_2 - \lambda \end{vmatrix} = 0$$

Where, $L = \frac{\mathrm{b}(\beta_1\mu + q\beta_2(1-e^{-\mu h}) + (1-v)q\beta_3 e^{-\mu h})}{\mu(q+\mu)}$ $\mathrm{P}_2 = \alpha + \delta + \mu$ and $\mathrm{P}_1 = \gamma + \eta + \mu$

Where λ the Eigen value and I is the identity matrix, so to find the $Det(\mathrm{J}_2(E^0) - \lambda I)$ as follow:

$$(p_1 + \lambda)(p_2 + \lambda) - \gamma L = 0$$

$$\Rightarrow \lambda^2 + (p_1 + p_2)\lambda + p_2 p_1 - \gamma L = 0$$

$$\Rightarrow \lambda_4 = \frac{-(p_1 + p_2) + \sqrt{(p_1 + p_2)^2 - 4p_2 p_1 + 4\gamma L}}{2}$$

$$\Rightarrow \lambda_5 = \frac{-(p_1 + p_2) - \sqrt{(p_1 + p_2)^2 - 4p_2 p_1 + 4\gamma L}}{2}$$

Here, the five Eigen values are: - $\lambda_1 = -\mu$,$\lambda_2 = -\mu$, $\lambda_3 = -(q+\mu)$

$$\lambda_4 = \frac{-(p_1 + p_2) + \sqrt{(p_1 + p_2)^2 - 4p_2 p_1 + 4\gamma L}}{2}$$

$$\lambda_5 = \frac{-(p_1 + p_2) - \sqrt{(p_1 + p_2)^2 - 4p_2 p_1 + 4\gamma L}}{2}$$

It is clear that λ_5 is negative.

Now all the Eigen values become negative and the equation (3.1) to (3.5) is stable if we are able to show λ_4 is negative. For λ_4 to be negative then, $\lambda_4 + \lambda_5 < 0$ and $\lambda_4\lambda_5 > 0$ must be satisfied which implies $\lambda_4 + \lambda_5 = -(p_1 + p_2) < 0$ and

$$\lambda_4\lambda_5 = \frac{(p_1+p_2)^2 - (p_1+p_2)^2 + 4p_2p_1 - 4\gamma L}{4} = p_2 p_1 - \gamma L > 0$$

$$\Rightarrow \gamma L < p_2 p_1$$

Since, $p_1 = \gamma + \eta + \mu$, $p_2 = \alpha + \delta + \mu$ *and* $L = \frac{\mathrm{b}(\beta_1\mu + q\beta_2(1-e^{-\mu h}) + (1-v)q\beta_3 e^{-\mu h})}{\mu(q+\mu)}$

Substituting we get

$$\frac{\gamma \mathrm{b}(\beta_1\mu + q\beta_2(1-e^{-\mu h}) + (1-v)q\beta_3 e^{-\mu h})}{\mu(q+\mu)} < (\gamma + \eta + \mu)(\alpha + \delta + \mu)$$

Dividing all the expression by $(\gamma+\eta+\mu)(\alpha+\delta+\mu)$ we get

$\frac{\gamma b(\beta_1\mu+q\beta_2(1-e^{-\mu h})+(1-v)q\beta_3 e^{-\mu h})}{\mu(q+\mu)(\gamma+\eta+\mu)(\alpha+\delta+\mu)} < 1$ Since, $R_0 = \frac{\gamma b(\beta_1\mu+q\beta_2(1-e^{-\mu h})+(1-v)q\beta_3 e^{-\mu h})}{\mu(q+\mu)(\gamma+\eta+\mu)(\alpha+\delta+\mu)}$

Finally, we get $R_0 < 1$.

$\det J(E^0) > 0$ When $R_0 < 1$

The real part of the Eigen values of $\det(J_2(E^0) - \lambda I) = 0$ are all negative when $R_0 < 1$. This shows that, the DFE point is locally asymptotically stable when the basic reproduction number $R_0 < 1$ and unstable when $R_0 > 1$.

3.3.4 Global stability of the disease free equilibrium point

Theorem 3.3: if $R_0 < 1$, then the DFE point is globally asymptotically stable in the region ϕ.

Proof: Let us rewrite the model equations (3.1) to (3.5) are written as follow:

$$\frac{dZ_1}{dt} = F(Z_1, Z_2) = \left(\frac{dS}{dt}, \frac{dV}{dt}, \frac{dR}{dt}\right)^T$$

$$\frac{dZ_2}{dt} = G(Z_1, Z_2) = \begin{bmatrix} E' \\ I' \end{bmatrix}$$

$$F(Z_1, 0) = \begin{bmatrix} S' \\ V' \\ R' \end{bmatrix}, \; G(Z_1, 0) = 0 \text{ Since, } I = E = 0$$

Where, $Z_1 = (S, V, R) \in R^3$ represents the class of uninfected individuals and $Z_2 = (E, I) \in R^2$ represents the class of infected individuals. The DFE point of the model is denoted by $U_0 = (Z_1^*, Z_2^*)$ Where, $Z_2^* = (E_0, I_0) = (0, 0)$ and

