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UNIVERSITÄT KOBLENZ - LANDAU

## MASTER'S THESIS

for the partial fulfillment of the requirements for a Master of Science in  
**Mathematical Modeling of Complex Systems**

# **Mathematical Modeling and Simulation of a Zombie Epidemic**

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# Declaration of Honour

I hereby, confirm that I have authored this thesis paper alone and on my own. I have not employed any resources or online materials other than those mentioned in the bibliography section. I did not submit or publish this thesis paper anywhere before or with any other examination procedure.



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10<sup>th</sup> October, 2021  
Koblenz, Germany

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# Abstract

Mathematical modeling is the process of describing a system using mathematical methods, language, concepts, and equations. Various mathematical models are being developed to understand, analyze, study, and predict different epidemiological and disease-inflicted situations in the human population. In this thesis paper, an attempt has been made to understand, study the scenario and predict the outcome of an epidemic caused by zombie infection on the human population. The development of this zombie epidemic model is based on the classical SIR model, which was originally proposed by Kermack-McKendrick in 1927. Based on this original SIR model, an analogous SZR model, where the possibility of a zombie epidemic is considered, is studied here. The SZR model is analyzed through different mathematical processes to check and verify its stability. It is also being checked the possibility of human survival in the long run if such an epidemic occurs in real life through introducing and analyzing perturbation parameter in the model. A graphical interactive computer program is created using Python as part of this study, where it is possible to change and modify the parameter values of the model and simulate as well as visualize the change in outputs instantly. Moreover, in the subsequent step, a more complicated quarantine model, namely Modified SEZQR is considered, where the stability of the human population is studied through the introduction of perturbation parameter. A basic reproduction number is calculated based on this model and the condition for disease-free equilibrium is investigated through the impact of this perturbation parameter in bifurcating the model from instability to stability.

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# Chapter 1

## Introduction

### 1.1 Background

In recent times, mathematical modeling has been an important method in studying the spread of infectious diseases, contamination, and viral outbreaks. This process of mathematical modeling helps us to interpret the real-world scenario of the disease or outbreak in terms of mathematical language and equations. As such, it is possible to study the ongoing dynamics of the disease and predict the future flow or path of the disease, analyze and track its progression and finally take necessary steps to prevent or contain the outbreak in a more efficient and effective way. Through this modeling process, the whole disease inflicted scenario is translated in the form of mathematical equations based on the empirical observations, which are then later solved using different methods, parameters, and variables that enable researchers to understand the whole outbreak situation in a more comprehensive way and make informed decisions accordingly.

A lot of works have been done in modeling different types of outbreaks in the human population and the works on this field continue to flourish even further and wider. One of the most notable works in this field of studying epidemics through mathematical modeling can be traced back to the research paper *A contribution to the mathematical theory of epidemics* [1], which was authored by Kermack and McKendrick in 1927. In this paper, the authors discussed about a deterministic modeling process, namely the SIR model, where an individual from a population would belong to one of the three categories- susceptible, infectious, or recovered. The model describes the transition of the disease through linear mass action law within these three compartments. This classical modeling approach of the SIR model has been taken as the basis of this thesis work. The modeling of the zombie infection follows an analogous process but also introduces and considers more variables and compli-

## 1 Introduction

cations to make it more pragmatic and fitting for the real-world scenario.

In this thesis work, zombie infection is considered as the reason for causing the epidemic. In the pop culture (as in movies, thriller novels, video games) of recent times, the zombie apocalypse has become a popular phenomenon. As per the folklore definition of the Oxford dictionary [2], a zombie is believed to be something that is dead but turned alive partially through magic and is not fully aware of its surroundings. However, in today's pop cultures, zombies are being depicted as some kind of undead, cannibalistic, mindless creatures, that can attack and infect other healthy individuals and then also turn them into zombies and thus cause havoc within a population. So like any other kind of viral infection or infectious disease, a zombie has the ability to infect people and spread a disease. It is not the point of interest of this thesis work to investigate the origin of zombie infection, whatever that might be. Rather, it has been tried to study the dynamics through the process of mathematical modeling by considering the zombie epidemic as just another kind of infectious disease epidemic. In this paper, an attempt has been made to analyze the mathematical models of a likable zombie infection, introduce perturbation parameters to investigate the likelihood of a probable stability of such kind of epidemic through a scientific and mathematical approach.

## 1.2 Related Work

A lot of research works have already been conducted in the field of mathematical modeling for the study of viral disease circulation among the population, both for humans and other types of animals. As already mentioned, the most notable pioneering work in this field comes from the SIR model developed by Kermack and McKendrick [1], where the authors had surmised a simple model of disease transmission within three compartments, namely from susceptible to infectious to recovered. Their work has turned into the ground basis for all kinds of future modeling approaches undertaken by different researchers in this field. An important work in understanding the process for developing mathematical equations and systems for epidemiological dynamics is described in detail in the book *An introduction to mathematical epidemiology* [3]. Another comprehensive introduction can be found in the book *Mathematical Epidemiology* [4], where the authors have discussed in detail regarding the preparation of mathematical models, along with the explanation for necessary mathematical concepts (such as calculus, differential equations, matrix algebra, probability) for understanding and simulating real-world outbreak scenario. Here, the authors have considered different real-world cases for infectious diseases such as Severe Acute Respiratory Syndrome (SARS), influenza, West Nile virus, etc. in explaining the process for developing a mathematical model. Also, to get some understanding of the concepts behind mathematical biology, the books *Mathematical Biology I and II* [5], [6] are some of the important works in this field of study.

However, in the simpler SIR model, a linear transformation of disease dynamics is considered and it is also assumed that an infected individual will receive immunity after a certain time. But this is not the actual case that happens in real-life scenarios. So, to understand the non-linearity, further studies are required. In this respect, *Some epidemiological models with nonlinear incidence* [7] provide some important insights. In this paper, the authors have investigated different types of dynamics based on multiple equilibria points and related periodic solutions. Here, the authors have also introduced one more compartment, called Exposed in building up their model. In another work, S. Ruan and W. Wang [8] attempted to study the global dynamics of the epidemic through a nonlinear saturated mass action incidence rate. Also, for studying disease models without immunity, the works of H. W. Hethcote and P. van den Driessche [9] provided some important directions. More study on the SEIR (susceptible-exposed-infectious-recovered) model with nonlinear incidence rates can be found in the works of M. Y. Li and J. S. Muldowney [10].

Numerous works have been done on modeling zombie epidemics. To get some

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primary idea, *Teaching Mathematical Modeling Using the Zombie Apocalypse* [11] can be a good starting point. For Bayesian analysis of the zombie epidemic and some other diseases, the works of C. Witkowski and B. Blais [12] provides some directions. Also, the book of A. Cartmel and R. J. Smith [13], provides a very rich and detailed overview for modeling zombies mathematically. Some other relevant papers for zombie epidemic modeling worth mentioning here are, the works of A. Alemi, M. Bierbaum [14], the works of E. Idu and R. Oladele [15], and the works of V. Tomotani [16].

However, the two research works that have contributed the most in writing this thesis paper are *Mathematical Modelling Of An Outbreak Of Zombie Infection* [17] and *Perturbations in Epidemiological Models* [18]. The first paper [17] introduces the SZR model, and the quarantine model SEZQR (or SIZQR) and investigated whether it is possible for human to survive such a zombie epidemic. The second paper [18], took the analysis to next level by introducing perturbation parameters in the existing models and analyzed the survivability of the human population during such an epidemic. This paper inferred the likelihood of healthy human survival and termination of the zombie apocalypse with respect to the proper perturbation parameter. These works are the main basis and inspiration for analyzing the SZR model and making new modifications to the SEZQR model that will be presented in the upcoming chapters of this thesis paper.

### 1.3 Structure of the Thesis

This thesis paper begins with a brief introduction to mathematical modeling for infectious diseases in chapter 1. Here, the process and importance of mathematical modeling are discussed, and also other related, relevant research works in this field are highlighted, that have served as the guiding directions for this thesis work.

In chapter 2, a brief introduction to the classical SIR model [1] has been given. This chapter explains the development of a simple model based on the three-class system, namely susceptible-infectious-recovered. This model describes the linear mass action law for the transmission of disease within a closed homogeneous population.

In chapter 3, a closer look has been given at the SZR model [18]. This model introduces zombies as the origin of the epidemic. Several mathematical analyses have been conducted on this basic model to check its feasibility and sustainability based on the perturbation parameter. An interactive graphical program is created using python to change the parameter values and simulate the changes in real-time in order to understand the dynamics in a more convenient way. The role of the perturbation parameter, as it changes values, on the model to test its stability has also been investigated here.

Finally, a more elaborate and complicated quarantine SEZQR model [17], [18] is studied in chapter 4. Some new modifications have been made on this model to give it a more pragmatic outlook and a new basic reproduction number is calculated based on this modified model. Later on, stability is checked for this modified model, and also the condition for the disease-free equilibrium is evaluated based on the perturbation parameter. Finally, the results of this modified model is compared with the original SEZQR model. Some special case scenarios have also been discussed at the end of this chapter.

# Chapter 2

## SIR Epidemic Model

### 2.1 Basic Introduction

In this chapter, a brief overview of the classical SIR model developed by Kermack-Mckendrick [1] in 1927, will be given. This model attempts to estimate and predict the distribution and number of infections for an infectious disease. The SIR model serves as the most primary ground in developing more elaborate and complicated epidemiological models.

The SIR model categorizes the whole population into three compartments. First, the susceptible compartment S, secondly the infected and infectious compartment I, and finally the recovered compartment R.

- The susceptible population S denotes the number of healthy people who are not yet infected but are prone or vulnerable to infection.
- The infectious population I denotes the people who are already infected and sick from the susceptible population. These people are also infectious and are waiting to be recovered.
- And lastly, the recovered population R, who are assumed to be recovered from the disease.

This model can be visualized in the picture below—

## 2 SIR Epidemic Model

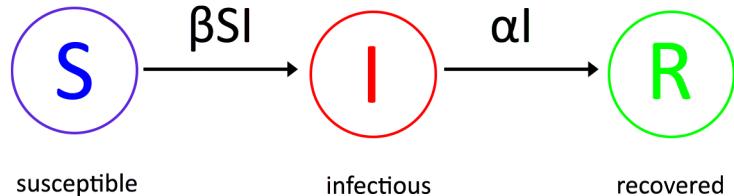


Figure 2.1: SIR Model

Here, the individuals transfer from the susceptible compartment S to the infectious compartment I at a rate of  $\beta SI$ , where  $\beta$  is a positive constant and the transmission rate from S to I. And finally, individuals transfer from the infectious compartment I to the recovered compartment R at a rate of  $\alpha I$ , where  $\alpha$  is again a positive constant and the recovery rate for individuals from I to R. Here, it is important to note that, the transmission rate from the susceptible population S to the infected population I depends both on the susceptible and infectious compartments and hence, the rate is defined as  $\beta SI$ .

So the model can be summarized as a system of ordinary differential equations as given below—

$$\begin{aligned} S'(t) &= -\beta SI \\ I'(t) &= \beta SI - \alpha I \\ R'(t) &= \alpha I \end{aligned} \tag{2.1}$$

Here, all the variables S, I, and R are functions of time, which means that they only change their values with respect to the time. It is also crucial that, the size of the whole population at any given time t, is the sum of all the individuals from the susceptible, infectious, and recovered compartments. That means—

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

Some other important fundamental characteristics of this model are—

- The whole population is closed. That means the number of total individuals remains constant within the given time t, i.e.  $N'(t) = S'(t) + I'(t) + R'(t) = 0$  and  $N = S(0) + I(0) + R(0)$ . The population is continuous in time.
- All the individuals receive immunity as soon as they enter the recovered compartment R, either by immunity from reinfection or by death. So the possibility

## 2 SIR Epidemic Model

for reinfection is omitted.

- The duration of the disease spread or epidemic is smaller than the lifespan of the population.
- The incubation period [19] for the disease is negligible. So any individual who gets infected is moved immediately to the infectious compartment I.
- The population is homogeneously [20] mixed. All the individuals within the population have an equal probability of getting into contact with each other and getting infected.
- The unit of transmission rate  $\beta = 1/(\text{population size} \times \text{unit of time})$ , and  
The unit of recovery rate  $\alpha = 1/(\text{unit of time})$  [3]

## 2.2 Example

A sample real life epidemic case can be solved here with the SIR model using python. For this, let us consider a dataset from an influenza epidemic that occurred in a boys boarding school in the north of England in 1978 [21], [22].

In this case, the epidemic lasted for two weeks. There were in total of 763 boys who were residents in that boarding school, including one who was infected initially.

So we can set the initial conditions—

Initial susceptible,  $S(0) = 762$

Initial infected,  $I(0) = 1$

Initial recovered,  $R(0) = 0$

Time period,  $t = 14$  days

Step size = 1

And the transmission rate as well as recovery rate values are taken from [5]

$\beta = 0.00218$

$\alpha = 0.441$

Now it is possible to model these data using python.

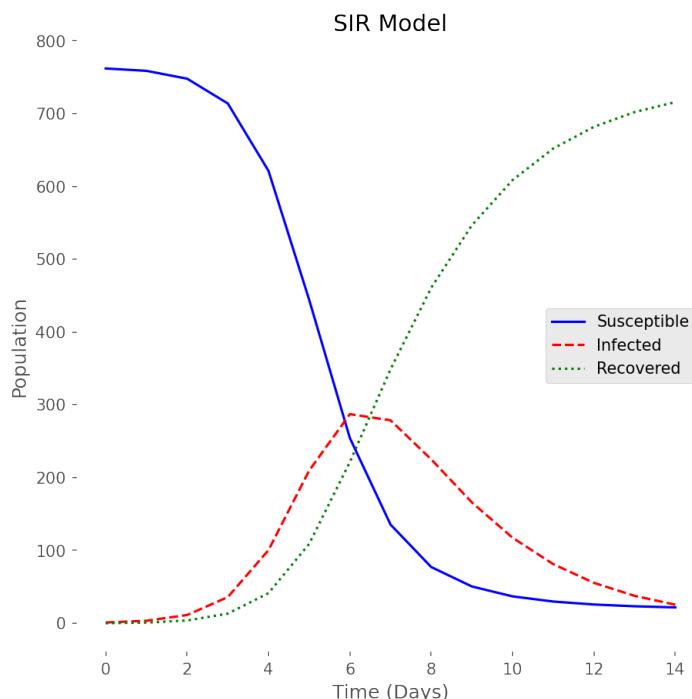


Figure 2.2: Numeric Solution of SIR Model for Example Data

## 2 SIR Epidemic Model

From the above graphs, it can be seen that, the susceptible population  $S'(t)$  is strictly decreasing with time, while the recovered population  $R'(t)$  is strictly increasing with time. But for the infectious population  $I'(t)$ , the values increase at first and then decrease to zero finally.

