



Faculty of Computer Science and Information Technology

**Formulation of the SVEIR Model for COVID-19 by Incorporating
Control Intervention in Pakistan**

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Formulation of SVEIR Model for COVID-19 by Incorporating Control Intervention in Pakistan

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DECLARATION

I declare that the work in this thesis was carried out in accordance with the regulations of Universiti Malaysia Sarawak. Except where due acknowledgements have been made, the work is that of the author alone. The thesis has not been accepted for any degree and is not concurrently submitted in candidature of any other degree.



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ABSTRACT

Like other countries around the world, Pakistan experienced a COVID-19 outbreak, starting from February 26, 2020, when the first two cases of COVID-19 were reported. To save the nation from this disease, the government of Pakistan took different strict measures. Along with the various aspects of the disease, including its epidemiology, transmission, clinical features, diagnosis, treatment, and prevention, it is widely accepted that mathematical models can be helpful to predict the occurrence of infectious diseases. However, the control interventions incorporating the Non-pharmaceutical interventions (NPI) measure for the current scenario in Pakistan, which include vaccination compartments, have not yet been identified for COVID-19. Therefore, the main objective of this study was to propose a new COVID-19 model by incorporating the vaccine factor to analyze the COVID-19 trends in Pakistan. In order to achieve the objective of research, a systematic process was followed, and an analogous existing model called STEQIR (Gill et al., 2020) was evaluated. Then, by using some modifications such as transitioning individuals from the susceptible population to a vaccinated population and by compartmental analysis, including the control intervention of the vaccine, a new model, namely the SVEIR (Susceptible, Vaccinated, Exposed, Infected, and Recovered) model, was derived. The proposed model is based on the assumption that Vaccination reduces the effective susceptible group, lowering the force of infection. The possibility of the analytical solution of the proposed SVEIR model was investigated. However, the analytical solution for the SVEIR model is quite tricky and impractical due to high non-linearity and the implicit nature of the governing equations. Therefore, the numerical solution of the proposed SVEIR model was computed using a higher-order Runge-Kutta method, which yields a stable solution of the SVEIR model. The numerical simulation of all five variables can project the outbreak well over the next few

months. It was established that despite the large population of Pakistan, the measured maximum percentage error (MAPE) was in an acceptable range for all five variables that fell between 9.72 and 15.42, and the results were statistically significant at 90% and 95% confidence levels. The validation of the proposed SVEIR model was also done by comparing a benchmarking method (Gill, 2020), and it was shown that the SVEIR model performs better for the Pakistan COVID-19 data. To assess the variations caused by the working parameters involved in the SVEIR model, a sensitivity analysis was conducted, and the impact of all parameters involved in the SVEIR model was analyzed. From the analysis, it was revealed that among all the parameters, the transmission rate, death rate ε , and the average number of contacts per day per case are sensitive as they produce more variations in almost all population classes. Finally, the simulation of the basic reproduction number R_0 regarding sensitive parameters and values was obtained. It was pointed out that the R_0 remains more dominant for the probability of susceptibility β , becoming infectious per contact, and death rate; for other parameters, it remains less than 1. The outcome and findings of this study may be essential for policymakers and public health officials in making informed decisions and formulating effective strategies to govern and mitigate the spread of COVID-19. The understanding gained from this research may guide targeted strategies, promote efficient resource allocation, and contribute to the continuing efforts to mitigate and control the COVID-19 pandemic in Pakistan. Future research may focus on extending the proposed SVEIR model by incorporating additional factors, such as the efficacy of various vaccination techniques, the effects of non-pharmaceutical therapies, demographic characteristics, economic determinants, and seasonal variations in environmental and weather conditions weather.