$Z_1^* = (S_0, V_0, R_0) = \left(\frac{b}{q+\mu}, \frac{\mu qb - vqbe^{-\mu h}}{\mu^2(q+\mu)}, \frac{vq\, be^{-\mu h}}{\mu^2(q+\mu)}\right)$. Since to prove global stability, we would be applied the Castillo-Chavez theorem we have: $\frac{dZ_1}{dt} = F(Z_1, Z_2) = \left(\frac{dS}{dt}, \frac{dV}{dt}, \frac{dR}{dt}\right)^T$

$$= \begin{bmatrix} b - \beta_1 S(t) I(t) - qS(t) - \mu S(t) \\ qS(t) - q\beta_2 I(t) \int_0^h e^{-\mu\tau} S(t-\tau) d\tau - vq \int_h^\infty e^{-\mu\tau} S(t-\tau) d\tau - (1-v) q\beta_3 I(t) \int_h^\infty e^{-\mu\tau} S(t-\tau) d\tau - \mu V(t) \\ vq \int_h^\infty e^{-\mu\tau} S(t-\tau) d\tau + \eta E(t) + \alpha I(t) - \mu R(t) \end{bmatrix}$$

$$\frac{dZ_2}{dt} = G(Z_1, Z_2) = \begin{bmatrix} E' \\ I' \end{bmatrix}$$

$$= \begin{bmatrix} \beta_1 S(t) I(t) + q\beta_2 I(t) \int_0^h e^{-\mu\tau} S(t-\tau) d\tau + (1-v) q\beta_3 I(t) \int_h^\infty e^{-\mu\tau} S(t-\tau) d\tau - \gamma E(t) - \eta E(t) - \mu E(t) \\ \gamma E(t) - \alpha I(t) - \delta I(t) - \mu I(t) \end{bmatrix}$$

First we show Z_1^* is the global asymptotically stable for the system, let us consider the reduced

System.

$$\frac{dZ_1}{dt} = F(Z_1, 0) = \begin{bmatrix} S' \\ V' \\ R' \end{bmatrix} = \begin{bmatrix} b - qS - \mu S \\ qS - vq \int_h^{\infty} e^{-\mu\tau} S(t-\tau)d\tau - \mu V \\ vq \int_h^{\infty} e^{-\mu\tau} S(t-\tau)d\tau - \mu R \end{bmatrix} \text{ where } I = E = 0$$

We can rewrite the system as: $S' = b - qS - \mu S$

$$V' = qS - vq \int_h^{\infty} e^{-\mu\tau} S(t-\tau)d\tau - \mu V$$

$$R' = vq \int_h^{\infty} e^{-\mu\tau} S(t-\tau)d\tau - \mu R$$

The general solution of the given ordinary differential equation $S' + (q + \mu)S = b$.

First to find the general solution of the homogenous ordinary differential equation $S' + (q + \mu)S = 0$

$$\frac{dS}{S} = -(q + \mu)dt$$

Both sides integrate $\int \frac{dS}{S} = -(q + \mu) \int dt \Rightarrow \ln S_c = -(q + \mu)t + f$ where f is constant of integration. So, $S_c = e^{-(q+\mu)t+f} = e^f e^{-(q+\mu)t}$

$$= c\, e^{-(q+\mu)t} \text{ where } c = e^f$$

To get the particular solution of the non-homogenous ordinary differential equation

Let $S_p = At + D \Rightarrow S_p' = A$ substituting this into the equation $S' + (q + \mu)S = b$

$$A + (q + \mu)(At + D) = b \Rightarrow A + (q + \mu)At + (q + \mu)D = b$$

$$\Longrightarrow (q + \mu)At + (q + \mu)D + A = 0t + b$$

Thus, $\Longrightarrow A = 0$ and $D = \frac{b}{q+\mu}$

$$\Longrightarrow S_p = \frac{b}{q + \mu}$$

Thus, the general solution of the non-homogenous ordinary differential equation is

$$S(t) = S_p(t) + S_c(t) = \frac{b}{q+\mu} + c\, e^{-(q+\mu)t}$$

For the initial condition t = 0, we find the particular solution with the initial condition as

$$S(t) = \frac{b}{q + \mu} + c\, e^{-(q+\mu)t} \Longrightarrow S(0) = \frac{b}{q + \mu} + c$$

$$\Rightarrow c = \mathrm{S}_0 - \frac{\mathrm{b}}{\mathrm{q}+\mu}$$

$$\mathrm{S(t)} = \frac{\mathrm{b}}{\mathrm{q}+\mu}\ ,\ \text{ since } \mathrm{S}_0 = \frac{\mathrm{b}}{\mathrm{q}+\mu}$$

Taking the limit as t goes to ∞ we obtain: $\mathrm{S}_\infty = \lim_{t\to\infty} S(t) = \frac{\mathrm{b}}{\mathrm{q}+\mu} = \mathrm{S}_0$

Similarly $\mathrm{V}_\infty = \frac{\mathrm{qb}}{\mu(\mathrm{q}+\mu)}$ *and* $\mathrm{R}_\infty = 0$. Here, $Z_1{}^* = (S^*, V^*, R^*) = \left(\frac{\mathrm{b}}{\mathrm{q}+\mu}, \frac{\mathrm{qb}}{\mu(\mathrm{q}+\mu)}, 0\right)$

Therefore, $Z_1{}^*$ the globally asymptotically stable for the model $\frac{dZ_1}{dt} = F(Z_1, 0)$

Secondly we will show that $\widehat{\mathrm{G}}\,(\mathrm{Z}_1, \mathrm{Z}_2) = \mathrm{AZ}_2 - \mathrm{G}(\mathrm{Z}_1, \mathrm{Z}_2)$ and $\widehat{\mathrm{G}}\ (\mathrm{Z}_1, \mathrm{Z}_2) \geq 0$ for $(\mathrm{Z}_1, \mathrm{Z}_2) \in \phi$ Where $\mathrm{A} = \frac{\partial \mathrm{G}}{\partial Z_2}(Z_1{}^*, 0)$ is a Meltzer matrix (off diagonal elements are non-negative). And ϕ is the region where the model makes biological sense.