Also, a phase portrait [34], [35], [36], [37] is a very convenient way to geometrically represent the trajectories of a dynamical system in a phase plane.

The phase portrait of the SIR model—

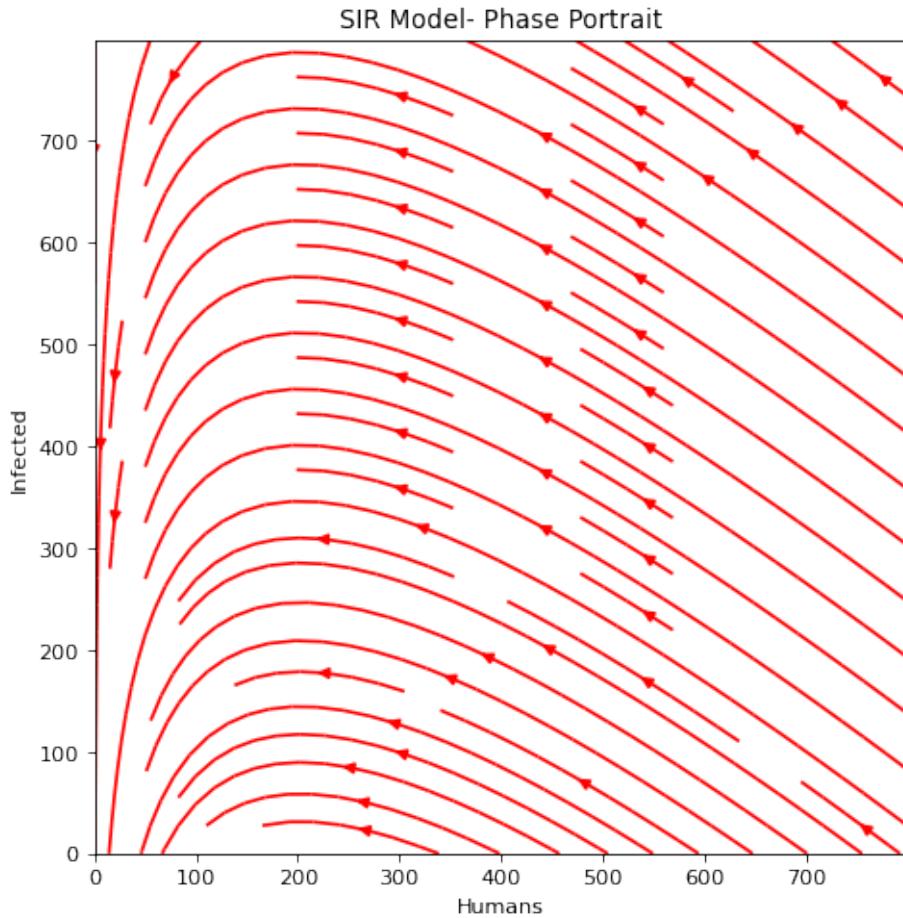


Figure 2.3: SIR Model- Phase Portrait

From the phase portrait, it can be seen that the SIR model is linearly stable and a disease free equilibrium exists. According to this very simple model, the survivability of human population in the long run is possible.

In Python code, `solve_ivp` function from Scipy library [23] was used to solve the SIR differential equations and later plotted with matplotlib library [24]. Also, Numpy library [25] was used for some additional calculations. And for the phase

## 2 SIR Epidemic Model

portrait, streamplot [46] function was used.

Some more related examples regarding SIR model can be found at [26], [38], [39], [40], [41], [42], [43].

Some studies on the recent Corona Virus Disease 2019 (COVID-19) using SIR model can be found at [44], [45].

The source of the Python codes for this SIR model can be found in the Codes section of this thesis paper.

# Chapter 3

## Zombie Epidemic Model

### 3.1 Basic Zombie Model Introduction

The basic SZR (susceptible-zombie-removed) model is a modification of the classical SIR model [1] which was first introduced in [17]. This model considers zombie infection as the cause of the epidemic.

Like the SIR model, this SZR model also categorizes the whole population into three compartments. It begins with the susceptible compartment denoted by S, then the compartment for the infected and infectious zombies Z and finally the compartment R for the removed population.

- The susceptible compartment S, denotes the group of the population who are healthy but are vulnerable to the zombie infection.
- The zombie compartment Z, denotes the group of the population who are infected with zombie infection and are also infectious. This group of people are capable to spread the disease.
- Finally, the people who have recovered from the zombie disease are categorized in the removed R compartment.

The whole model can be visualized as below—

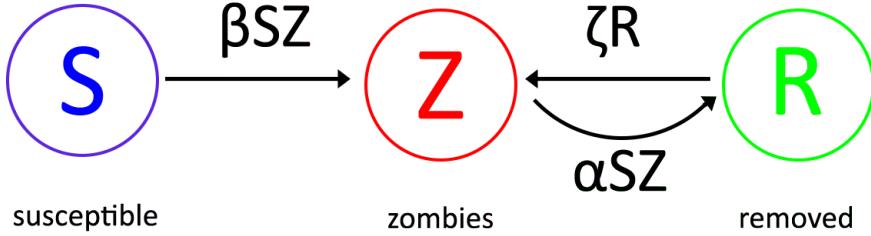


Figure 3.1: Basic SZR Model

The dynamics of the spread of disease within this model can be summarized as below—

- Individuals from the susceptible compartment S transfer to the compartment of zombies Z at a rate of  $\beta SZ$ . Here  $\beta$  is a positive constant and is the transfer rate from the compartment S to I. The transfer rate of individuals from the susceptible to the zombies depends both on the current population number of S and Z.
- The transfer rate of individuals from the zombies compartment Z to the removed R is defined as  $\alpha SZ$ , where  $\alpha$  is a positive constant and the removal rate from the compartment Z to R. This removal rate also depends on the total number of individuals for both of the susceptible and zombies compartments.
- Finally, the reinfection rate  $\zeta R$ , that denotes the transfer of individuals from the removed compartment to the zombies compartment. This rate is assumed to be dependent only on the total number of individuals inside the R compartment.

So now, the SZR model can be written as a system of ordinary differential equations as given below—

$$\begin{aligned} S'(t) &= -\beta SZ \\ Z'(t) &= \zeta R + (\beta - \alpha)SZ \\ R'(t) &= \alpha SZ - \zeta R \end{aligned} \tag{3.1}$$

As before, all the variables S, Z and R are functions of time, t. And the total size of the population remains constant within the given time and the sum of all the compartments is equal to the whole population size N. Which in turn means that,

### 3 Zombie Epidemic Model

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

Equation (3.1) can be reduced in the following form, with the following substitution  $R = N - S - Z$ ,

$$\begin{aligned} S'(t) &= -\beta SZ \\ Z'(t) &= \zeta(N - S - Z) + (\beta - \alpha)SZ \end{aligned} \tag{3.2}$$

Some important assumptions of this model—

- Unlike the SIR model, in the SZR model, no type of immunity is promised to the individuals of the population. So the possibility of reinfection is considered here. Hence, comes the reinfection rate  $\zeta R$  from the removed compartment to the compartment of zombies. So the removed individuals in the compartment R can be reinfected or resurrected and can be returned to the Z compartment.
- Here, zombies are removed only through the interaction with human population. All types of other natural causes like starvation, natural disaster or accident are ignored in this model.
- As soon as a susceptible individual gets infected, that person is transferred to the zombies compartment. The incubation period is negligible and can be omitted.
- Like the SIR model, the population is homogeneously mixed. Every individual possesses an equal probability of getting infected.

In [17], the authors tried to analyze the linear stability of the disease free equilibrium of this model, in order to determine the possible survivability of the human species. The authors concluded that, the survival of the human race is not possible in the long run of this model and thus the disease free equilibrium is nonexistent.

## 3.2 Example of SZR Model

To simulate the basic SZR model, an imaginary example can be considered.

For this example, let us consider the following values,

The total population size,  $N = 1000$

Initial susceptible population,  $S(0) = 830$

Initial zombie population,  $Z(0) = 70$

Initial removed population,  $R(0) = 100$

Number of days,  $t = 4000$

And for the estimates of the parameters, those values can be taken from [17],

Parameter	Description	Estimate
$\beta$	transmission rate for the zombie infection	0.0095
$\alpha$	removal rate of infected zombies	0.005
$\zeta$	reinfection or resurrection rate for removed individuals	0.0001

Table 3.1: Parameter Estimates for the Basic SZR Model

Now it is possible to solve the system of differential equations (3.1) numerically using python with the above set of values.

At first, the system is numerically solved for  $t = 10$  days, with total steps of 100, so it is easier to visualize the decrease of the susceptible population.

### 3 Zombie Epidemic Model

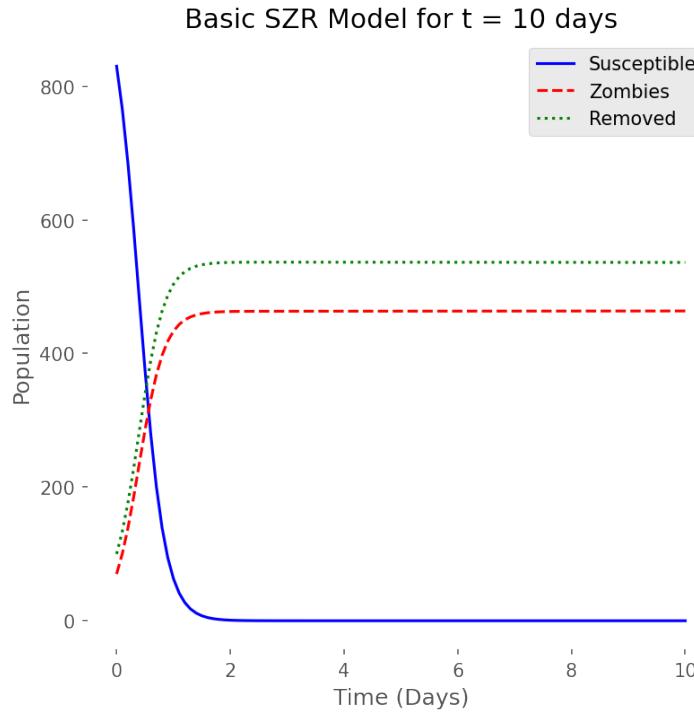


Figure 3.2: Basic SZR Model Numeric Solution for  $t = 10$  Days

Finally, the system is solved for  $t = 4000$  days, with total steps of 4000. As can be seen from the Figure 3.3, the number of zombies increases, while the removed population decreases on a straight manner.

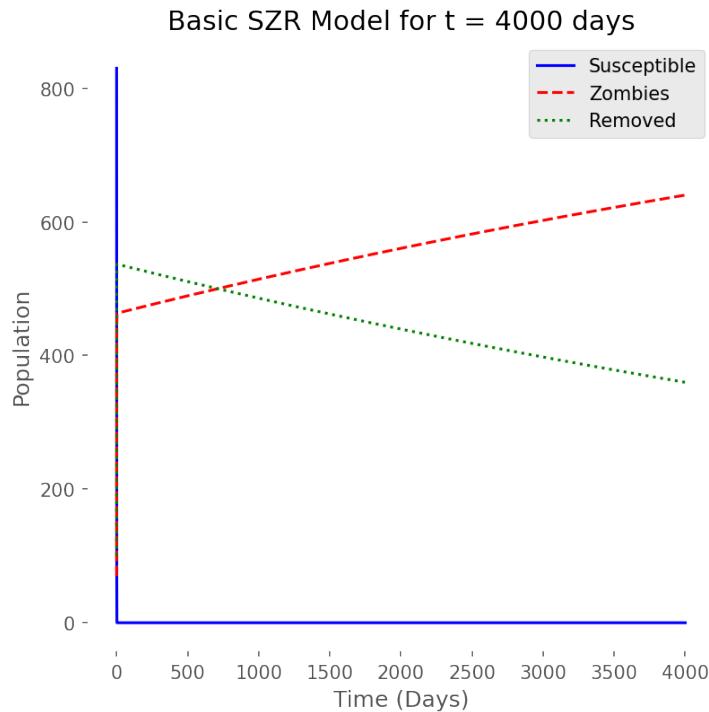


Figure 3.3: Basic SZR Model Numeric Solution for  $t = 4000$  Days

### 3 Zombie Epidemic Model

And also the phase portrait for the system—

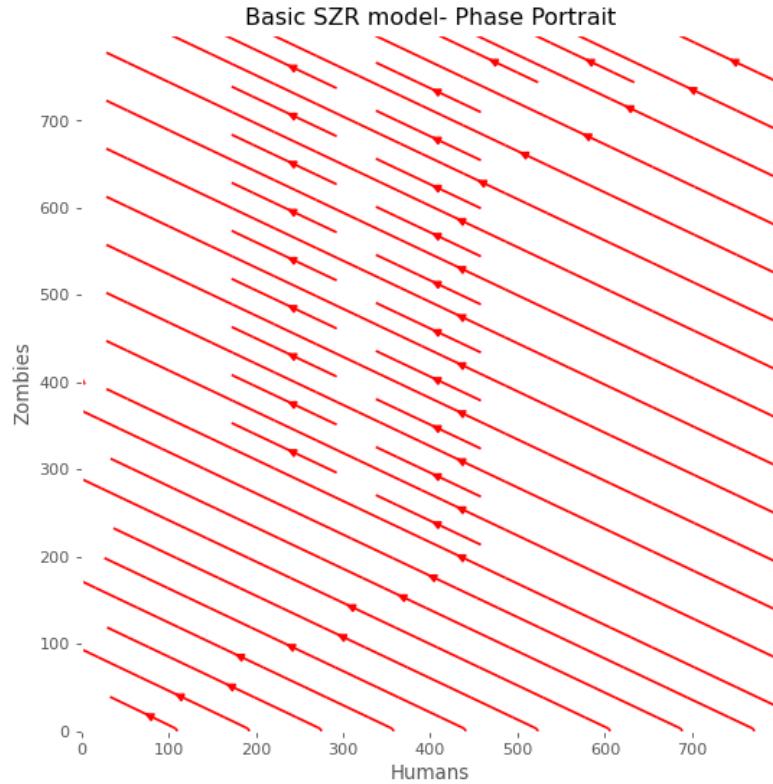


Figure 3.4: Basic SZR Model- Phase Portrait

As can be seen from Figure 3.4, the phase portrait of the basic SZR model, the system is unstable and the survival of the healthy human population is not possible in this model.

### 3.3 SZR Model with Perturbation

#### 3.3.1 Model Introduction

Now comes the scope for the modification of the basic SZR model. In [18], the authors Allen et al. introduced a new parameter to perturb the basic model.