Keywords: COVID-19 in Pakistan. SVEIR model, vaccination, sensitivity analysis

**Perumusan Model SVEIR untuk COVID-19 dengan Menggabungkan Intervensi
Kawalan di Pakistan**

ABSTRAK

Seperti negara-negara lain, Pakistan juga telah mengalami wabak COVID-19 bermula dari 26 Februari 2020 apabila dua kes COVID-19 pertama dilaporkan. Kerajaan Pakistan mengambil pelbagai langkah untuk mengatasi masalah ini. Model matematik amat berguna dalam ramalan penyakit berjangkit ini dengan mengambilkira ini pelbagai aspek penyakit ini, termasuk epidemiologinya, penularan, ciri-ciri klinikal, diagnosis, rawatan, dan pencegahan.. Walau bagaimanapun, intervensi kawalan yang menggabungkan langkah-langkah Intervensi Bukan Farmaseutikal (NPI) untuk senario semasa di Pakistan termasuk kompartmen vaksinasi belum lagi dikenal pasti untuk COVID-19. Oleh itu, objektif utama kajian ini adalah untuk mencadangkan model COVID-19 baharu dengan memasukkan faktor vaksin untuk menganalisis trend COVID-19 di Pakistan. Untuk mencapai objektif penyelidikan, satu proses sistematik telah diambil dan satu model sedia ada yang serupa dipanggil STEQIR (Gill et al., 2020) telah dinilai. Setelah itu, dengan menggunakan beberapa pengubahsuaian seperti dengan memindahkan individu dari populasi terdedah kepada populasi Vaksinasi dan dengan analisis kompartmen termasuk intervensi kawalan vaksin, satu model baru yang dikenali sebagai model SVEIR (Terdedah, Vaksinasi, Terdedah, Dijangkiti, dan Pulih) telah diperolehi. Model yang dicadangkan adalah berdasarkan andaian bahawa Vaksinasi mengurangkan kumpulan terdedah dengan menurunkan daya jangkitan. Kemungkinan penyelesaian analitik bagi model SVEIR yang dicadangkan telah disiasat tetapi didapati bahawa penyelesaian analitik untuk model SVEIR adalah agak sukar dan tidak praktikal disebabkan oleh ketidaklinieran yang tinggi dan sifat implisit persamaan pengawalan. Oleh itu, penyelesaian numerik bagi model SVEIR yang dicadangkan telah dikira menggunakan kaedah Runge-Kutta order tinggi yang menghasilkan penyelesaian stabil bagi model SVEIR. Simulasi

numerik bagi semua lima pembolehubah dapat meramalkan wabak dengan baik untuk beberapa bulan ke hadapan. Walaupun populasi Pakistan agak besar, kesilapan peratus maksimum yang diukur (MAPE) berada dalam julat yang boleh diterima untuk semua lima pembolehubah yang jatuh antara 9.72 dan 15.42 dan hasilnya adalah signifikan secara statistik pada tahap signifikan 90% dan 95%. Pengesahan model SVEIR yang dicadangkan juga dilakukan dengan membandingkan kaedah penanda aras Gill (2020) dan ditunjukkan bahawa model SVEIR berprestasi lebih baik untuk data COVID-19 Pakistan. Penilaian variasi yang disebabkan oleh parameter yang terlibat dalam model SVEIR, analisis kepekaan telah dijalankan dan kesan semua parameter telah dianalisis. Hasil daripada analisis tersebut, didapati bahawa antara semua parameter, kadar penularan, kadar kematian ϵ dan purata bilangan kontak setiap hari bagi setiap kes adalah sensitif kerana ia menghasilkan lebih banyak variasi dalam hampir semua kelas populasi. Akhir sekali, simulasi sensitiviti untuk nombor pembiakan asas R_0 telah diperoleh. Simulasi menunjukkan bahawa R_0 kekal lebih dominan untuk kebarangkalian kerentanan β , menjadi berjangkit per kontak dan kadar kematian, untuk parameter lain ia kekal kurang daripada 1. Hasil dan penemuan kajian ini penting bagi pembuat dasar dan pegawai kesihatan awam dalam membuat pilihan yang berpengetahuan dan merumuskan strategi yang berkesan untuk mengawal dan mengawal penyebaran COVID-19. Pemahaman yang diperoleh daripada penyelidikan ini mungkin dapat membimbing strategi yang disasarkan, mempromosikan pengagihan sumber yang cekap, dan menyumbang kepada usaha berterusan untuk mengurangkan dan mengawal pandemik COVID-19 di Pakistan. Penyelidikan masa depan mungkin akan menumpukan pada pengembangan model SVEIR yang dicadangkan dengan penambahan faktor-faktor lain seperti keberkesanan pelbagai teknik vaksinasi, kesan terapi bukan farmaseutikal, demografi, penentu ekonomi dan kesan variasi bermusim dalam persekitaran dan cuaca.