Consider a matrix $\mathrm{A} = \frac{\partial \mathrm{G}}{\partial Z_2}(Z_1{}^*, 0) = \begin{pmatrix} \frac{\partial \mathrm{G}_1}{\partial E} & \frac{\partial \mathrm{G}_1}{\partial I} \\ \frac{\partial \mathrm{G}_2}{\partial E} & \frac{\partial \mathrm{G}_2}{\partial I} \end{pmatrix}$

$$= \begin{bmatrix} -\gamma - \eta - \mu & \beta_1 S^* + \mathrm{q}\,\beta_2 S^* \int_0^{\mathrm{h}} \mathrm{e}^{-\mu\tau}\mathrm{d}\tau + (1-\mathrm{v})\mathrm{q}\beta_3 S^* \int_{\mathrm{h}}^{\infty} \mathrm{e}^{-\mu\tau}\mathrm{d}\tau \\ \gamma & -\alpha - \delta - \mu \end{bmatrix}$$

Hence, A is a Meltzer matrix (off diagonal elements are non-negative).here,

$$\widehat{\mathrm{G}}\ (\mathrm{Z}_1, \mathrm{Z}_2) = \mathrm{AZ}_2 - \mathrm{G}(\mathrm{Z}_1, \mathrm{Z}_2)$$

$$\widehat{\mathrm{G}}\ (\mathrm{Z}_1, \mathrm{Z}_2) = \begin{bmatrix} -\gamma - \eta - \mu & \beta_1 S^* + \mathrm{q}\,\beta_2 S^* \int_0^{\mathrm{h}} \mathrm{e}^{-\mu\tau}\mathrm{d}\tau + (1-\mathrm{v})\mathrm{q}\beta_3 S^* \int_{\mathrm{h}}^{\infty} \mathrm{e}^{-\mu\tau}\mathrm{d}\tau \\ \gamma & -\alpha - \delta - \mu \end{bmatrix} \begin{bmatrix} \mathrm{E} \\ I \end{bmatrix} - \mathrm{G}(\mathrm{Z}_1, \mathrm{Z}_2)$$

$$= \begin{bmatrix} -\gamma - \eta - \mu & \beta_1 S^* + \mathrm{q}\,\beta_2 S^* \int_0^{\mathrm{h}} \mathrm{e}^{-\mu\tau}\mathrm{d}\tau + (1-\mathrm{v})\mathrm{q}\beta_3\, S^* \int_{\mathrm{h}}^{\infty} \mathrm{e}^{-\mu\tau}\mathrm{d}\tau \\ \gamma & -\alpha - \delta - \mu \end{bmatrix} \begin{bmatrix} \mathrm{E} \\ I \end{bmatrix}$$

$$- \begin{bmatrix} \beta_1 \mathrm{S\,I\,(t)} + \mathrm{q}\,\beta_2 \mathrm{I} \int_0^{\mathrm{h}} \mathrm{e}^{-\mu\tau}\mathrm{S}(\mathrm{t}-\tau)\mathrm{d}\tau + (1-\mathrm{v})\mathrm{q}\beta_3 \mathrm{I} \int_{\mathrm{h}}^{\infty} \mathrm{e}^{-\mu\tau}\mathrm{S}(\mathrm{t}-\tau)\mathrm{d}\tau - \gamma\mathrm{E} - \eta\mathrm{E} - \mu\mathrm{E} \\ \gamma\mathrm{E} - \alpha\,\mathrm{I} - \delta\mathrm{I} - \mu\mathrm{I} \end{bmatrix}$$

$$= \begin{bmatrix} -\gamma E - \eta E - \mu E + \beta_1 S^* I + q\,\beta_2 I S^* \int_0^h e^{-\mu\tau} d\tau + (1-v) q \beta_3 I S^* \int_h^\infty e^{-\mu\tau} d\tau \\ \gamma E - \alpha I - \delta I - \mu I \end{bmatrix}$$

$$- \begin{bmatrix} \beta_1 S I + q\,\beta_2 I \int_0^h e^{-\mu\tau} S(t-\tau) d\tau + (1-v) q \beta_3 I \int_h^\infty e^{-\mu\tau} S(t-\tau) d\tau - \gamma E - \eta E - \mu E \\ \gamma E - \alpha I - \delta I - \mu I \end{bmatrix}$$

$$= \begin{bmatrix} 0 \\ 0 \end{bmatrix} \geq 0$$

Therefore, by Castillo-Chavez theorem the DFE point of the system is globally asymptotically stable when $R_0 < 1$.

3.3.5 Existence of endemic equilibrium point

An endemic equilibrium (EE) point is a steady state in which at least one of its coordinates in the infected compartment is non-zero. We denote $E_1 = (S^*, V^*, E^*, I^*, R^*)$ as the EE point of the model. It can be obtained by setting each equation of the system equal to zero:

$0 = b - \beta_1 S^* I^* - q S^* - \mu S^*$ …… ….. (3.10)

$0 = \beta_1 S^* I^* + q\,\beta_2 I^* S^* \int_0^h e^{-\mu\tau} d\tau + (1-v) q \beta_3 I^* S^* \int_h^\infty e^{-\mu\tau} d\tau - \gamma E^* - \eta E^* - \mu E^*$ … (3.11)

$0 = \gamma E^* - (\alpha + \delta + \mu) I^*$ …… (3.12)