The authors considered a new parameter  $\mu$ , with  $\mu \in (0, \infty)$ , to set up a non-linearity inside the model. Here, the removal rate from the zombies compartment  $Z$  to the removed compartment  $R$  is defined as  $\alpha S^{(1+\mu)} Z$ .

This parameter  $\mu$  is introduced to slightly perturb the original basic model in order to provide rooms for new possibilities and equilibriums as well as to give it a nonlinear nature. For more methodologies on perturbation parameters, interested reader is directed to [27], [28], [29], [30], [31], [32], [33].

The newly modified model can be visualized in the figure below—

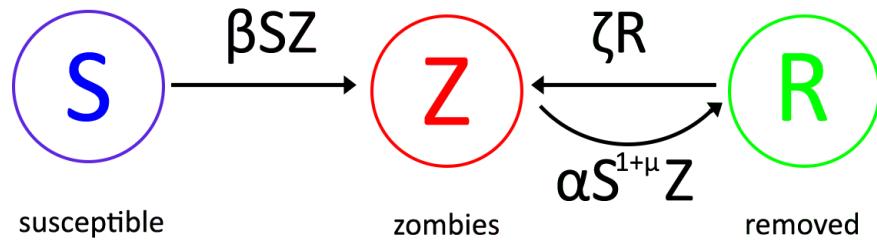


Figure 3.5: Perturbed SZR Model

All the other assumptions and considerations from the basic SZR model remains same and unchanged in this modified and slightly perturbed SZR model.

It is expected that this small perturbation in the original SZR model will open the scope for human survival and provide a new disease free equilibrium.

According to this modification, a new system of differential equations can be developed—

$$\begin{aligned}
 S'(t) &= -\beta SZ \\
 Z'(t) &= \zeta R + \beta SZ - \alpha S^{1+\mu} Z \\
 R'(t) &= \alpha S^{1+\mu} Z - \zeta R
 \end{aligned} \tag{3.3}$$

### 3 Zombie Epidemic Model

Or, these equations can be reduced with the substitution of  $R = N - S - Z$ , in the following form—

$$\begin{aligned} S'(t) &= -\beta SZ \\ Z'(t) &= \zeta(N - S - Z) + \beta SZ - \alpha S^{1+\mu} Z \end{aligned} \tag{3.4}$$

As per [18], the condition for the perturbation parameter  $\mu$  to make the model linearly stable and to introduce a disease free equilibrium, is as given below—

$$\mu > \frac{\ln\left(\frac{\beta N - \zeta}{\alpha}\right)}{\ln(N)} - 1 \tag{3.5}$$

### 3.3.2 Example

This modified SZR model with perturbation can be numerically solved using an imaginary example, so that it is easier to understand and predict its behavior.

For this imaginary example, let us consider the following initial conditions—

The total population size,  $N = 1000$

Initial susceptible population,  $S(0) = 800$

Initial zombie population,  $Z(0) = 200$

Initial removed population,  $R(0) = 0$

Number of days,  $t = 1000$

And for the estimates of the parameters, those values can be taken from [17] and [18],

Parameter	Description	Estimate
$\beta$	transmission rate for the zombie infection	0.0095
$\alpha$	removal rate of infected zombies	0.005
$\zeta$	reinfection or resurrection rate for removed individuals	0.0001
$\mu$	perturbation value	0.175

Table 3.2: Parameter Estimates for the Perturbed SZR Model

Now the model is solved numerically with the above set of values using Python `solve_ivp` [23] function. This function uses Runge-Kutta method of order five (RK45) [61], [62], [63], as the integration method.

First the system is solved for 10 days, with a step size of 0.1. So, it easier to visualize the changes in the zombie population.

### 3 Zombie Epidemic Model

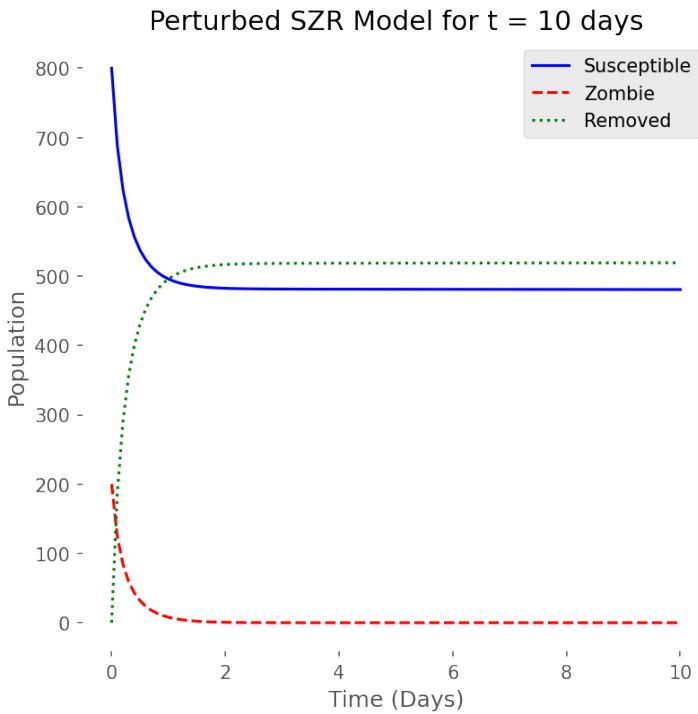


Figure 3.6: Perturbed SZR Model Numeric Solution for  $t = 10$  Days

And finally, the system is solved for 1000 days, with a step size of 1. It can be seen that, the impact of the perturbation parameter  $\mu$  has caused the decline of the zombie population and the size of the removed population increases gradually.

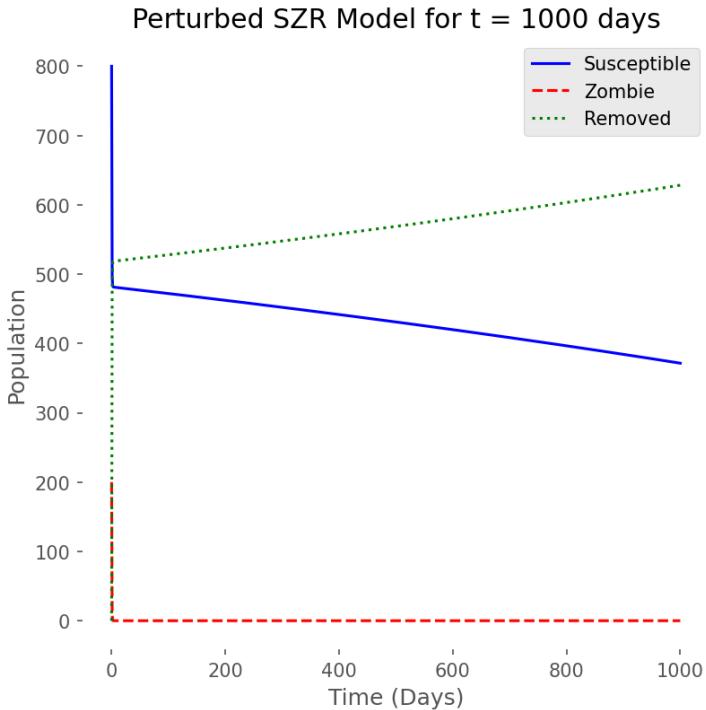


Figure 3.7: Perturbed SZR Model Numeric Solution for  $t = 1000$  Days

### 3 Zombie Epidemic Model

Now, for the phase portrait of the perturbed SZR model, it can be seen that the perturbation parameter  $\mu$  has a deep impact on the stability of the model. While comparing with the Figure 3.4, it is noticeable that this perturbation parameter has caused a noticeable change in the behavior of the model.

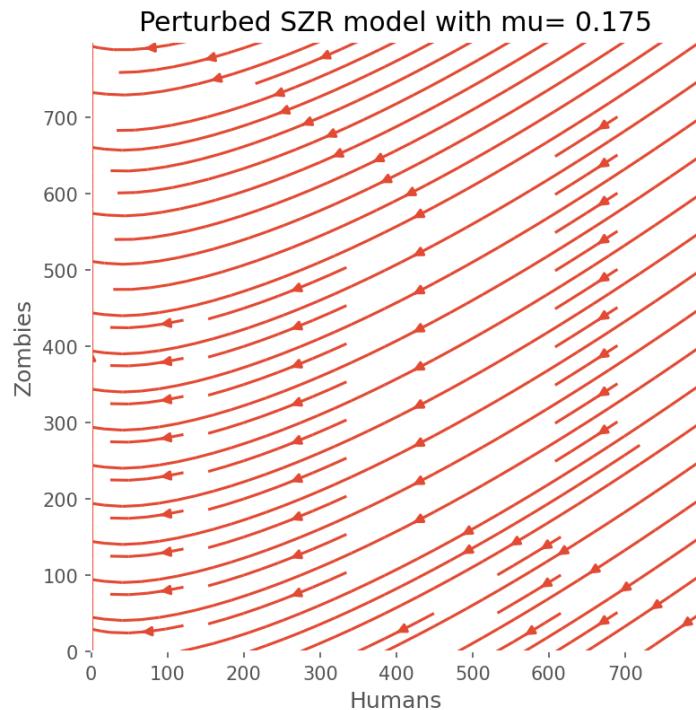


Figure 3.8: Perturbed SZR Model- Phase Portrait

So due to this perturbation parameter  $\mu$ , this model is stable. The number of zombies will decrease to zero and the whole population will go back to its healthy state gradually.

### 3.3.3 Change of Stability as Per Perturbation Parameter

In order to investigate the change of stability and behavior of the perturbed SZR model, a simple python program was written. This program will plot the phase portraits of this model, starting from  $\mu = 0.0$  (at  $\mu = 0.0$ , this model is just the basic and unperturbed SZR model), and will increase the value of  $\mu$  by 0.005 at each step, until the model reaches linear stability and a disease free equilibrium exists. The value of  $\mu$  is checked against the condition stated in equation (3.5), to find the first value of  $\mu$  corresponding to the stability of the model.