Kata kunci: COVID-19 di Pakistan. Model SVEIR, vaksinasi, analisis sensitiviti

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LIST OF ABBREVIATIONS

ARIMA	Autoregressive Integrated Moving Average
BIBP	Beijing Institute of Biological Products
CDC	Centers for Disease Control
COVID	Coronavirus
COVAX	COVID-19 Vaccine Global Access
DFE	Disease Free Equilibrium
IBMs	Institute of Biomedical Science
LSE	Least Squares Error
M	Semi-susceptible
MCO	Movement Control Order
MERS	Middle East Respiratory Syndrome
MLE	Maximum Likelihood Estimation
MoNHSRC	Ministry of National Health Services, Regulation and Coordination
MPE	Mean Percentage Error
NDMA	National Disaster Management Authority
NGM	Next Generation Matrix
NPI	Non-pharmaceutical interventions
ODEs	Ordinary Differential Equations
PBS	Pakistan Bureau of Statistics
R	Coefficient of correlation
RK	Runge-Kutta
RMSE	Root Mean Square Error

SARIMA	Seasonal Autoregressive Integrated Moving Average
SARS	Severe Acute Respiratory Syndrome
SEIARD	Susceptible Exposed Asymptomatic Infected Recovered and Deceased
SEIHRD	Susceptible Exposed Infected Hospitalized Recovered Death
SEIQR	Susceptible Exposed Infected Quarantine and Recovered
SEIR	Susceptible Exposed Infected Recovered
SEIRD	Susceptible Exposed Infected Recovered Death
SEQAIPTR	Susceptible Exposed Quarantine Incubated Infected Symptomatic Infectious Population Negative test result Population and Recovered
SIR	Susceptible Infected Recovered
SMEIHRDV	Susceptible Semi-Susceptible Exposed Infected Hospitalized Recovered Dead and Vaccinated
SOP	Standard Operating Procedure
SSE	Sum of Squared Error
STEQIR	Susceptible Traced Exposed Quarantine Infected and Recovered
WHO	World Health Organization

LIST OF SYMBOLS (NOMENCLATURE)

$\%$	Percentage
ω	Vaccine wane rate
β	The probability of susceptibility becoming infectious per contact
ϕ	Incubation period
$\gamma = \frac{1}{D}$	Recovery rate
R_0	Basic reproductive number
$1/\gamma$	Infectious period
ε	The death rate due to COVID-19
ξ	The average number of contacts per day per case
τ	People in the vulnerable groups are receiving vaccination rates
μ	Natural death rate (constant for all classes)
q	The proportion of close contacts traced per day
κ	The proportion of exposed persons who performed effective precautions
λ	Different rates at which individuals move into the susceptible compartment
δ	The mean daily rate at which infectious cases are isolated
τ	People in the vulnerable group start receiving a vaccination rate
N	Total Population
$\frac{d}{dt}$	Derivative of variables with respect to time
E_q	Positive test results are undergoing quarantine
I_q	The infected isolated population

CHAPTER 1

INTRODUCTION

This chapter presents a concise overview of the COVID-19 disease, highlights the aim and objectives of the study, and emphasizes the formulation of a suitable mathematical model to predict COVID-19 trends in Pakistan.

1.1 Study Background

COVID-19, a zoonotic disease caused by the beta coronavirus SARS-CoV-2, is believed to have first infected humans around November 2019 near the city of Wuhan in Hubei Province, China. Since then, it has spread globally, resulting in a pandemic (Zhu et al., 2020; Gallego et al., 2020). On March 11, 2020, the World Health Organization (WHO) officially declared COVID-19 a global pandemic. By December 2023, the virus had infected over 275,000 people worldwide and claimed more than 11,000 lives. Despite significant public health efforts to interrupt its transmission, the number of COVID-19 cases and deaths continued to rise throughout 2020.

Research has shown that the COVID-19 virus spreads primarily through respiratory droplets released when an infected person coughs, sneezes, talks, or breathes. It can also be transmitted by touching contaminated surfaces and then touching the mouth, nose, or eyes. The symptoms of COVID-19 can vary significantly, ranging from mild to severe illness. Common symptoms include fever, cough, fatigue, muscle aches, loss of smell or taste, and difficulty breathing. Some individuals may also experience gastrointestinal symptoms such as diarrhea, nausea, and vomiting. The virus can survive on surfaces for several hours to days, depending on factors such as exposure to sunlight, temperature, and the type of surface.

Social distancing reduces the risk of contact with contaminated surfaces and infectious individuals outside the home (Huang et al., 2020).

The majority of COVID-19 cases and deaths initially occurred in China, South Korea, Italy, and Iran (WHO, 2020). The virus also severely affected other Asian countries, including Pakistan. Located in South Asia, Pakistan shares borders with India to the east, Afghanistan to the west and north, Iran to the southwest, and China to the northeast. The country reported its first two COVID-19 cases on February 26, 2020—both individuals had recently traveled from Iran. This marked the beginning of the virus's spread within Pakistan.