From the above equation (3.11) we have

$$\left(\beta_1 + q\,\beta_2 \int_0^h e^{-\mu\tau} d\tau + (1-v) q \beta_3 \int_h^\infty e^{-\mu\tau} d\tau\right) S^* = (\gamma + \eta + \mu) \frac{E^*}{I^*} \quad \text{…… (3.13)}$$

From the above equation (3.12) we have $\frac{E^*}{I^*} = \frac{(\alpha + \delta + \mu)}{\gamma}$ ……..……. (3.14)

Considering (3.13) and (3.14), we get

$$\left(\beta_1 + q\,\beta_2 \int_0^h e^{-\mu\tau} d\tau + (1-v) q \beta_3 \int_h^\infty e^{-\mu\tau} d\tau\right) S^* = \frac{(\gamma+\eta+\mu)(\alpha+\delta+\mu)}{\gamma}$$

$$S^* = \frac{\mu(\gamma+\eta+\mu)(\alpha+\delta+\mu)}{\gamma(\mu\beta_1 + q\,\beta_2(1-e^{-\mu h}) + (1-v) q \beta_3 e^{-\mu h})}$$

Here let us express S^* in terms of R_0. Now, $R_0 = \frac{\gamma b(\beta_1 \mu + q\,\beta_2 (1-e^{-\mu h}) + (1-v) q \beta_3 e^{-\mu h})}{(q+\mu)\mu(\gamma+\eta+\mu)(\alpha+\delta+\mu)}$

$S^* = \frac{b}{(q+\mu)R_0}$ From the equation (3.10) $I^* = \frac{(q+\mu)(R_0-1)}{\beta_1}$ Where, $S^* = \frac{b}{(q+\mu)R_0}$

And taking into account (3.14) we obtain: $\mathrm{E}^* = \frac{(\mathrm{q}+\mu)(\mathrm{R}_0-1)(\alpha+\delta+\mu)}{\beta_1\gamma}$

Therefore, we say that the equations (3.10) to (3.12) have a unique EE point that is

$$E_1 = (\mathrm{S}^*, \mathrm{E}^*, \mathrm{I}^*, V^*, R^*) = \left(\frac{\mathrm{b}}{(\mathrm{q}+\mu)\mathrm{R}_0}, \frac{(\mathrm{q}+\mu)(\alpha+\delta+\mu)(\mathrm{R}_0-1)}{\gamma\beta_1}, \frac{(\mathrm{q}+\mu)(\mathrm{R}_0-1)}{\beta_1}, V^*, R^*\right)$$ When $\mathrm{R}_0 > 1$

And, $V^* = \frac{\mathrm{qb}\mu - \mathrm{vqbe}^{-\mu\mathrm{h}}}{\mu^2(\mathrm{q}+\mu)\mathrm{R}_0} - \frac{\beta_2\mathrm{qb}(\mathrm{R}_0-1)(1-\mathrm{e}^{-\mu\mathrm{h}})+(1-v)qb\beta_3(\mathrm{R}_0-1)\mathrm{e}^{-\mu\mathrm{h}}}{\mathrm{R}_0\beta_1\mu^2}$

$$R^* = \frac{\mathrm{vqbe}^{-\mu\mathrm{h}}}{(\mathrm{q}+\mu)\mathrm{R}_0\mu^2} + \frac{\eta(\mathrm{q}+\mu)(\alpha+\delta+\mu)(\mathrm{R}_0-1)+\gamma\alpha(\mathrm{q}+\mu)(\mathrm{R}_0-1)}{\mu\gamma\beta_1}$$

3.3.6 Local Stability of the Endemic Equilibrium point

Theorem3.4: The EE point E_1 of the model equation (3.1) to (3.5) is locally asymptotically stable in the region ϕ for $\mathrm{R}_0 > 1$.

Proof: The Jacobean matrix at E_1 is given by:

$$J = \begin{pmatrix} -\beta_1\mathrm{I} - \mathrm{q} - \mu & 0 & 0 & -\beta_1\mathrm{S} & 0 \\ \mathrm{q} - \mathrm{q}\beta_2\mathrm{I}\,\mathrm{S}\int_0^{\mathrm{h}}\mathrm{e}^{-\mu\tau}\mathrm{d}\tau - \mathrm{vq}\,\mathrm{S}\int_{\mathrm{h}}^{\infty}\mathrm{e}^{-\mu\tau}\mathrm{d}\tau - (1-\mathrm{v})\mathrm{q}\beta_3\mathrm{I}\,\mathrm{S}\int_{\mathrm{h}}^{\infty}\mathrm{e}^{-\mu\tau}\mathrm{d}\tau & -\mu & 0 & -\mathrm{q}\,\beta_2\mathrm{S}\int_0^{\mathrm{h}}\mathrm{e}^{-\mu\tau}\mathrm{d}\tau & 0 \\ \beta_1\mathrm{I} + \mathrm{q}\,\beta_2\mathrm{IS}\int_0^{\mathrm{h}}\mathrm{e}^{-\mu\tau}\mathrm{d}\tau + (1-\mathrm{v})\mathrm{q}\beta_3\mathrm{IS}\int_{\mathrm{h}}^{\infty}\mathrm{e}^{-\mu\tau}\mathrm{d}\tau & 0 & 0 & \beta_1\mathrm{S} + \mathrm{q}\,\beta_2\mathrm{S}\int_0^{\mathrm{h}}\mathrm{e}^{-\mu\tau}\mathrm{d}\tau + (1-\mathrm{v})\mathrm{q}\beta_3\mathrm{S}\int_{\mathrm{h}}^{\infty}\mathrm{e}^{-\mu\tau}\mathrm{d}\tau & -\gamma-\eta-\mu \\ 0 & 0 & 0 & -\alpha-\delta-\mu & \gamma \\ \mathrm{vq}\,\mathrm{S}\int_{\mathrm{h}}^{\infty}\mathrm{e}^{-\mu\tau}\mathrm{d}\tau & 0 & -\mu & \alpha & \eta \end{pmatrix}$$