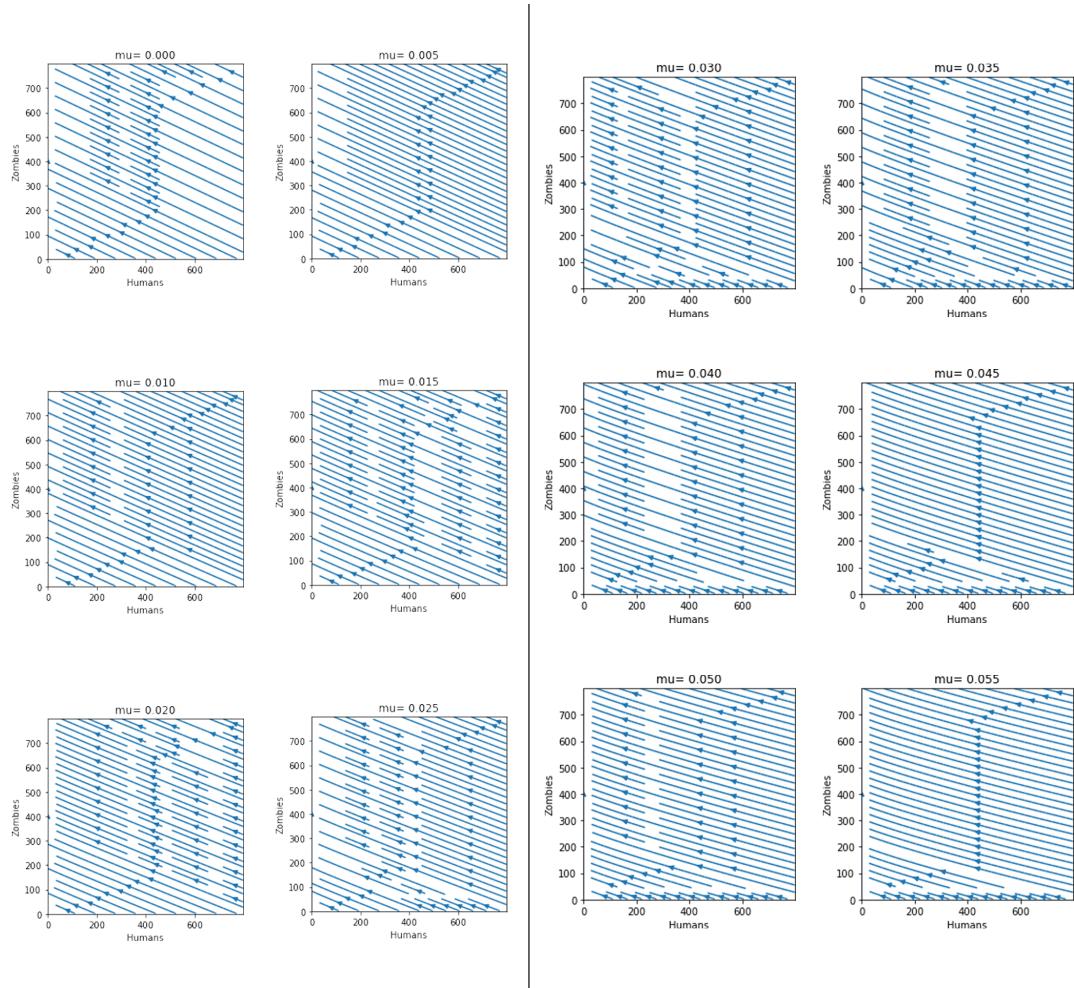


Figure 3.9: Change of Stability,  $\mu = 0.000$  to 0.055

### 3 Zombie Epidemic Model

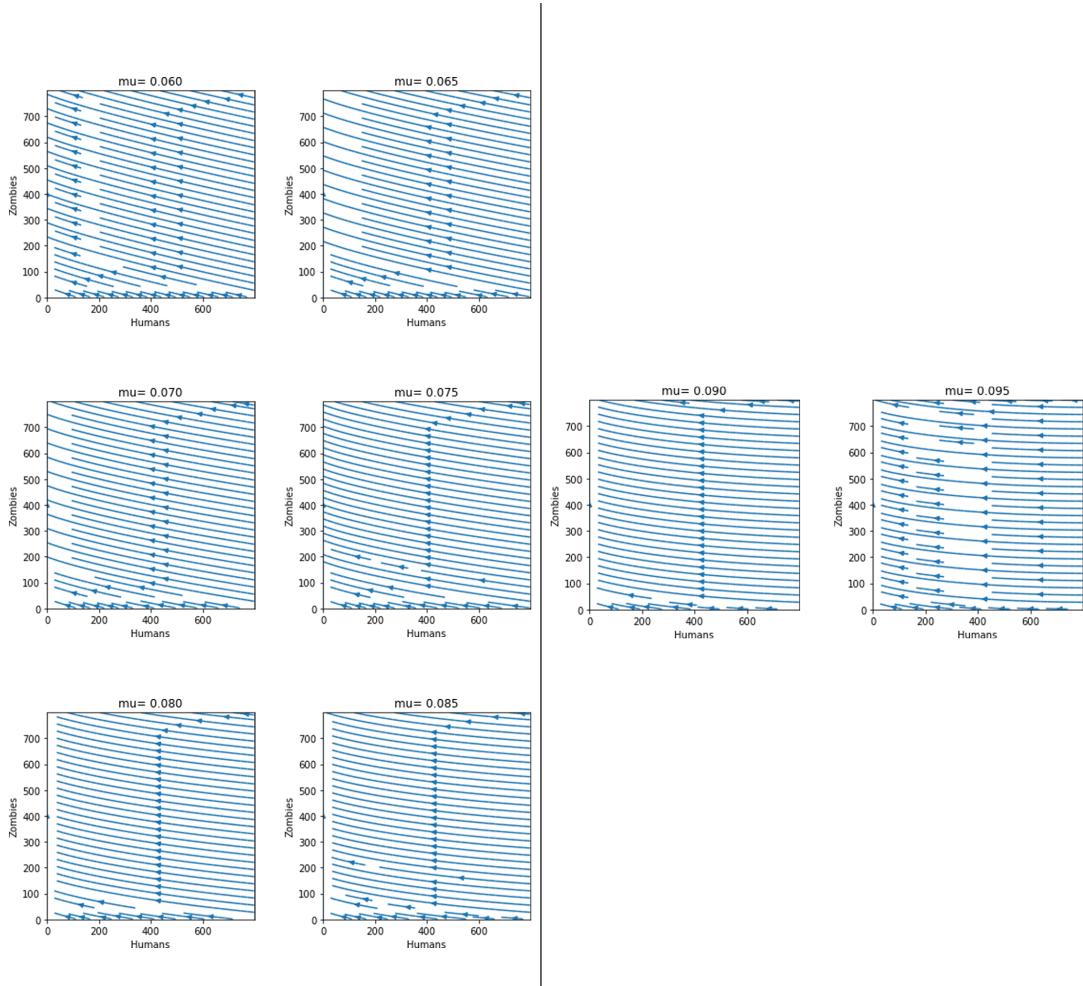


Figure 3.10: Change of Stability,  $\mu = 0.060$  to  $0.095$

So, according to the condition stated in equation (3.5) and parameter values stated in Table (3.2), the model reaches its first stability at the value of the perturbation parameter,  $\mu = 0.095$ . Starting at this perturbation value, zombie population starts to vanish gradually and the human population in the x-axis starts to increase. With each value increase of the perturbation parameter, the straight lines in the phase portraits, transform into a slightly curve lines.

This change in stability for the perturbed SZR model, can be visualized more conveniently with the bifurcation diagram as given below—

### 3 Zombie Epidemic Model

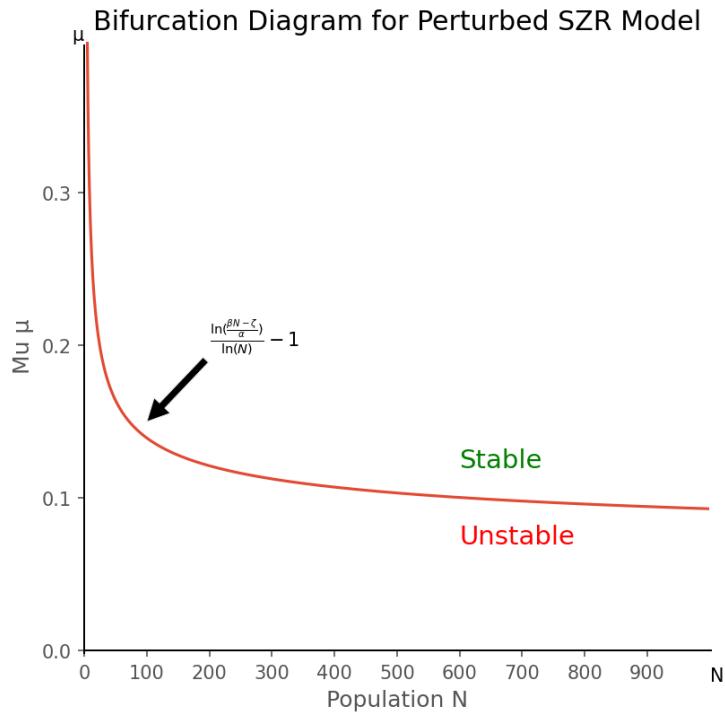


Figure 3.11: Bifurcation Diagram for Perturbed SZR Model

From the Figure 3.11, it is easily visible that the region above the curve line is stable as it satisfies the condition stated in equation (3.5). And for any value of perturbation parameter in the region below the curve line will make the model unstable. The curve line bifurcates the model, from instability to stability.

### 3.3.4 Graphical Interface Program

As part of writing this thesis paper, a program was created using python to develop a graphical user interface for generating phase portraits for the perturbed SZR model. This program provides the user with a simple and user friendly graphical interface to input the values of parameters  $\alpha$ ,  $\beta$ ,  $\zeta$ , the perturbation parameter  $\mu$ , the population size  $N$ ; and generate the phase portrait of the perturbed SZR model. It is also possible to save the generated phase portrait plot into the computer through the interactive window. So, without any more heavy coding , it is now possible to generate phase portraits and study the stability of the perturbed SZR model, just by entering the numeric parameter values inside this graphical program.

Some images of this interactive graphical program are given below—

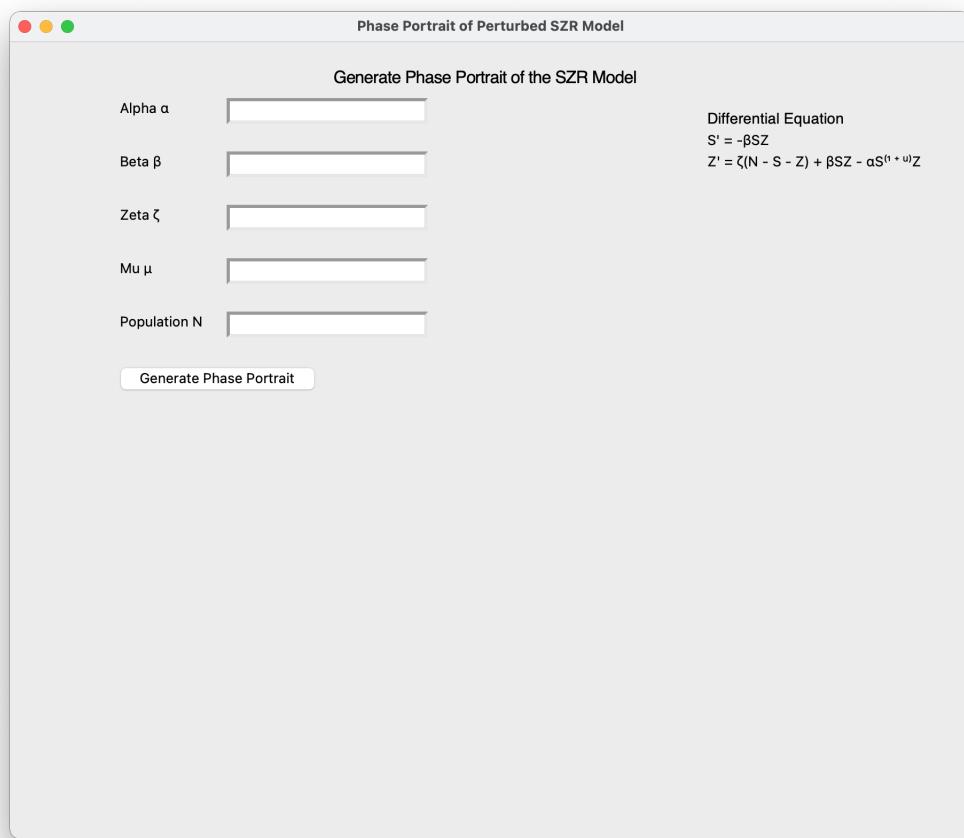


Figure 3.12: GUI Program for Generating Phase Portraits, Sample 01

### 3 Zombie Epidemic Model

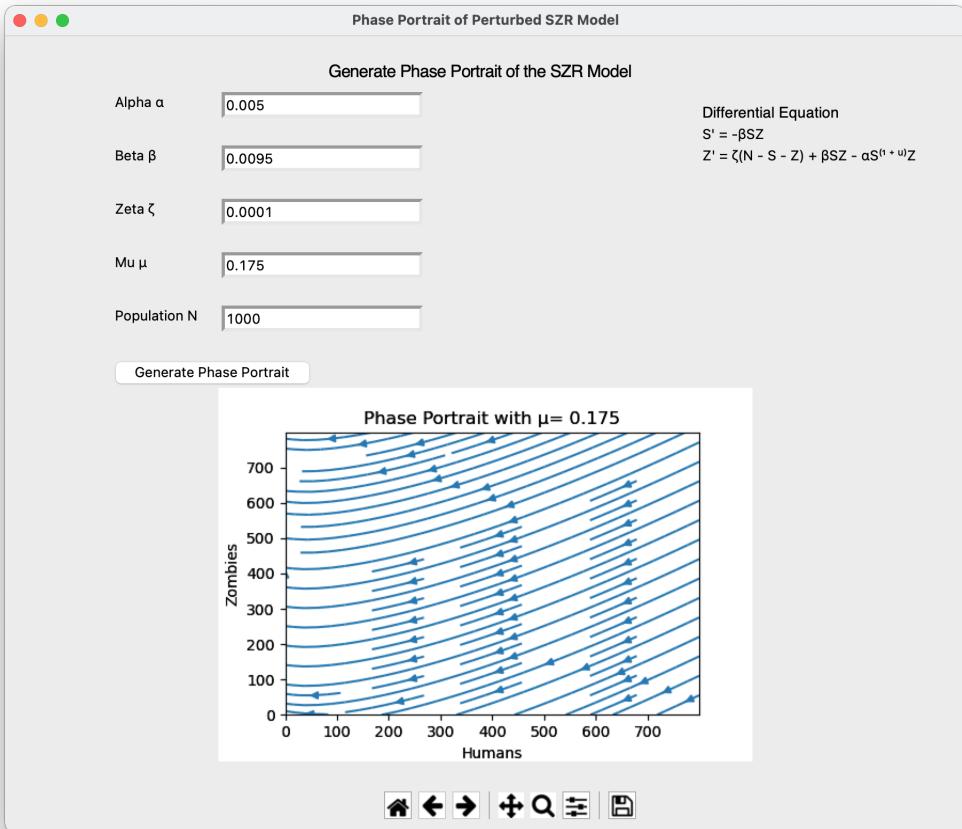


Figure 3.13: GUI Program for Generating Phase Portraits, Sample 02

This program was written using python and the Tkinter [47] library was used to develop the graphical user interface (GUI) for the code. This library is very fast, efficient and effective in building simple GUI applications for desktop using python.

The source code for this program (PerturbedSZR\_PhasePortrait\_GUI.py) is listed in the Codes section, at the end of this thesis paper. All code files are uploaded in a GitHub repository and the relevant links for downloading the source codes are also provided.

### 3.3.5 Effects of Perturbation Parameter

In order to visualize the impact of the perturbation parameter, on the model and corresponding zombie population more efficiently, two new graphs have been plotted. As for the first one, the perturbed SZR model is solved for  $t = 1000$  days, and the population of zombies at the final 1000<sup>th</sup> day is observed against the increase of the perturbation parameter  $\mu$ .

During this calculation, the initial conditions were,

The total population size,  $N = 1000$

Initial susceptible population,  $S(0) = 800$

Initial zombie population,  $Z(0) = 200$

Initial removed population,  $R(0) = 0$

Number of days,  $t = 1000$

And the parameter values for  $\beta$ ,  $\alpha$ ,  $\zeta$  remain same as given on the previous Table 3.2.

And then the system of differential equations for the perturbed SZR model was solved using the same solve\_ivp function [23] in python.

The final plot looks like this as given below—

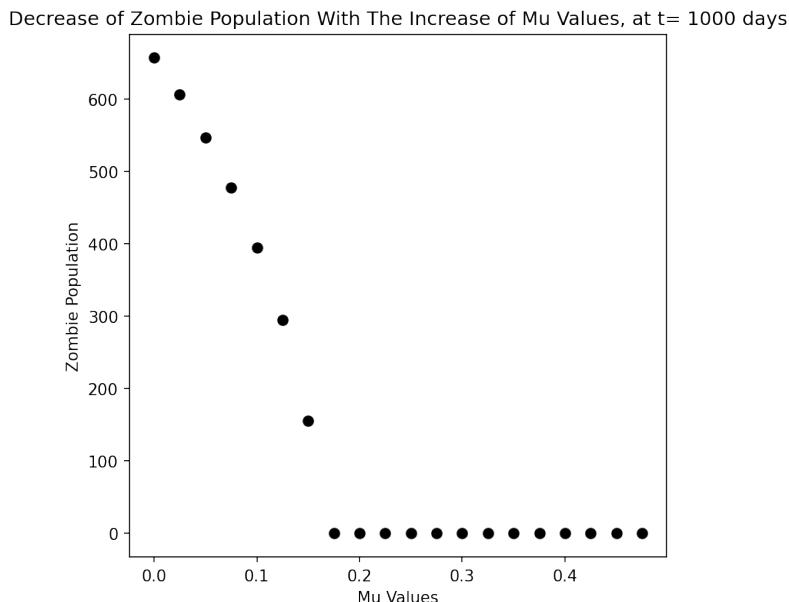


Figure 3.14: Perturbed SZR- Relation Between Zombie Population and Perturbation Parameter

### 3 Zombie Epidemic Model

As can be seen from the Figure 3.14, at the final day count or at 1000<sup>th</sup> day, the value of the zombie population decreases rapidly with the increase of perturbation parameter  $\mu$ . The more the value of  $\mu$  increases, the smaller it gets for the value of the zombie population at the 1000<sup>th</sup> day position. And at one point, the zombie population vanishes on the 1000<sup>th</sup> day position.

Also the Figure 3.15, demonstrates the whole zombie population with respect to different perturbation parameters. For different values of perturbation parameter, the zombie population is plotted in different colors, and it is visible that, with the increase of perturbation parameter values, the zombie populations decrease accordingly, and in disproportionate relation. This graph is plotted for the first 10 days only, with a step size of 0.01. So it is easier to identify the changes in the initial days.