In response, the government quickly implemented measures to control the outbreak. Since then, several studies have been conducted to better understand the epidemiology, transmission, clinical features, and management of COVID-19 in the country. Epidemiological findings indicate that most cases in Pakistan occurred among adults, with a slightly higher incidence in males than females. The virus is more prevalent in urban areas compared to rural regions (Ishtiaq et al., 2021).

Jefferson et al. (2023) and Javed et al. (2023) discussed the patterns of COVID-19 transmission in Pakistan. They emphasized the importance of physical distancing and mask-wearing in reducing the spread of the virus. Pakistan has experienced multiple waves of COVID-19, each with varying timing and severity. Data suggest that the third wave began in late February 2021, intensified throughout March and April, and peaked in April 2021, making it the most severe wave. During this period, the country witnessed a sharp rise in cases and deaths, which overwhelmed the healthcare system. In response, the government implemented various control measures, including lockdowns, social distancing, and nationwide vaccination campaigns.

On February 2, 2021, Pakistan launched its COVID-19 vaccination program. As of August 1, 2022, the country had reported 1,048 COVID-19 cases with three deaths. By October 2022, the number of cases had decreased to 47, and the number of deaths had increased to seven (WHO, 2020).

Figure 1.1 presents a summarized time series plot of COVID-19 cases in Pakistan from March 2020 to December 2022. The new cases and 7-day average trend exhibit the different waves of COVID-19 throughout Pakistan. The peak cases have been observed in July 2020, December 2020, May 2021, October 2021 and February 2022. After May 2022 the new cases of COVID-19 decrease monotonically and disease has undergone to vanish. Similarly, the trends of COVID-19 cases for all four provinces, Punjab, Sindh, Khyber Pakhtunkhwa, and Baluchistan, as well as the capital territory of Islamabad and other administrative regions, including Gilgit-Baltistan and Azad Jammu and Kashmir, are shown in Figures 1.2 to 1.7. The spread of COVID-19 disease shows the different trends for the different provinces and administrative territories. In Figure 1.2 the Behavior of COVID-19 cases in the largest Punjab province of Pakistan is exhibited. The peak cases have been observed in June 2020, April 2021, September 2021, and February 2022. After May 2022 the new cases of COVID-19 had decreased asymptotically. Figure 1.3 expresses the Behavior of COVID-19 cases in the second largest province Sindh of Pakistan. It can be observed that in May 2020, June 2020, December 2020, May 2021 and February 2022 the COVID-19 spread was high in Sindh. After June 2022 the new cases of COVID-19 had reduced smoothly. The number of new COVID-19 cases in June 2020, April 2021, May 2021, and February 2022 was higher in the Khyber Pakhtunkhwa province of Pakistan, as shown in Figure 1.4. After March 2022, the new cases of COVID-19 had reduced in Khyber Pakhtunkhwa. Figure 1.5 exhibits the

trend of COVID-19 cases in the Balochistan province of Pakistan. Since this province has the least population compared to other provinces of Pakistan therefore there was not a significant spread of COVID-19. However, most of the new cases have been observed in July 2020, September 2020, May 2021, and August 2021. Figure 1.6 exhibits the Behavior of the COVID-19 cases in the Gilgit-Baltistan region of Pakistan. At the peak number of cases was observed from June 2020 to January 2021 and from May 2021 to September 2021, then after April 2022, the number of cases has been reduced in Gilgit-Baltistan. Similarly, Figure 1.7 shows the trend of COVID-19 in the Pakistan-administered Azad Jammu and Kashmir. The high number of cases was observed from May 2021 to September 2021 and in March 2022. After April 2022, a decline was observed in the number of cases in Azad Jammu and Kashmir.