$\mathrm{c}_1 = -\beta_1\mathrm{I}^* - \mathrm{q} - \mu$, $\mathrm{c}_2 = \mathrm{q} - \mathrm{q}\,\beta_2\mathrm{I}^*\,\mathrm{S}^*\int_0^{\mathrm{h}}\mathrm{e}^{-\mu\tau}\mathrm{d}\tau - \mathrm{vq}\mathrm{S}^*\int_{\mathrm{h}}^{\infty}\mathrm{e}^{-\mu\tau}\mathrm{d}\tau - (1-\mathrm{v})\mathrm{q}\beta_3\mathrm{I}^*\,\mathrm{S}^*\int_{\mathrm{h}}^{\infty}\mathrm{e}^{-\mu\tau}\mathrm{d}\tau$,

$\mathrm{c}_3 = -\mathrm{q}\,\beta_2\mathrm{S}^*\int_0^{\mathrm{h}}\mathrm{e}^{-\mu\tau}\mathrm{d}\tau$, $\mathrm{c}_4 = \beta_1\,\mathrm{I}^* + \mathrm{q}\,\beta_2\mathrm{I}^*\mathrm{S}^*\int_0^{\mathrm{h}}\mathrm{e}^{-\mu\tau}\mathrm{d}\tau + (1-\mathrm{v})\mathrm{q}\beta_3\mathrm{I}^*\mathrm{S}^*\int_{\mathrm{h}}^{\infty}\mathrm{e}^{-\mu\tau}\mathrm{d}\tau$,

$\mathrm{c}_5 = \beta_1\mathrm{S}^* + \mathrm{q}\,\beta_2\mathrm{S}^*\int_0^{\mathrm{h}}\mathrm{e}^{-\mu\tau}\mathrm{d}\tau + (1-\mathrm{v})\mathrm{q}\beta_3\mathrm{S}^*\int_{\mathrm{h}}^{\infty}\mathrm{e}^{-\mu\tau}\mathrm{d}\tau$

$\mathrm{c}_6 = -\gamma - \eta - \mu$, $\mathrm{c}_7 = \mathrm{vq}\,\mathrm{S}^*\int_{\mathrm{h}}^{\infty}\mathrm{e}^{-\mu\tau}\mathrm{d}\tau$, $\mathrm{c}_8 = -\alpha - \delta - \mu$

$$\mathrm{J}_{\mathrm{E}_1} = \begin{pmatrix} \mathrm{c}_1 & 0 & 0 & -\beta_1\mathrm{S} & 0 \\ \mathrm{c}_2 & -\mu & 0 & \mathrm{c}_3 & 0 \\ \mathrm{c}_4 & 0 & 0 & \mathrm{c}_5 & \mathrm{c}_6 \\ 0 & 0 & 0 & \mathrm{c}_8 & \gamma \\ \mathrm{c}_7 & 0 & -\mu & \alpha & \eta \end{pmatrix}$$

$$\mathrm{Det}(\lambda\mathrm{I} - \mathrm{J}_{\mathrm{E}_1}) = 0$$

$$\begin{vmatrix} \lambda - \mathrm{c}_1 & 0 & 0 & \beta_1\mathrm{S} & 0 \\ -\mathrm{c}_2 & \lambda - \mu & 0 & -\mathrm{c}_3 & 0 \\ -\mathrm{c}_4 & 0 & \lambda & -\mathrm{c}_5 & -\mathrm{c}_6 \\ 0 & 0 & 0 & \lambda - \mathrm{c}_8 & -\gamma \\ -\mathrm{c}_7 & 0 & \mu & -\alpha & \lambda - \eta \end{vmatrix} = 0$$

$\Rightarrow (\lambda - c_1)\left((\lambda - \mu)(\lambda((\lambda - c_8)(\lambda - \eta) - \alpha\gamma) + \gamma\mu c_5 + \mu c_6(\lambda - c_8))\right) - \beta_1 S(-(\lambda - \mu)(-c_4\mu\gamma + c_7\lambda\gamma)) = 0$

$\Rightarrow (\lambda - c_1)(\lambda^4 - \lambda^3(\eta + c_8 + \mu) + \lambda^2(\eta c_8 - \alpha\gamma + \mu c_6 + (\eta + c_8)\mu) + \lambda(\gamma\mu c_5 - \mu c_6 c_8 - \mu(\eta c_8 - \alpha\gamma) - \mu^2 c_6) - \gamma\mu^2 c_5 + \mu^2 c_6 c_8) - \beta_1 S c_4\mu\gamma\lambda + \beta_1 S c_7\lambda^2\gamma + \beta_1 S c_4\mu^2\gamma - \beta_1 S c_7\lambda\gamma\mu = 0$

$\Rightarrow \lambda^5 - \lambda^4(\eta + c_8 + \mu + c_1) + \lambda^3(\eta c_8 - \alpha\gamma + \mu c_6 + \eta\mu + c_8\mu + c_1(\eta + c_8 + \mu)) + \lambda^2(\gamma\mu c_5 - \mu c_6 c_8 - \mu\eta c_8 + \alpha\gamma\mu - \mu^2 c_6 + \beta_1 S c_7\gamma - c_1(\eta c_8 - \alpha\gamma + \mu c_6 + \eta\mu + c_8\mu)) - \lambda(\gamma\mu^2 c_5 - \mu^2 c_6 c_8 + \beta_1 S c_4\mu\gamma + \beta_1 S c_7\gamma\mu + c_1(\gamma\mu c_5 - \mu c_6 c_8 - \mu\eta c_8 + \alpha\gamma\mu - \mu^2 c_6)) + \gamma\mu^2 c_5 c_1 - \mu^2 c_6 c_8 c_1 + \beta_1 S c_4\mu^2\gamma = 0$