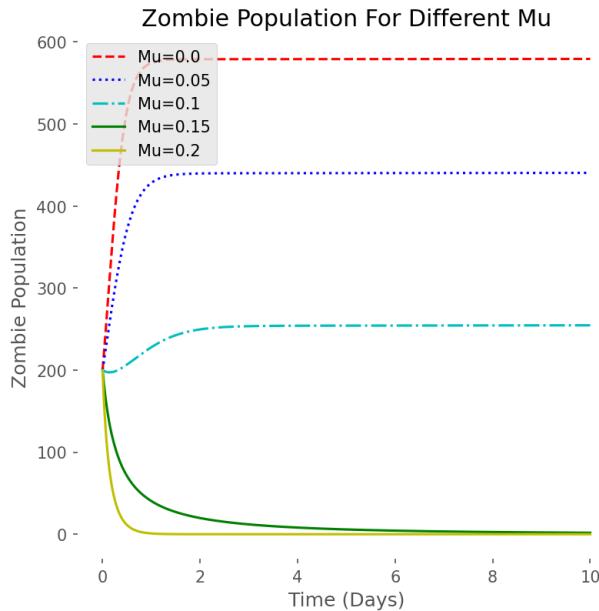


Figure 3.15: Perturbed SZR- Zombie Population with Increasing Perturbation Parameter

So it can be easily theorized that, the bigger the value of this perturbation parameter  $\mu$  is, the faster the zombie population will disappear. The possibility to increase the value of this perturbation parameter depends on increasing the capability of human skills, equipment and methods in removing the zombies, that are available to the human population in real world.

# Chapter 4

## Quarantine Model

### 4.1 Basic Introduction

In order to make the zombie epidemic model or the SZR model, a more practical and realistic one, a quarantine model had been developed. The quarantine model was first introduced in [17], and later the perturbation parameter was added in [18]. In this quarantine model, it is assumed that the infected people do not turn into zombies immediately. Rather, before becoming zombies they belong to the exposed category. And in this model, a possibility has been considered to quarantine the people from the exposed category as well as from the zombie category. Hence, it opens up the scope for the introduction and consideration of quarantining people in the model. In [17], the authors estimated that the survival of a healthy human population is not possible according to the model and after some time the healthy human population will go extinct due to this zombie apocalypse. However, in [18], the authors introduced the perturbation parameter in the original model and conjectured the possibility of human survival.

The perturbed SEZQR (susceptible-exposed-zombie-quarantined-removed) model looks like as the following figure —

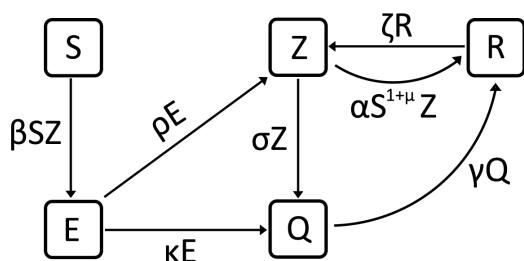


Figure 4.1: Perturbed SEZQR Model

## 4 Quarantine Model

With this perturbed SEZQR model, the transformation of individuals within different compartments is given as follows-

- Individuals from susceptible compartment S enter the exposed compartment E at a rate of  $\beta SZ$ . This rate depends both on the number of population within the compartments susceptible and zombies.
- In the exposed compartment E, individuals are infected with the zombie infection, but are not yet infectious. From this compartment, individuals either enter the zombie compartment Z at a rate of  $\rho E$  or enter the quarantine compartment Q at a rate of  $\kappa E$ .
- In the zombie compartment Z, individuals are infected, infectious and thus hostile. They are capable of spreading the disease among other healthy people. From this compartment, individuals transform to the quarantine category Q at a rate of  $\sigma Z$ . Or, they can also be transformed to removed compartment R (i.e. killed by humans) at a rate of  $\alpha S^{(1+\mu)} Z$ . Here, in this transformation rate, the perturbation parameter  $\mu$  is introduced.
- In this model, the possibility of quarantining individuals is considered. Hence, here comes the quarantine compartment Q. From this compartment, individuals can be transferred to the removed compartment R at a rate of  $\gamma Q$ .
- Finally, comes the removed compartment R, where resides all the individuals who either recovered from the compartment Q or are being killed, terminated or neutralized from the compartment Z. However, in this model, no type of immunity is promised or guaranteed. So it is possible that a removed individual can be reinfected or resurrected and can be returned to the zombie compartment again at a rate of  $\zeta R$ .
- All the entities used in the above transformation rates  $\beta$ ,  $\alpha$ ,  $\rho$ ,  $\kappa$ ,  $\sigma$ ,  $\gamma$ ,  $\zeta$ , and the perturbation parameter  $\mu$  are positive constants
- Zombies are removed only through human intervention and interaction. All other natural causes are ignored here.
- The whole population is homogeneously mixed and every individual has the equal possibility of getting infected.

So, this whole perturbed SEZQR model can be summarized as a system of dif-

## 4 Quarantine Model

ferential equations —

$$\begin{aligned} S' &= -\beta SZ \\ E' &= \beta SZ - (\rho + \kappa)E \\ Z' &= \rho E + \zeta R - \sigma Z - \alpha S^{1+\mu} Z \\ Q' &= \kappa E + \sigma Z - \gamma Q \\ R' &= \alpha S^{1+\mu} Z + \gamma Q - \zeta R \end{aligned} \tag{4.1}$$

## 4.2 Modified Quarantine Model with Perturbation

However, there are still room for some improvements for the perturbed SEZQR model which was discussed in the previous section, to make it a more pragmatic model.

Two modifications can be considered in the existing perturbed SEZQR model. For the first one, the transfer rate of individuals from the zombie compartment  $Z$  to the quarantine compartment  $Q$  should also depend on the susceptible population  $S$ . Because it is logical to theorize that the contribution of the susceptible population is required to quarantine the zombies from the compartment  $Z$  to  $Q$ . The susceptible people are the only healthy population that are capable of impacting or accelerating the process of quarantining infectious zombies. So, the transfer rate from the zombie compartment  $Z$  to the quarantine compartment  $Q$  should possibly be  $\sigma SZ$ .

Now as for the second modification, it is also logical to consider the possibility of people (or zombies) breaking free from the quarantine compartment  $Q$  and joining the zombie compartment  $Z$  again. It will not always be possible to keep all the individuals in perfect isolation while in the compartment  $Q$ . Some individuals will turn into zombies, or some will break free due to the various reasons, or zombies from the compartment  $Z$  can infiltrate the  $Q$  compartment and transform some of the individuals from  $Q$  compartment into zombies. So this possibility can be examined. The transfer rate of individuals from the compartment  $Q$  to the zombie compartment  $Z$  can be taken as  $\omega Q$ , where  $\omega$  is a positive constant.

This newly modified SEZQR model with the existing perturbation parameter can be visualized in the Figure 4.2

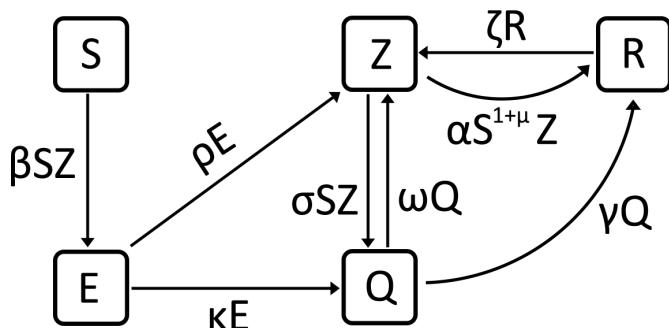


Figure 4.2: Modified SEZQR Model with Perturbation

#### 4 Quarantine Model

So, for this newly modified SEZQR model, the system of differential equations will look like —

$$\begin{aligned} S' &= -\beta SZ \\ E' &= \beta SZ - (\rho + \kappa)E \\ Z' &= \rho E + \zeta R - \sigma SZ - \alpha S^{1+\mu} Z + \omega Q \\ Q' &= \kappa E + \sigma SZ - \gamma Q - \omega Q \\ R' &= \alpha S^{1+\mu} Z + \gamma Q - \zeta R \end{aligned} \tag{4.2}$$

As before, all the variables S, E, Z, Q and R are functions of time, which means that they only change values with respect to the time. And the full size of the population at any given time t, is the grand total of all the individuals from all of the compartments. Which in turn means that,

$$\text{Total population size, } N = S(t) + E(t) + Z(t) + Q(t) + R(t)$$

So, alternatively, equation (4.2) can be reduced to the following form,

$$\begin{aligned} S' &= -\beta SZ \\ E' &= \beta SZ - (\rho + \kappa)E \\ Z' &= \rho E + \zeta(N - S - E - Z - Q) - \sigma SZ - \alpha S^{1+\mu} Z + \omega Q \\ Q' &= \kappa E + \sigma SZ - \gamma Q - \omega Q \end{aligned} \tag{4.3}$$

Also, the whole population is closed. The number of total individuals remains fixed and constant within the given time period t, i.e.  $N'(t) = 0$ . The population is continuous in time. The population is homogeneously mixed and, each and every individual has an equal probability of coming into contact with each other as well as getting infected.

In the upcoming sections, this modified SEZQR model will be analyzed mathematically for linear stability. An attempt has been made to find out the condition for disease free equilibrium on the basis of basic reproduction number and the condition for the perturbation parameter  $\mu$  to make the modified SEZQR model stable.

### 4.3 Basic Reproduction Number for Modified SEZQR Model

The expected number of secondary infection cases which are produced by a single or typical infection or infected individual in a completely susceptible population is known as the basic reproduction number  $R_0$  [48], [49], [50], [51], [52]. For the modified SEZQR model, this basic reproduction number is the number of individuals who are infected with the zombie disease by a single zombie. In this section, this basic reproduction will be derived based on the modified SEZQR model. But before that, some important terminologies are introduced below.

**Definition 4.1 Spectral Radius:** The largest absolute value of all the eigenvalues (supremum of all the absolute values of the elements in its spectrum) of a square matrix or a bounded linear operator is known as the spectral radius of that matrix or operator [53].

If  $X$  is an  $n \times n$  matrix with real or complex elements, and having eigenvalues  $\lambda_1, \dots, \lambda_n$ ; then the spectral radius  $\rho(X)$  of  $X$  is defined as,

$$\rho(X) = \max_{1 \leq i \leq n} |\lambda_i|$$

**Definition 4.2 Jacobian Matrix:** The Jacobian matrix of a vector valued function having several variables is the matrix that contains all the first order partial derivatives of its variables [54], [55].

For a given set  $y = f(x)$ , having  $n$  equations with  $n$  variables  $x_1, \dots, x_n$ , which can be explicitly written as,

$$y = \begin{bmatrix} f_1(x) \\ f_2(x) \\ \vdots \\ f_n(x) \end{bmatrix}$$

Then, the Jacobian matrix is defined as,

$$J(x_1, \dots, x_n) = \begin{bmatrix} \frac{\partial y_1}{\partial x_1} & \dots & \frac{\partial y_1}{\partial x_n} \\ \vdots & \ddots & \vdots \\ \frac{\partial y_n}{\partial x_1} & \dots & \frac{\partial y_n}{\partial x_n} \end{bmatrix}$$

**Definition 4.3 Upper Triangular Matrix:** If all the entries of a square matrix below the main diagonal are zero, then that square matrix is called upper

## 4 Quarantine Model

triangular matrix [56].

A square matrix X is upper triangular if,

$$X_{ij} = \begin{cases} a_{ij} & \text{for } i \leq j \\ 0 & \text{for } i > j \end{cases}$$

Or more explicitly,

$$X = \begin{bmatrix} a_{11} & a_{12} & \dots & a_{1n} \\ 0 & a_{22} & \dots & a_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \dots & a_{nn} \end{bmatrix}$$

So, now, it is possible to start calculating the value of basic reproduction number, following the methods as described on [18], and some instructions from [60]. As per the system (4.3) and Figure 4.2 of the modified SEZQR model, let us construct a next-generation matrix [57], [58], [59] that focuses only on the compartments that introduce new infections or the spread or transition of infections within the compartments. As such, it is only necessary to focus on the  $E'$ ,  $Z'$  and  $Q'$  equations.

From this, it is now possible to form the new-infection matrix  $\mathcal{F}$  and the transition matrix  $\mathcal{V}$  in such a way that,

$$[E' \ Z' \ T']^T = \mathcal{F} - \mathcal{V}$$

So, for the system (4.3), the new infection matrix  $\mathcal{F}$  and the transition matrix  $\mathcal{V}$  are given by,

$$\mathcal{F} = \begin{bmatrix} \beta SZ \\ 0 \\ 0 \end{bmatrix}$$

$$\mathcal{V} = \begin{bmatrix} (\rho + \kappa)E \\ \alpha S^{1+\mu}Z + \sigma SZ - \rho E - \zeta(N - S - E - Z - Q) - \omega Q \\ \gamma Q + \omega Q - \kappa E - \sigma SZ \end{bmatrix}$$

Then the basic reproduction number is calculated as per the spectral radius of  $FV^{-1}$ , where F and V are the Jacobian matrices of  $\mathcal{F}$  and  $\mathcal{V}$  respectively, which is evaluated at the disease free equilibrium  $(N, 0, 0, 0, 0)$ .