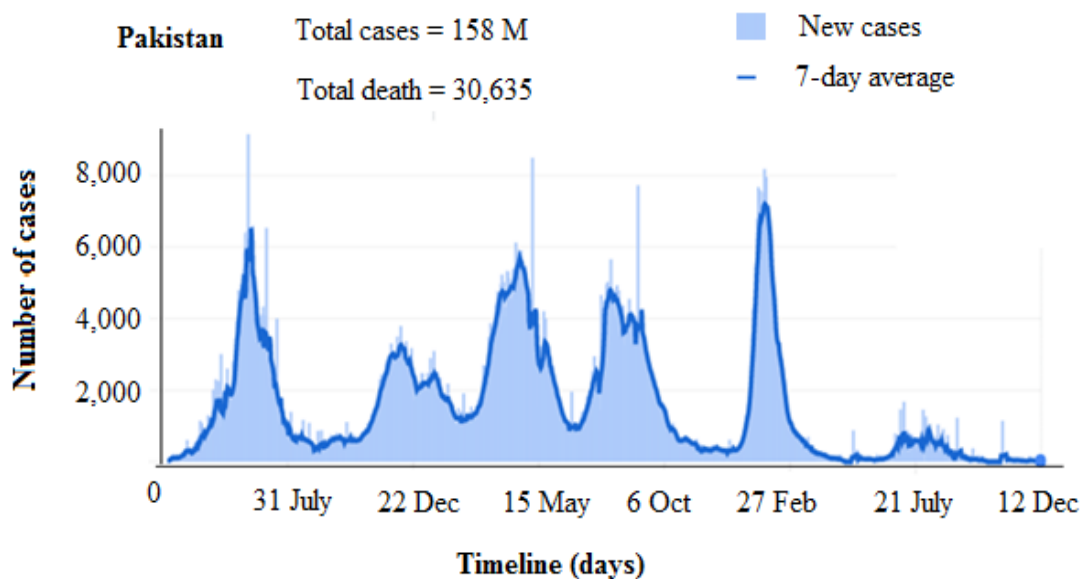


Figure 1.1: COVID-19 case numbers and the 7-day average in Pakistan from March 15, 2020, to December 12, 2022

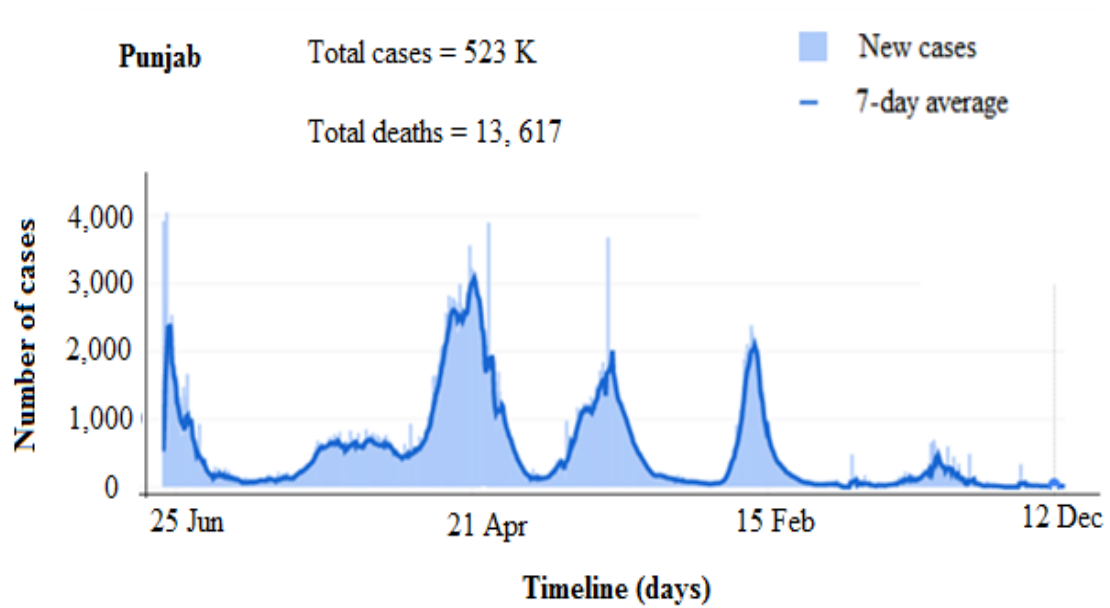


Figure 1.2: COVID-19 case numbers and the 7-day average in Punjab Province of Pakistan from June 11, 2020, to December 12, 2022