Therefore, we have a characteristic equation

$\Rightarrow P(\lambda) = \lambda^5 - b_1\lambda^4 + b_2\lambda^3 + b_3\lambda^2 - b_4\lambda + b_5 = 0$ ……3.15

Where, $b_1 = (\eta + c_8 + \mu + c_1)$, $b_2 = (\eta c_8 - \alpha\gamma + \mu c_6 + \eta\mu + c_8\mu + c_1(\eta + c_8 + \mu))$,

$b_3 = (\gamma\mu c_5 - \mu c_6 c_8 - \mu\eta c_8 + \alpha\gamma\mu - \mu^2 c_6 + \beta_1 S c_7\gamma - c_1(\eta c_8 - \alpha\gamma + \mu c_6 + \eta\mu + c_8\mu))$,

$b_4 = (\gamma\mu^2 c_5 - \mu^2 c_6 c_8 + \beta_1 S c_4\mu\gamma + \beta_1 S c_7\gamma\mu + c_1(\gamma\mu c_5 - \mu c_6 c_8 - \mu\eta c_8 + \alpha\gamma\mu - \mu^2 c_6))$,

$b_5 = \gamma\mu^2 c_5 c_1 - \mu^2 c_6 c_8 c_1 + \beta_1 S c_4\mu^2\gamma$.

Using the characteristic polynomial representation in equation (3.15) the Routh Hurwitz criterion Matrix are given by:

$H_1 = [b_1]$, $\det(H_1) = b_1 > 0$……..…..……(*)

$H_2 = \begin{bmatrix} b_1 & 1 \\ 0 & b_2 \end{bmatrix}$, $\det(H_2) = b_1 b_2 > 0$ or $b_1 > 0$ and $b_2 > 0$……..(**)

$H_3 = \begin{pmatrix} b_1 & 1 & 0 \\ b_3 & b_2 & b_1 \\ 0 & 0 & b_3 \end{pmatrix}$, $\det(H_3) = (b_1 b_2 - b_3)b_3 > 0$, $b_3 > 0$, and $b_1 b_2 > b_3$……..(***)

$H_4 = \begin{pmatrix} b_1 & 1 & 0 & 0 \\ b_3 & b_2 & b_1 & 0 \\ 0 & b_4 & b_3 & b_2 \\ 0 & 0 & 0 & b_4 \end{pmatrix}$, $\det(H_4) = b_4(b_1 b_2 b_3 - {b_3}^2 - {b_1}^2 b_4) > 0$, $b_1 > 0$, $b_3 > 0$, $b_4 > 0$

and $b_1 b_2 b_3 > {b_3}^2 + {b_1}^2 b_4$. ……..(****)

$H_5 = \begin{pmatrix} b_1 & 1 & 0 & 0 & 0 \\ b_3 & b_2 & b_1 & 0 & 0 \\ b_5 & b_4 & b_3 & b_2 & b_1 \\ 0 & 0 & b_5 & b_4 & b_3 \\ 0 & 0 & 0 & 0 & b_5 \end{pmatrix}$,

$\det(H_5) = b_1 b_2 b_3 b_4 b_5 + b_2 b_3 {b_5}^2 + b_1 b_4 b_5 - (b_1 {b_2}^2 {b_5}^2 + b_5 {b_1}^2 {b_4}^2 + b_4 b_5 {b_3}^2) > 0$

$= b_5(b_1 b_2 b_3 b_4 + b_2 b_3 b_5 + b_1 b_4 - (b_1 {b_2}^2 b_5 + {b_1}^2 {b_4}^2 + b_4 {b_3}^2)) > 0$

$b_5 > 0$ and $b_1 b_2 b_3 b_4 + b_2 b_3 b_5 + b_1 b_4 > \left(b_1 {b_2}^2 b_5 + {b_1}^2 {b_4}^2 + b_4 {b_3}^2\right)$ ……..(*****)

When all the conditions from (*) to (*****) holds. Hence all the roots of the characteristic polynomial of equation (3.15) are negative this verify that the model equation (3.1) to (3.5) is locally asymptotically stable when $R_0 > 1$ and unstable when $R_0 < 1$ .When $R_0 > 1$, Here the DFE point is unstable from the model equation when the solution converges to the EE point.

Table 1:- Summary for stability of the SVEIR model.

	Sign of R_0	**Type of stability**	**Mode of Epidemic**
DFE	$R_0 < 1$	Locally and globally asymptotically stable	No Epidemic
	$R_0 > 1$	Unstable	Epidemic
EE	$R_0 > 1$	locally asymptotically stable	Epidemic

CHAPTER FOUR

NUMERICAL SIMULATIONS WITH DISCUSSION, CONCLUSION AND RECOMMENDATION

4.1 Numerical simulations with discussion

The numerical simulations of the model were carried out to graphically illustrate with the help of python program to discuss the dynamical behavior of the model .The sources of these parameters are mainly from the reference as well as the assumptions.