## 4 Quarantine Model

So here we have,

$$F = \begin{bmatrix} 0 & \beta N & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

and

$$V = \begin{bmatrix} (\rho + \kappa) & 0 & 0 \\ (\zeta - \rho) & \alpha N^{1+\mu} + \sigma N + \zeta & \zeta - \omega \\ -\kappa & -\sigma N & \gamma + \omega \end{bmatrix}$$

So now the inverse of V,

$$V^{-1} = \frac{1}{(\rho + \kappa)[(\gamma + \omega)(\alpha N^{1+\mu} + \sigma N + \zeta) + \sigma N(\zeta - \omega)]} \cdot$$

$$\begin{bmatrix} (\gamma + \omega)(\alpha N^{1+\mu} + \sigma N + \zeta) + \sigma N(\zeta - \omega) & 0 & 0 \\ -[(\zeta - \rho)(\gamma + \omega) + \kappa(\zeta - \omega)] & (\rho + \kappa)(\gamma + \omega) & -[(\rho + \kappa)(\zeta - \omega)] \\ -\sigma N(\zeta - \rho) + \kappa(\alpha N^{1+\mu} + \sigma N + \zeta) & \sigma N(\rho + \kappa) & (\rho + \kappa)(\alpha N^{1+\mu} + \sigma N + \zeta) \end{bmatrix}$$

Here the determinant of V,  $\det(V) = (\rho + \kappa)[(\gamma + \omega)(\alpha N^{1+\mu} + \sigma N + \zeta) + \sigma N(\zeta - \omega)]$

And the adjugate of V,

$$\begin{bmatrix} \det(V) * \text{inv}(V) = \\ (\gamma + \omega)(\alpha N^{1+\mu} + \sigma N + \zeta) + \sigma N(\zeta - \omega) & 0 & 0 \\ -[(\zeta - \rho)(\gamma + \omega) + \kappa(\zeta - \omega)] & (\rho + \kappa)(\gamma + \omega) & -[(\rho + \kappa)(\zeta - \omega)] \\ -\sigma N(\zeta - \rho) + \kappa(\alpha N^{1+\mu} + \sigma N + \zeta) & \sigma N(\rho + \kappa) & (\rho + \kappa)(\alpha N^{1+\mu} + \sigma N + \zeta) \end{bmatrix}$$

So, now we can calculate  $FV^{-1}$ ,

$$FV^{-1} = \begin{bmatrix} 0 & \beta N & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \cdot \frac{1}{(\rho + \kappa)[(\gamma + \omega)(\alpha N^{1+\mu} + \sigma N + \zeta) + \sigma N(\zeta - \omega)]} \cdot$$

$$\begin{bmatrix} (\gamma + \omega)(\alpha N^{1+\mu} + \sigma N + \zeta) + \sigma N(\zeta - \omega) & 0 & 0 \\ -[(\zeta - \rho)(\gamma + \omega) + \kappa(\zeta - \omega)] & (\rho + \kappa)(\gamma + \omega) & -[(\rho + \kappa)(\zeta - \omega)] \\ -\sigma N(\zeta - \rho) + \kappa(\alpha N^{1+\mu} + \sigma N + \zeta) & \sigma N(\rho + \kappa) & (\rho + \kappa)(\alpha N^{1+\mu} + \sigma N + \zeta) \end{bmatrix}$$

#### 4 Quarantine Model

$$= \frac{-\beta N[(\zeta - \rho)(\gamma + \omega) + \kappa(\zeta - \omega)]}{(\rho + \kappa)[(\gamma + \omega)(\alpha N^{1+\mu} + \sigma N + \zeta) + \sigma N(\zeta - \omega)]} \cdot \begin{bmatrix} 1 & \frac{\beta N(\rho + \kappa)(\gamma + \omega)}{-\beta N[(\zeta - \rho)(\gamma + \omega) + \kappa(\zeta - \omega)]} & \frac{-\beta N(\rho + \kappa)(\zeta - \omega)}{-\beta N[(\zeta - \rho)(\gamma + \omega) + \kappa(\zeta - \omega)]} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

This is an upper triangular matrix. So we have the only non-zero eigenvalue, which is the basic reproduction number,

$$R_0(\mu) = \frac{-\beta N[(\zeta - \rho)(\gamma + \omega) + \kappa(\zeta - \omega)]}{(\rho + \kappa)[(\gamma + \omega)(\alpha N^{1+\mu} + \sigma N + \zeta) + \sigma N(\zeta - \omega)]} \quad (4.4)$$

Here , it must be the case that,

$$[(\zeta - \rho)(\gamma + \omega) + \kappa(\zeta - \omega)] < 0 \quad (4.5)$$

Then, with the condition stated in (4.5),  $R_0(\mu)$  will be positive for all values of  $\mu$ .

## 4.4 Stability Condition for Perturbation Parameter

In order to determine the value of  $\mu$  for which the disease free equilibrium is linearly stable for the modified SEZQR model, we determine the calculation when  $R_0(\mu) < 1$ .

Then we have,

$$R_0(\mu) < 1$$

$$\text{or, } \frac{-\beta N[(\zeta - \rho)(\gamma + \omega) + \kappa(\zeta - \omega)]}{(\rho + \kappa)[(\gamma + \omega)(\alpha N^{1+\mu} + \sigma N + \zeta) + \sigma N(\zeta - \omega)]} < 1$$

or,

$$N^{1+\mu} > \frac{\beta N[(\zeta - \rho)(\gamma + \omega) + \kappa(\zeta - \omega)] + (\rho + \kappa)[\sigma N(\zeta - \omega) + (\gamma + \omega)(\zeta + \sigma N)]}{-\alpha(\gamma + \omega)(\rho + \kappa)} \quad (4.6)$$

Since  $\alpha(\gamma + \omega)(\rho + \kappa) > 0$ , it must be the case that,

$$\beta N[(\zeta - \rho)(\gamma + \omega) + \kappa(\zeta - \omega)] + (\rho + \kappa)[\sigma N(\zeta - \omega) + (\gamma + \omega)(\zeta + \sigma N)] < 0$$

Which in turn requires that,

$$N > \frac{-(\rho + \kappa)[\sigma N(\zeta - \omega) + (\gamma + \omega)(\zeta + \sigma N)]}{\beta[(\zeta - \rho)(\gamma + \omega) + \kappa(\zeta - \omega)]} \quad (4.7)$$

Finally, in order for the basic reproduction number  $R_0(\mu) < 1$ , we have,

$$\mu > \frac{\ln\left(\frac{\beta N[(\zeta - \rho)(\gamma + \omega) + \kappa(\zeta - \omega)] + (\rho + \kappa)[\sigma N(\zeta - \omega) + (\gamma + \omega)(\zeta + \sigma N)]}{-\alpha(\gamma + \omega)(\rho + \kappa)}\right)}{\ln(N)} - 1$$

**Theorem 4.1:** The disease free equilibrium of the modified SEZQR system, satisfying the conditions stated in (4.5) and (4.7), is linearly stable if and only if,

$$\mu > \frac{\ln\left(\frac{\beta N[(\zeta - \rho)(\gamma + \omega) + \kappa(\zeta - \omega)] + (\rho + \kappa)[\sigma N(\zeta - \omega) + (\gamma + \omega)(\zeta + \sigma N)]}{-\alpha(\gamma + \omega)(\rho + \kappa)}\right)}{\ln(N)} - 1 \quad (4.8)$$

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It is possible to draw the bifurcation diagram for this modified SEZQR model, with the following set of parameter values. For the estimates of the parameters, those values can be taken from [17], [18]. Also a new value for the parameter  $\omega$  is assumed in this table below-

Parameter	Description	Estimate
$\beta$	transmission rate for the zombie infection	0.0095
$\alpha$	removal rate of infected zombies	0.005
$\zeta$	reinfection or resurrection rate for removed individuals	0.0001
$\rho$	conversion rate from exposed to zombies	0.005
$\kappa$	quarantine rate of exposed individuals	0.001
$\sigma$	quarantine rate of zombies	0.001
$\gamma$	removal rate of quarantined individuals	0.0001
$\omega$	conversion rate of quarantined individuals to zombies	0.009
$\mu$	perturbation value	0.175

Table 4.1: Parameter Estimates for the Modified SEZQR Model

For the population size of 1000, the bifurcation diagram is given as below,

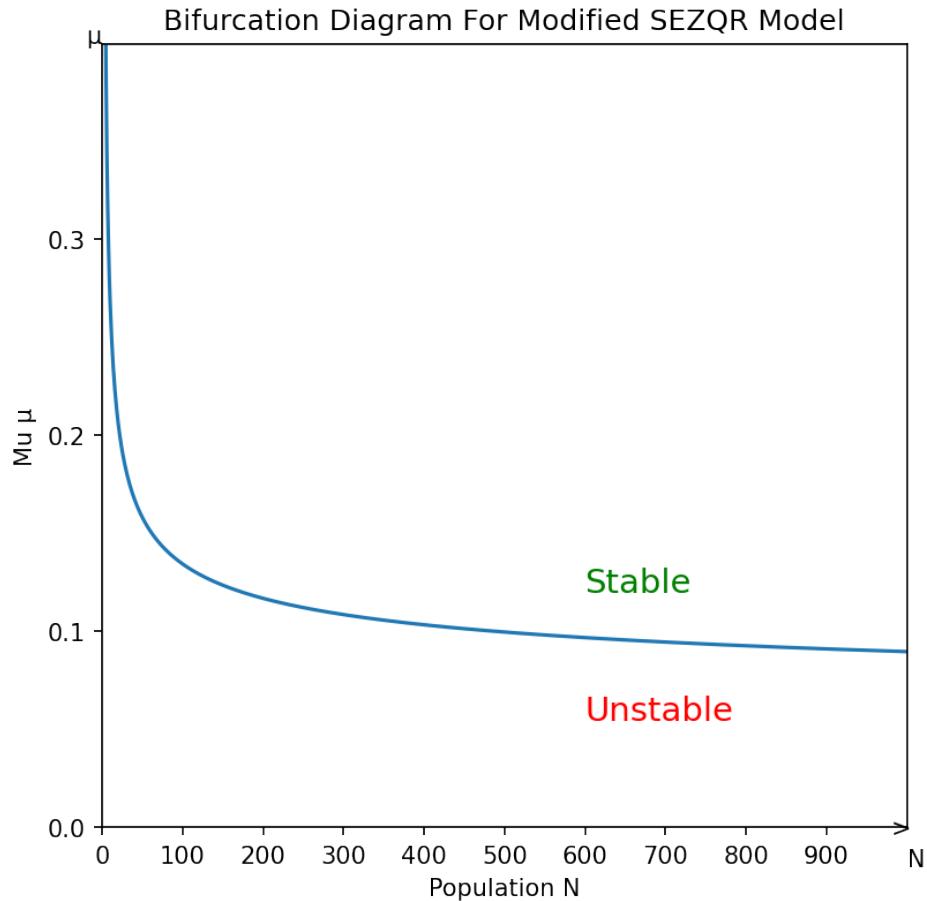


Figure 4.3: Bifurcation Diagram for Modified SEZQR Model

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In the figure 4.3, the bifurcation diagram clearly distinguishes the stable and unstable regions according to the perturbation parameter.

And for the given set of values stated on Table 4.1, the conditions stated in (4.5) and (4.7) are also satisfied. So, the Theorem 4.1 states the necessary condition of perturbation parameter to make the modified SEZQR model stable.

## 4.5 Example of Modified SEZQR Model

This newly modified SEZQR model with the perturbation parameter, can be numerically solved using an imaginary example, so that it is easier to interpret its behavior.

For this imaginary example, let us consider the following initial conditions—

The total population size,  $N = 1000$

Initial susceptible population,  $S(0) = 700$

Initial exposed population,  $E(0) = 100$

Initial zombie population,  $Z(0) = 130$

Initial quarantined population,  $Q(0) = 70$

Initial removed population,  $R(0) = 0$

Number of days,  $t = 1000$

And for the other parameter values, those are taken from the Table 4.1.

So, now it is possible to solve the system numerically. First the model is solved for 10 days with a step size of 0.1. So that, it is easier to understand and visualize the initial decline of the zombie population.

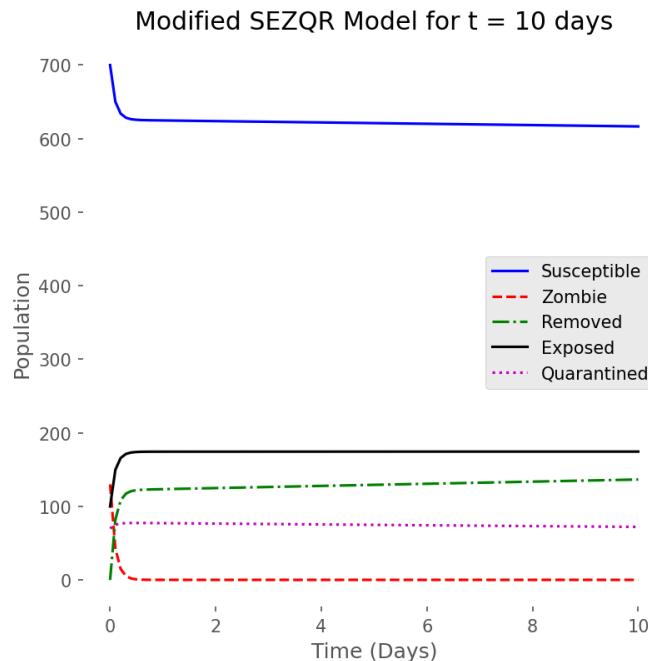


Figure 4.4: Modified SEZQR Model for  $t = 10$  days

And then, the system is solved for  $t = 1000$  days with a step size of 0.1.

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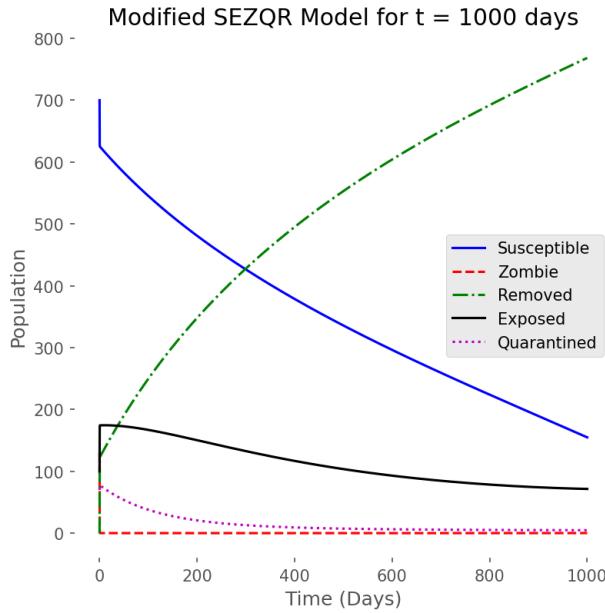


Figure 4.5: Modified SEZQR Model for  $t = 1000$  days

From the figure 4.5, it is easy to understand that, the removed population  $R$  will increase gradually and the zombies will vanish. So it indicates that, the model is stable and a disease free equilibrium is possible in the long run for the perturbation parameter,  $\mu = 0.175$ .

However, to understand the impact of the perturbation parameter  $\mu$  over this modified SEZQR model, the same model is solved again for 1000 days and with a step size of 0.1. But this time, the value of the perturbation parameter  $\mu$  is set to zero.

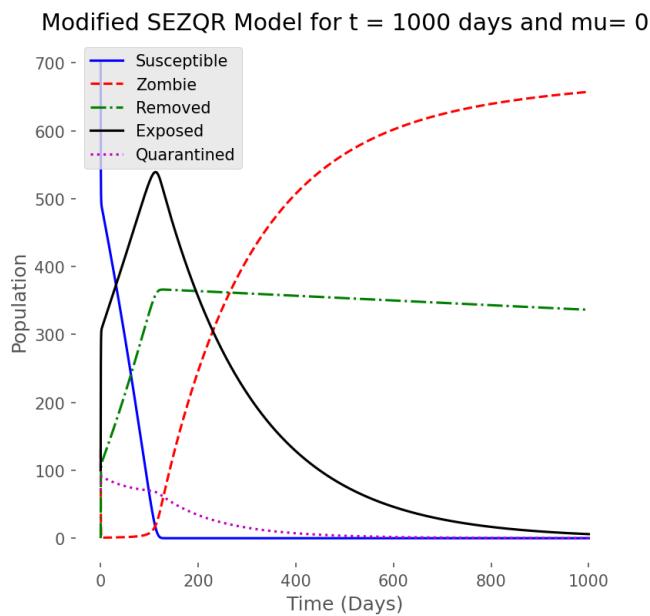


Figure 4.6: Modified SEZQR Model without Perturbation for  $t = 1000$  days

## 4 Quarantine Model

From the Figure 4.6, it can be seen that without the perturbation this model is unstable and eventually the zombie population will infect the whole population and cause the extinction of the healthy human population. The susceptible, exposed and quarantined population will vanish in the long run.