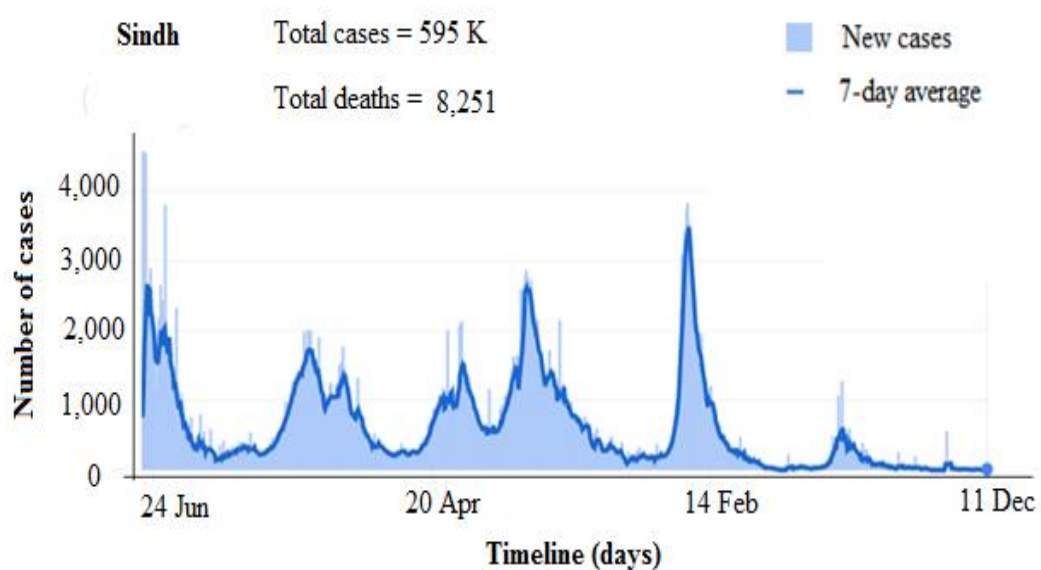


Figure 1.3: COVID-19 case numbers and the 7-day average in Sindh Province of Pakistan from June 11, 2020, to December 12, 2022

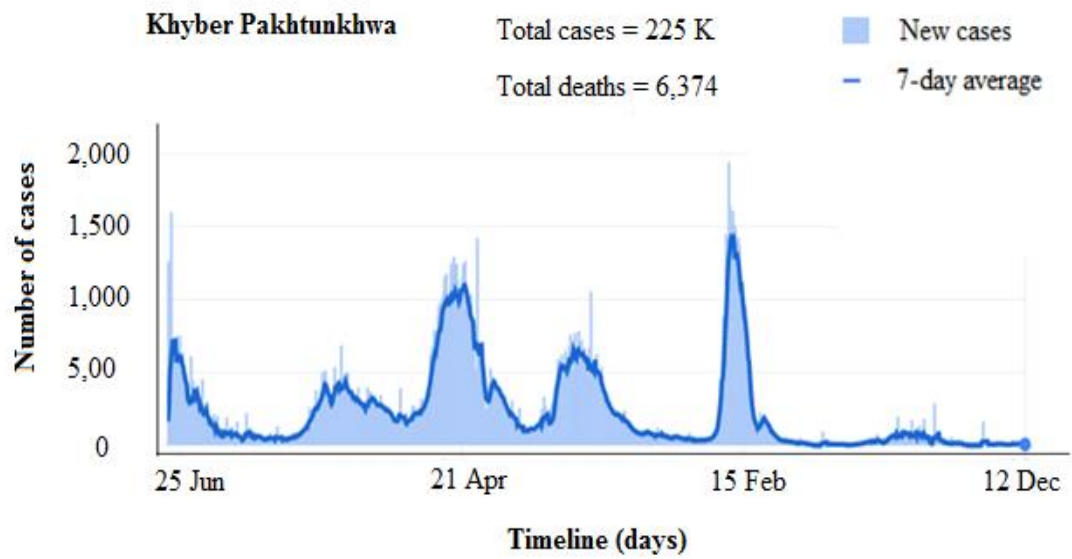


Figure 1.4: COVID-19 case numbers and the 7-day average in Khyber Pakhtunkhwa, Pakistan from June 11, 2020, to December 12, 2022