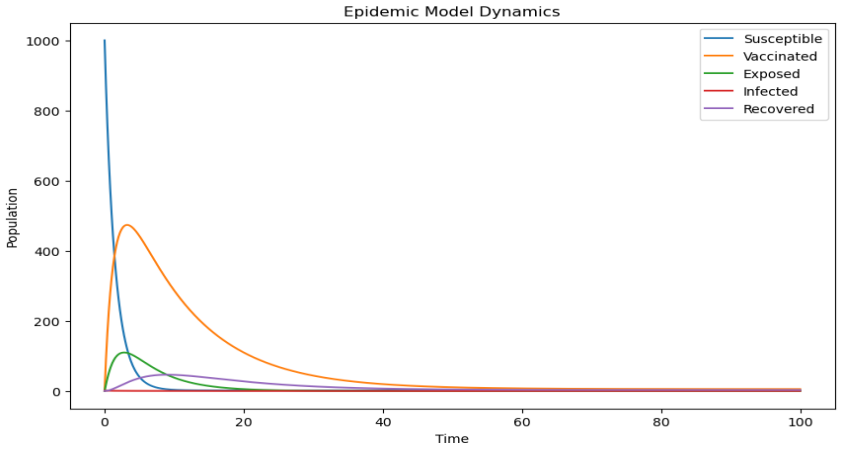
Table 3 below shows the set of parameter values we used to support the analytical results of the model. And also initial conditions of the variables are: $S_0 = 1000\,, V_0 = 0\ \,, E_0 = 0\ \ , I_0 = 1\ \ , R_0 = 0$

Table 2:- Numerical values of the parameters.

Parameters	Values	Reference
b	1.0	[14]
β_1	0.1	[18]
β_2	0.2	[4]
β_3	0.3	[8]
v	0.5	Assumed
μ	0.1	[12]
γ	0.2	[16]
α	0.3	[17]
δ	0.1	[1]
η	0.1	[14]
h	10	Assumed
q	0.5	[7]

The following figure $(\mathbf{2-4})$ could be expressing the dynamics behavior of the SVEIR model:

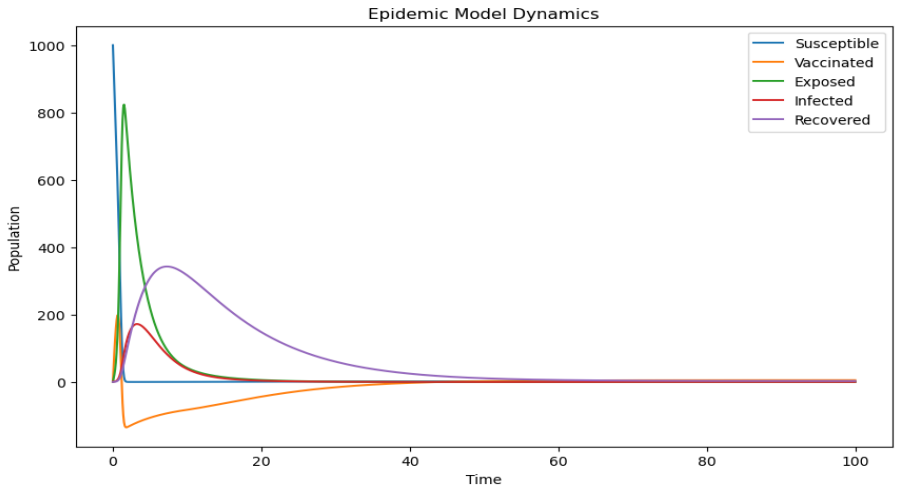
Figure 2: The infected rate $(\boldsymbol{\gamma}) = \mathbf{0.0012}$.



Consider in figure 2 illustrates the typical dynamics of an infectious disease within a closed population, characterized by:

- An initial rise in infections leading to a peak, followed by a decline.
- A corresponding increase in recoveries, indicating successful recovery rates.
- The role of vaccination in reducing the number of susceptible individuals and consequently the number of infections.

Figure 3: The infected rate $(\boldsymbol{\gamma}) = \mathbf{0.1}$.

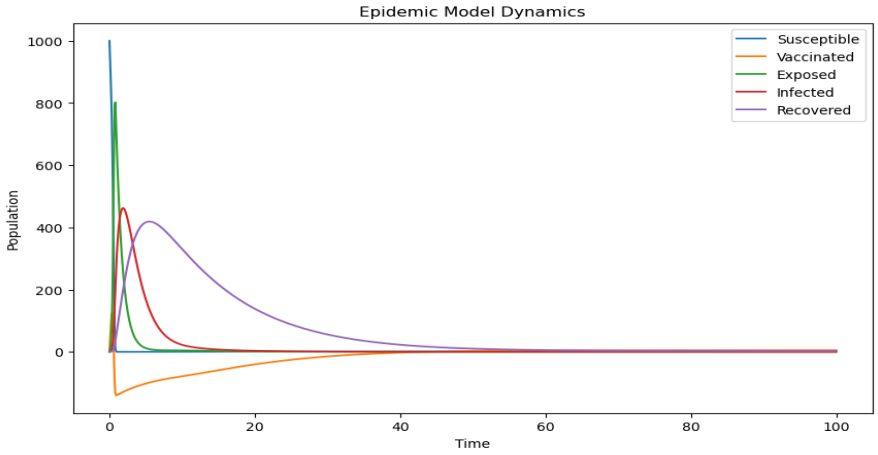


Consider in figure 3 illustrates a classic infectious disease model:

- ✓ Initial Outbreak: A rapid increase in infections leads to a peak burden on the population.

- ✓ Decline in Infections: After the peak, the number of infections declines as individuals recover or die.
- ✓ Increase in Recoveries: The recovered population grows as more individuals move from the infected compartment to recovery.