For the above numerical solutions, the `solve_ivp` function [23] was used in the python code. This function uses Runge-Kutta method of order five (RK45) [61], [62], [63], as the integration method. In this method, the error is controlled assuming the accuracy from the fourth-order method, while the steps are taken using the accurate formula of fifth-order.

And the phase portrait for the modified SEZQR model with perturbation—

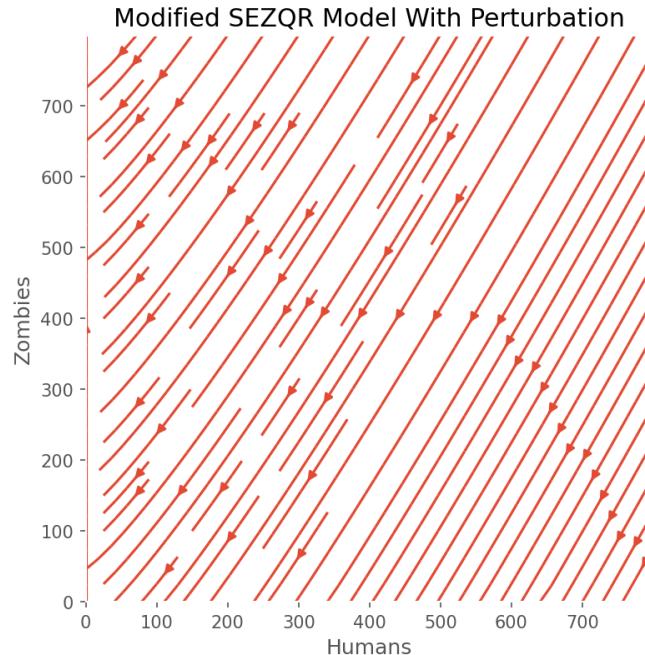


Figure 4.7: Modified SEZQR Model- Phase Portrait

It is noticeable from the phase portrait also, that with the perturbation, the modified SEZQR model is stable and provides scope for disease free equilibrium. Here, the x-axis (human population) is an attracting set.

## 4.6 Effect of Perturbation Parameter on Modified SEZQR Model

So, to visualize the impact of the perturbation parameter, on the modified SEZQR model and the corresponding zombie population more effectively and efficiently, here another graph is plotted.

In this plot, the modified SEZQR model is solved for  $t = 1000$  days, and the population of zombies at the final 1000<sup>th</sup> day is observed against the increase of the perturbation parameter  $\mu$ .

As again, the parameter values are taken from the Table 4.1. And initial conditions are still same as mentioned on the Section 4.5.

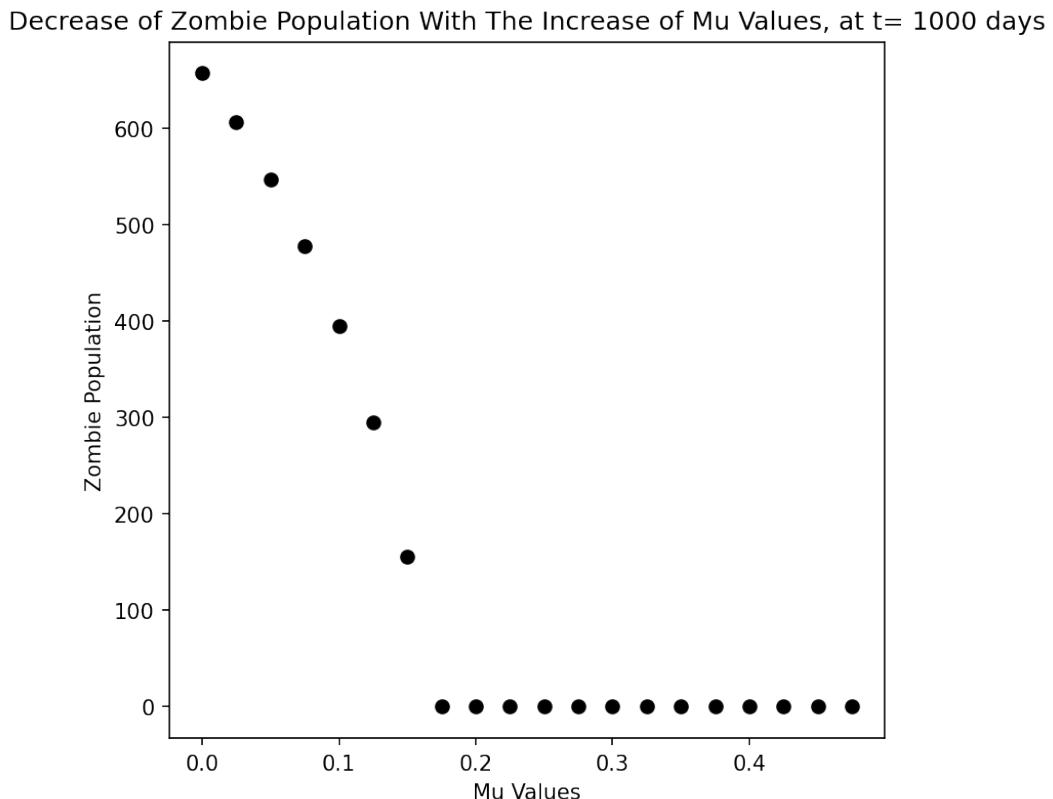


Figure 4.8: Modified SEZQR- Relation Between Zombie Population and Perturbation Parameter

As can be seen from the Figure 4.8, the value of zombie population at the final 1000<sup>th</sup> day position, falls sharply with the increase of perturbation parameter  $\mu$ . The more the value of the perturbation parameter  $\mu$  increases, the lower it gets for the zombie population number at the final 1000<sup>th</sup> day. And at some certain value of

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perturbation parameter  $\mu$ , the population of zombie totally vanishes at the 1000<sup>th</sup> day.

Also, if we solve the modified SEZQR system, plot only the zombie population as per different values of perturbation parameter, then another interesting graph can be obtained.

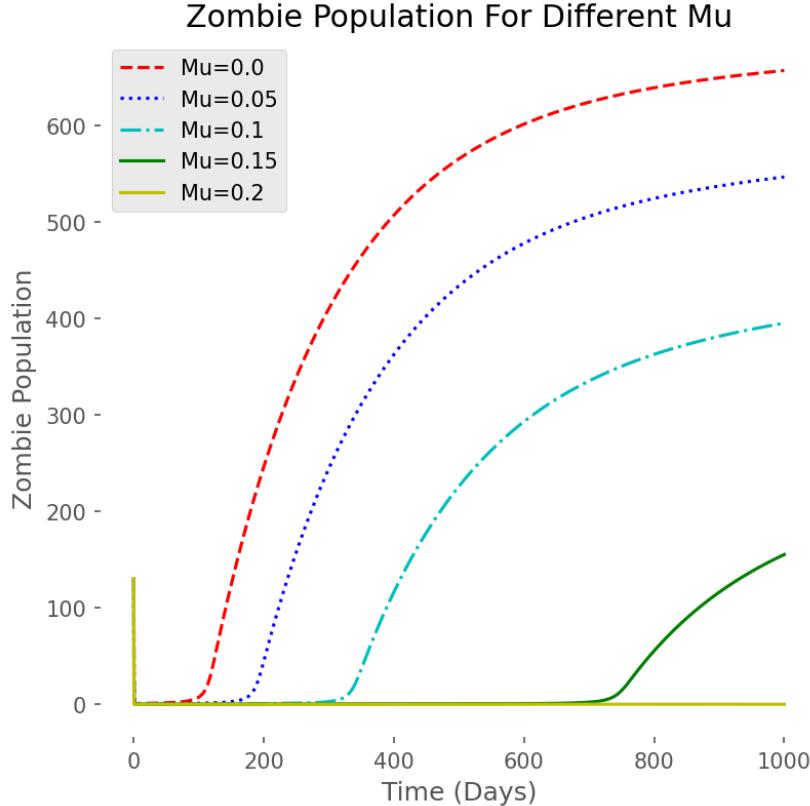


Figure 4.9: Modified SEZQR- Zombie Population with Different Perturbation Parameters

In the Figure 4.9, different zombie populations have been plotted for different values of perturbation parameter  $\mu$ . The perturbation parameter  $\mu$  value increases from 0.0 until 0.2, with a step size of 0.05. And at the same time, the corresponding zombie population has also been plotted with respect to that particular perturbation parameter  $\mu$ . As the perturbation parameter  $\mu$  value increases, the corresponding zombie population also declines gradually. This plot is generated for 1000 days, with the step size of 0.1.

So the higher the value of perturbation parameter  $\mu$  goes, the faster the zombie population will go extinct. The value of this perturbation parameter  $\mu$  depends on the human capacity and skills to remove and neutralize zombies in the real world.

## 4.7 Comparison of Models

In this section, some basic comparisons will be made for the Modified SEZQR model, with the perturbed SEZQR model from [18], which was discussed in the Section 4.1 of this chapter. The perturbed SEZQR model is already depicted in Figure 4.1 and the related system of differential equations was expressed in equation (4.1).

In the Theorem 2 of [18], the condition for the perturbation parameter of the SEZQR model, to introduce a disease-free equilibrium is defined as,

$$\mu > \frac{\ln\left(\frac{\beta N(\zeta\kappa + \gamma(\zeta - \rho)) + (\rho + \kappa)(\zeta\sigma + \gamma(\zeta + \sigma))}{-\alpha\gamma(\rho + \kappa)}\right)}{\ln(N)} - 1 \quad (4.9)$$

So, according to this condition, the bifurcation diagram for the SEZQR model looks like the figure given below. The parameter values are same as of Table 4.1 and the population size is 1000.

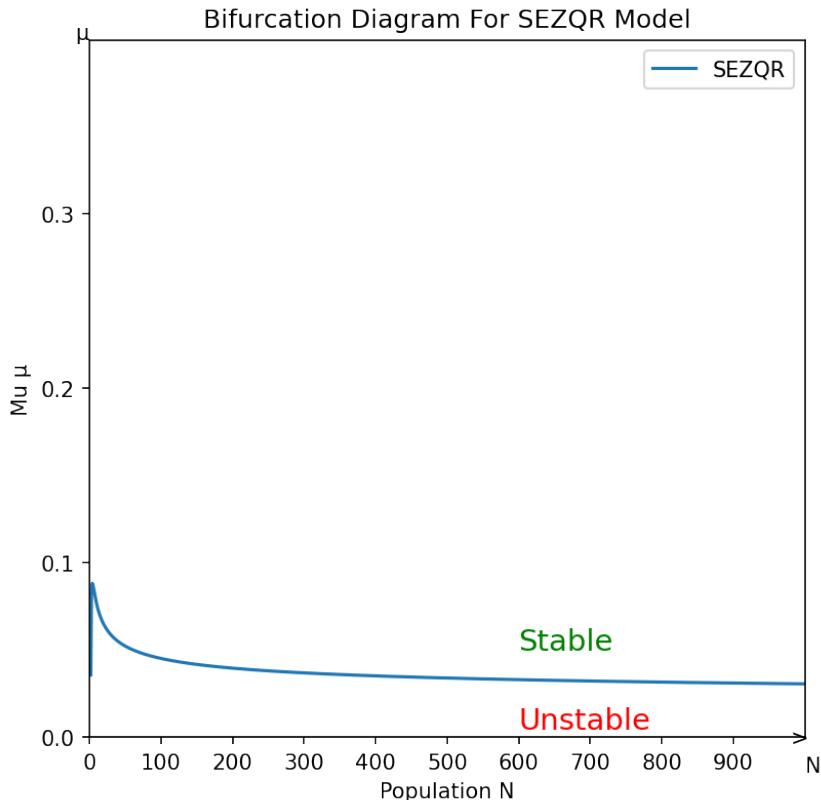


Figure 4.10: Bifurcation Diagram for SEZQR Model

Now, the bifurcation diagrams for both the SEZQR model and the modified SEZQR model are plotted within a single frame,

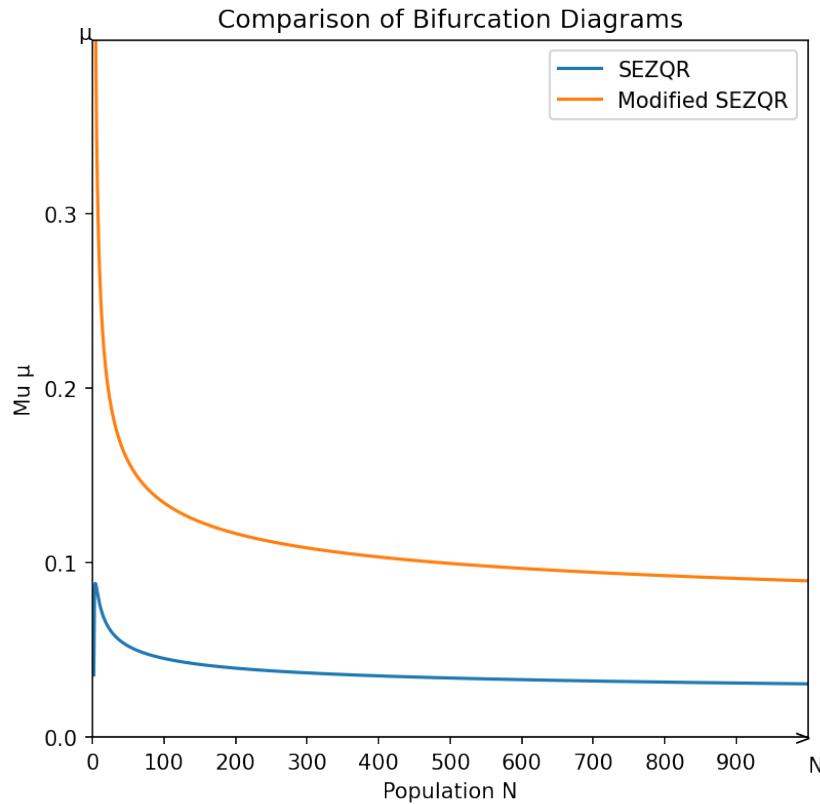


Figure 4.11: Bifurcation Diagrams Comparison

In the Figure 4.11, the bifurcation diagram for the modified SEZQR model is plotted using a yellow line, while the bifurcation line for the regular perturbed SEZQR model uses a magenta line. Any area above the curve line is stable for that line, and the area below the curve line marks the unstable region for that line.