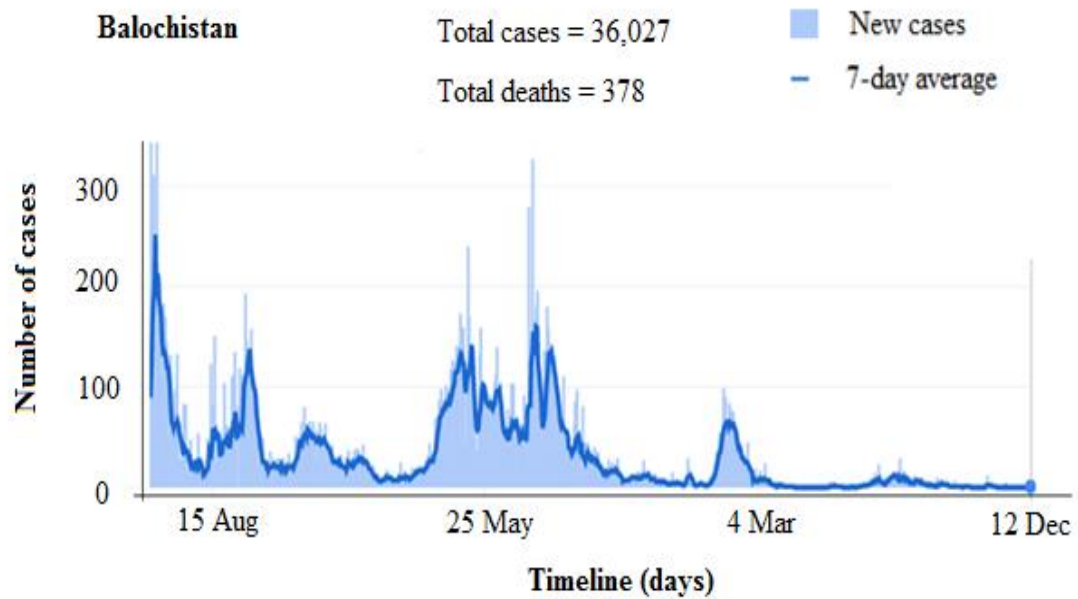


Figure 1.5: COVID-19 case numbers and the 7-day average in Balochistan, Pakistan from June 11, 2020, to December 12, 2022

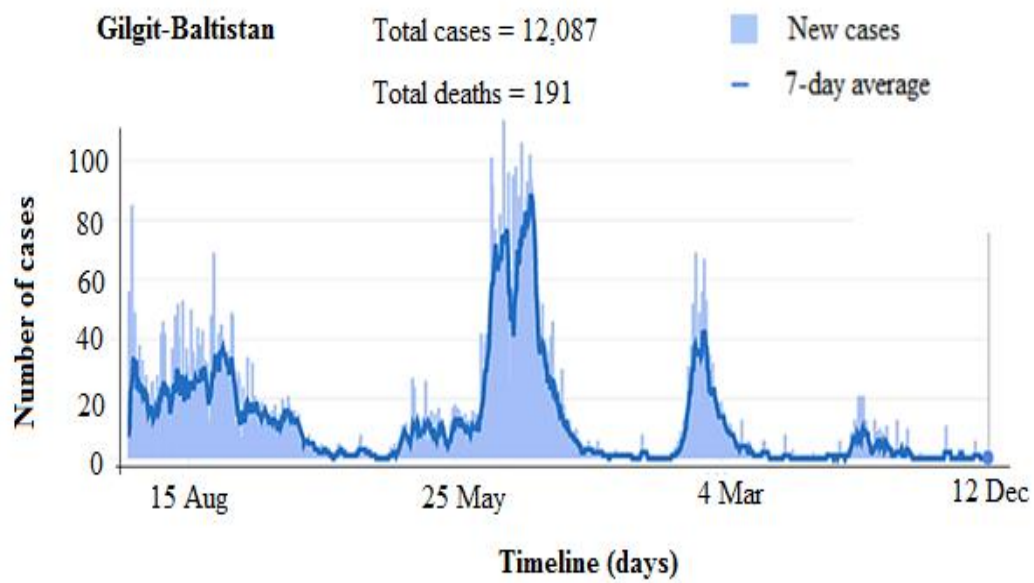


Figure 1.6: COVID-19 case numbers and the 7-day average in Gilgit Baltistan Province of Pakistan from June 11, 2020, to December 12, 2022