Figure 4: The infected rate $(\boldsymbol{\gamma}) = \mathbf{0.9}$.



Consider in figure 4 effectively illustrates the typical dynamics of an infectious disease in a closed population with:

- ❖ Initial Rise: The early phase of the outbreak sees a rapid increase in infections.
- ❖ Peak Infection: The peak of the infected population indicates the critical point of the outbreak.
- ❖ Decline Phase: After reaching the peak, the infected population decreases as individuals recover or die, while the recovered population continues to grow.

4.2 Conclusion

When it is carried out immunization with the vaccine, not only the vaccinated individual is protected against infectious disease, but also indirectly, it is prevented from infecting other individuals. Therefore, if the number of vaccinated individuals against the disease in the population is how much higher, the probability of the occurrence of that disease is lower at that rate. It is even possible to eliminate some diseases completely. For example, through successful vaccination programs, diseases such as smallpox, measles, and polio have been completely eradicated or have been reduced to almost non-existent levels. This situation has increased the interest to models with vaccine in dynamical systems.

In this project, it has been obtained the disease-free dynamics of a time delayed **SVEIR** epidemic model with a different perspective from the models in the literature. For the model it has been obtained the threshold quantity R_0, called as the basic reproduction number. Next, as $R_0 < 1$, it has been shown that disease-free equilibrium is locally asymptotically stable and is globally attractive, and as a result of this is globally asymptotically stable. Vaccination always has a strong effect for disease control by decreasing the basic reproduction number. So, when $R_0 < 1$, effective, preventative and sustained vaccinations the disease can disappear ultimately. Most of the individuals undergoing treatment join the recovered class .Increasing vaccination rate and aware individual has a significant impaction the spread rate of disease transmission. There is also inverse relationship between the basic reproduction number and these rates. When we increase the vaccination and aware individual the basic reproduction number, decreases and become less than one that means the disease die out from the population. It was also realized that, in the absence of mass vaccination program, the transmission of the disease cannot be eradicated from the population. The proper treatment about the disease transmission can help reduce the disease in a population. The results have also shown that effective contact with the infectious individuals cause a major increase of the disease transmission; hence individuals with active infectious disease must be detected as early as possible in order to reduce high transmission in a population.

4.3 Recommendation

To control infectious disease from the population we strongly recommended the following points.

- ✓ The public health administration focus on all susceptible individuals should be getting the infectious disease.
- ✓ The analysis shows that the outbreak of the disease largely depends on the contactrate q; therefore effort should be made to minimize unnecessary contact as well as how to take care of infected individuals so that he/she might not infect others.
- ✓ More people should be educated in order to create awareness about the outbreak of the infectious disease as well as the control strategy of it.

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Appendix

Python form of

- **Figure 2**

```
import numpy as np
import matplotlib.pyplot as plt
from scipy.integrate import odeint
from scipy.integrate import quad

# Parameters
b = 0.1      # Birth rate
beta1 = 0.3  # Infection rate for S and I
q = 0.2      # Rate of transition from S to V
mu = 0.01    # Natural death rate
beta2 = 0.4  # Infection rate for E and I
v = 0.5      # Fraction of exposed individuals that become vaccinated
beta3 = 0.2  # Another infection rate
gamma = 0.0012  # Rate of recovery from E to I
eta = 0.05   # Rate of recovery from E
alpha = 0.1  # Rate of loss of immunity
delta = 0.1  # Rate of disease death
h = 1        # Time threshold for transitions

# Initial conditions
S0 = 1000    # Initial susceptible population
I0 = 50      # Initial infected population
E0 = 0       # Initial exposed population
V0 = 0       # Initial vaccinated population
R0 = 0       # Initial recovered population
y0 = [S0, I0, E0, V0, R0]

# Time span
t = np.linspace(0, 100, 500)  # Time from 0 to 100

def model(y, t):
    S, I, E, V, R = y

    # Define the integral terms
    integral_0_h = quad(lambda tau: np.exp(-mu * tau) * S, 0, h)[0]
    integral_h_inf = quad(lambda tau: np.exp(-mu * tau) * S, h, np.inf)[0]

    # System of equations
    dSdt = b - beta1 * S * I - q * S - mu * S
    dIdt = gamma * E - alpha * I - delta * I - mu * I
    dVdt = (q * S
            - q * beta2 * I * integral_0_h
            - v * q * integral_h_inf
            - (1 - v) * q * beta3 * I * integral_h_inf
            - mu * V)
    dEdt = (beta1 * S * I
            + q * beta2 * I * integral_0_h
            + (1 - v) * q * beta3 * I * integral_h_inf
```

```
            - gamma * E
            - eta * E
            - mu * E)
    dRdt = (v * q * integral_h_inf
            + eta * E
            + alpha * I
            - mu * R)

    return [dSdt, dIdt, dEdt, dVdt, dRdt]

# Solve the system of equations
result = odeint(model, y0, t)

# Plot results
plt.figure(figsize=(10, 6))
plt.plot(t, result[:, 0], label='Susceptible (S)', color='blue')
plt.plot(t, result[:, 1], label='Infected (I)', color='red')
plt.plot(t, result[:, 2], label='Exposed (E)', color='green')
plt.plot(t, result[:, 3], label='Vaccinated (V)', color='black')
plt.plot(t, result[:, 4], label='Recovered (R)', color='magenta')
plt.xlabel('Time')
plt.ylabel('Population')
plt.title('Disease Model Dynamics')
plt.legend()
plt.grid()
plt.show()
```