It is easily visible that, the stability region for the perturbation parameter  $\mu$  of the regular SEZQR model is bigger than the stability region of the modified SEZQR model. The modified SEZQR model has a bigger unstable region for the perturbation parameter  $\mu$ . The possibilities of individuals breaking free from the quarantine compartment Q and returning to the zombie compartment Z as well as the influence of the susceptible population in quarantining zombies from the compartment Z to Q, that were introduced in the modified SEZQR model have caused the change in the region of stability for this model.

Also, if we numerically solve the SEZQR model for 1000 days with the same set of data used in the example of Section 4.5 of this chapter and compare it side by side with the solution of the modified SEZQR model (from the Figure 4.5), we will get the following scenario,

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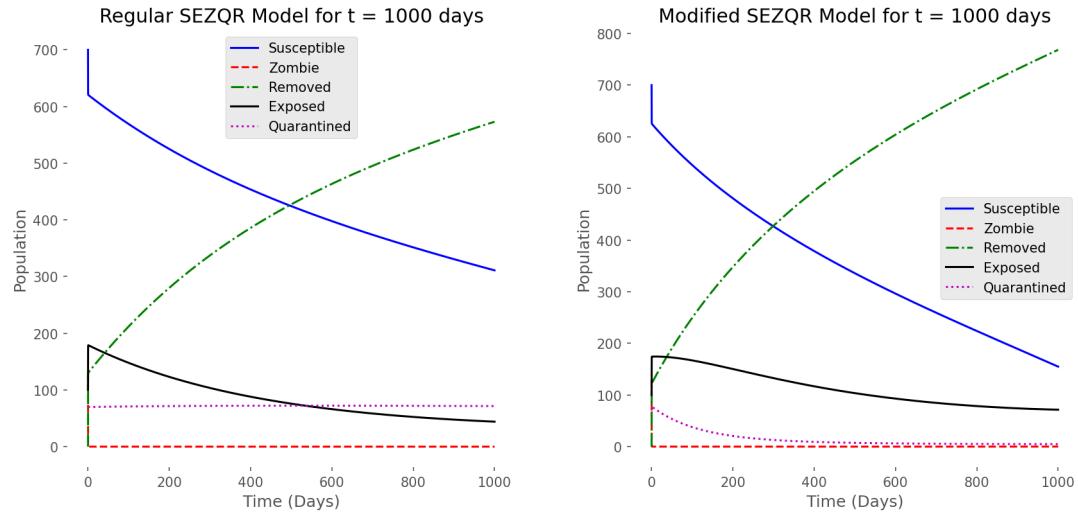


Figure 4.12: Solution Comparison- SEZQR vs. Modified SEZQR

In the Figure 4.12, both the solutions are plotted using the same set of data and for 1000 days. It can be seen that, the susceptible population line for the modified SEZQR model falls rapidly when compared to the susceptible line of the regular SEZQR model. On the other hand, the removed population line on the modified SEZQR model rises faster than that of the regular SEZQR model. While the zombie population lines remain almost similar for both of the graphs, there are some changes in behavior for the exposed and quarantined population lines. In the modified SEZQR model, the quarantined population line also goes downward gradually. The changes introduced in the modified SEZQR model have caused the dynamics of this model to act differently than the regular perturbed SEZQR model.

## 4.8 Special Case 01: Exposed = 0

Let us consider a special scenario, in which  $E = 0$ . That means, there is no individual in the exposed population. As such, no new individual can be turned into zombies  $Z$  or can be transferred to the quarantined compartment  $Q$  from the exposed compartment  $E$ .

Also it is important to note that, in the modified SEZQR model, the transfer rates  $\alpha S^{(1+\mu)} Z$  (from compartment  $Z$  to  $R$ ) and  $\sigma SZ$  (from compartment  $Z$  to  $Q$ ) are still depending on the initial susceptible population  $S$ . But as there is no exposed population  $E$ , the original susceptible population  $S$  is also absent in the field. So it is no longer possible for the susceptible population  $S$  to impact the transfer rates of zombies  $Z$ .

So, now the population transformation dynamics will be confined within the compartments  $Z$ ,  $Q$  and  $R$ . This can be visualized as below–

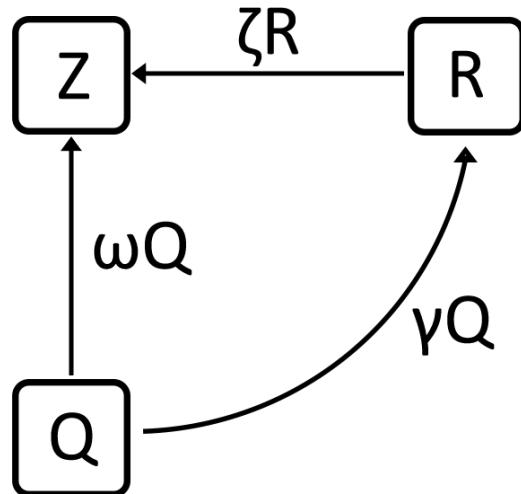


Figure 4.13: Special Case 01

And, the new set of differential equations will look like, with  $E$  being 0 and  $S$  being absent,

## 4 Quarantine Model

$$\begin{aligned} Z' &= \zeta R + \omega Q \\ Q' &= -\gamma Q - \omega Q \\ R' &= \gamma Q - \zeta R \end{aligned} \tag{4.10}$$

Which can be reduced in the short form as below,

$$Z' = \zeta(N - Z - Q) + \omega Q \tag{4.11}$$

$$Q' = -\gamma Q - \omega Q \tag{4.12}$$

Here, equation (4.12), is a first order linear ordinary differential equation. Solving this equation, we get the exact solution,

$$Q = c_1 e^{-(\gamma+\omega)t} \tag{4.13}$$

Where,  $c_1$  is a constant.

Putting this value in the equation (4.11), we get,

$$\begin{aligned} Z' &= \zeta N - \zeta Z + (\omega - \zeta)Q \\ \text{or, } Z' &= -\zeta Z + f(t) \end{aligned} \tag{4.14}$$

Where,

$$\begin{aligned} f(t) &= \zeta N + (\omega - \zeta)Q \\ &= \zeta N + (\omega - \zeta)(c_1 e^{-(\gamma+\omega)t}) \end{aligned}$$

Equation (4.14) is a nonhomogeneous linear differential equation.

The system of equations (4.10) can be solved numerically, with the same set of parameter values mentioned in Table 4.1 and initial conditions discussed in the example of Section 4.5 of this chapter.

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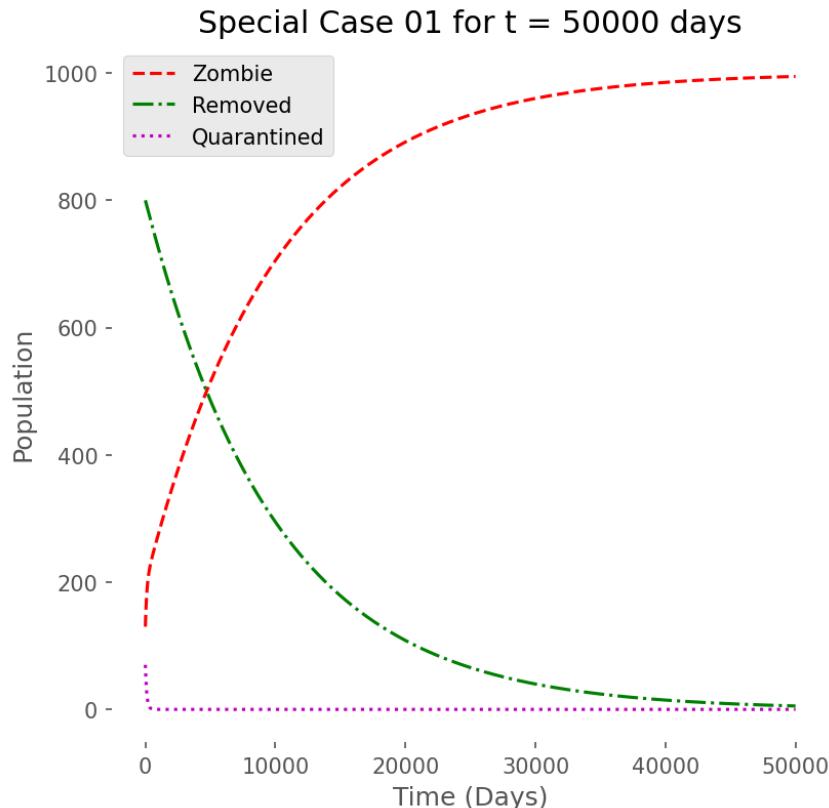


Figure 4.14: Special Case 01 Numerical Solution

Here the system is solved for 50,000 days, with a step size of 1. It can be seen that, in the long run the whole population turns into zombies, and the removed population as well as the quarantined population all disappear eventually. The perturbation parameter is absent from the equations, so there is no way to impact or perturb the dynamics of the model here.

This type of scenario (that the exposed population being zero) is only possible when all the individuals from the susceptible S population are already put into the Z or Q compartments and no new human is left for interaction or infection.

Or, the Z, Q and R categories are being isolated in such a closed system that they cannot interact with any new population. For example these categories can be put into a location or city which is totally disconnected or cut off with the rest of the country/world.

## 4.9 Special Case 02: Zombies = 0

For the special case 02, let us consider the circumstance when the population of Z compartment turns into zero. It means that there are no new zombies left to contaminate or infect new people in the susceptible population S (because the transfer rate  $\beta SZ$  and  $\alpha S^{(1+\mu)}Z$  will be zero, as  $Z = 0$ ). As such, the population of the compartments E, Q will gradually turn into zero and the whole system will be stable again with the healthy people only.

So, the new system will look like—

$$\begin{aligned} S' &= 0 \\ E' &= -(\rho + \kappa)E \\ Z' &= \rho E + \zeta R + \omega Q \\ Q' &= \kappa E - \gamma Q - \omega Q \\ R' &= \gamma Q - \zeta R \end{aligned} \tag{4.15}$$

This system can be reduced in the form given below,

$$\begin{aligned} E' &= -(\rho + \kappa)E \\ Z' &= \rho E + \zeta(N - S - E - Q) + \omega Q \\ Q' &= \kappa E - (\gamma + \omega)Q \end{aligned} \tag{4.16}$$

But it is also important to note that, here as all the zombies have vanished ( $Z = 0$ ), so it is not possible to produce new zombies or spread the infection anymore. As such the transfer rates  $\zeta R$ ,  $\omega Q$ ,  $\gamma Q$ ,  $\rho E$ ,  $\kappa E$  will turn into meaningless entities. So it is not logical to model or simulate this system of differential equations, as it is no longer relevant or realistic.

As all the zombies have been vanished, the whole population will be filled with healthy people only and no new infection is possible. Thus, it is no longer possible or sensible to transfer individuals within the given E, Z, Q, R compartments. These compartments do not exist anymore.

# Chapter 5

## Conclusion

In this thesis work, some attempts have been made to study the classical SIR model, and derive a more complicated yet pragmatic mathematical model from it to simulate and understand the real-world disease scenario. The zombie epidemic model that has been studied and analyzed here provides room for further studies on other types of infectious diseases that may cause epidemics in the human population. The simple zombie SZR model has been analyzed mathematically here and the graphical interface program that has been developed during this thesis work will provide scope for visualizing the model fast and easily in accordance with different sets of parameter values. This tool will ease the way to study and compare different model states under different circumstances.

Furthermore, in the more advanced and detailed modified SEZQR model, some more practical variables have been considered that may impact the zombie epidemic. Based on the modified model, a basic reproduction number is calculated and also the condition for initiating stability based on the perturbation parameter is derived. The value of the perturbation parameter depends on the human ability and capacity to contain and control the epidemic in the real world. During these analyses, some imaginary values of the conversion rate parameters were assumed. However, actual data need to be analyzed in the real world during the epidemic to get the most realistic estimates for these parameter values. Based on these parameter values, this modified model will be able to best predict and simulate the epidemic.

Even though many variables and situations have been considered in the modified model, there are still opportunities to include and consider many more situations that may occur in the real-world scenario. In the modified SEZQR model, the population nature is assumed to be homogenous. However, in further studies, there are scopes for analyzing the dynamics of the disease in a heterogeneous population. It can also be studied what may happen if the individuals are not contained within a

## 5 Conclusion

closed region, rather they are moving within a wider and more diversified geographical area. The effects of modern medical treatment, vaccines, public awareness, weather, age, gender, food habit, quarantine facility, health condition, communication, etc. also play vital roles in understanding infectious disease dynamics. These are some of the example variables that may be considered in the future to expand and elaborate on the efficacy of this modified SEZQR model in studying new types of infectious diseases. However, in this thesis paper, the investigations have been kept confined within its theoretical dimensions. The example and comparisons are conducted to explain the model in a more comprehensive way. Finally, two best thought special cases are also considered that may alter the model in significant ways.

# Codes

All the codes for this thesis work were written using Python programming language [64], version 3.7. This language was chosen as it provides sophisticated tools and libraries for a fast and convenient mathematical analysis and visualization. All the graphs were plotted using the Matplotlib [24] library. And all the differential equations were solved using the `solve_ivp` function [23]. This function uses Runge-Kutta method of order five (RK45) [61], [62], [63] by default, as the integration method. In this RK45 method, the error is controlled assuming the accuracy from the fourth-order method, while the steps are taken using the accurate formula of fifth-order. However, it is also possible to implement other types of explicit Runge-Kutta methods (such as RK23, DOP853) or implicit methods (such as Radau, BDF) in this function. More details on these methods can be found at [23]. The default RK45 method seems to produce the most accurate results for the works of this thesis and thus it has been kept unchanged. There is another old function called `odeint` [65] available in python for integrating a system of ordinary differential equations. However, the use of this very old `odeint` function was avoided in these codes as it was creating unexpected overflow error [66] and hampering the calculation. The interactive graphical interface program for generating phase portraits, which was discussed in Chapter 3.3.4, was created using the Tkinter [47] module.

All the code files are uploaded to GitHub online repository under the link-  
<https://github.com/tariquldipu/Masterarbeit>

All the codes are available in two formats. Firstly, the codes are available in Anaconda Jupyter Notebook (as in .ipynb) format and are organized inside the Jupyter folder. The codes and their outputs are also saved in PDF formats inside this directory. And secondly, the codes are also available as separate python files (as in .py format) and are organized in different folders as per their chapter names.

Some brief informations about each and every code file are also provided in the *README.md* file inside the GitHub repository.

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