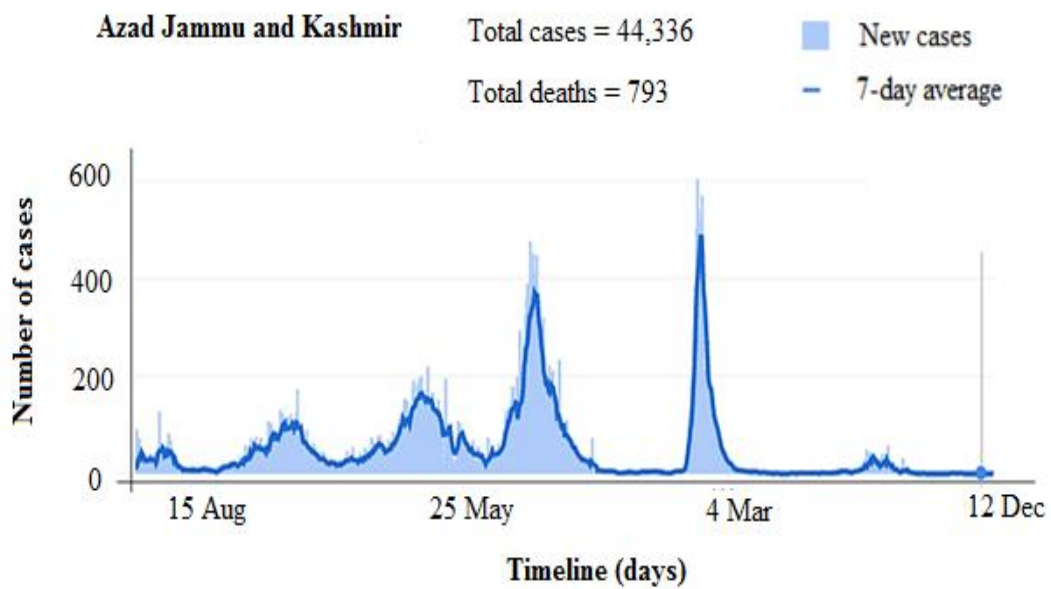


Figure 1.7: COVID-19 case numbers and the 7-day average in Azad Jammu and Kashmir of Pakistan from June 11, 2020, to December 12, 2022

The above Figures 1.1-1.7 provide valuable insights into the intensity and progression of the disease during different waves and periods in Pakistan.

1.2 Mathematical Modelling of COVID-19

Studies on COVID-19 have examined various aspects of the disease, including its epidemiology, transmission, clinical features, diagnosis, treatment, and prevention. It is widely accepted that mathematical models can be used to predict the occurrence and spread of infectious diseases. Compartmental models, in particular, provide a fundamental mathematical framework for studying the complex dynamics of epidemiological processes (Rao et al., 2019). To date, several investigations have successfully used various mathematical and statistical models to predict the spread of the COVID-19 pandemic (Wrapp et al., 2020).

The classical disease model known as the SIR (Susceptible–Infected–Recovered) model has been widely adopted for analyzing COVID-19 trends (Mirzaie et al., 2021; Oud et al., 2021; M. A. et al., 2021). This model assumes homogeneous mixing within the population and offers insights into the epidemic's dynamics, such as the peak number of infections and the optimal timing of interventions. Based on the availability of data and specific modeling needs, additional compartments have been proposed to enhance the model's accuracy.

For instance, the SEIR (Susceptible–Exposed–Infected–Recovered) and SEIRD (Susceptible–Exposed–Infected–Recovered–Deceased) models (Ilyas et al., 2020) incorporate factors such as the incubation period and disease-related mortality. The SEIHRD (Susceptible–Exposed–Infected–Hospitalized–Recovered–Deceased) model (Mirzaie et al.,

2021) further accounts for hospitalization and includes Behavioral aspects by assuming that the proportion of deaths among infected individuals may influence public adherence to social distancing measures.

To better reflect real-world conditions, especially after the introduction of vaccines, the concept of "semi-susceptible" individuals, those partially susceptible to infection, was introduced. This led to the development of the SMEIHRDV model (Susceptible–Semi-susceptible–Exposed–Infected–Hospitalized–Recovered–Deceased–Vaccinated), which refines epidemic predictions by incorporating vaccination and nuanced Behavioral dynamics (Mirzaie et al., 2021).

Simulation results using this model were compared with real-world data from Egypt, Belgium, Japan, Nigeria, Italy, and Germany, as released by the WHO during the second quarter of 2020. In related research, Peter et al. (2021) expanded the SEIR model into the SEIRQ model by including a quarantine compartment, while Li et al. (2021) utilized the SEIARD model to analyze the spread and impact of COVID-19.

Gill et al. (2020) discussed an innovative new mathematical model called STEQIR, based on Malaysian data. In this model, the researchers introduced three additional compartments: the traced close-contact population with a negative test result (T), the traced exposed close-contact population with a positive test result undergoing quarantine (Eq), and the isolated infected population (Iq). They suggested that measures such as isolation, quarantine, and, particularly, the Movement Control Order (MCO) should be implemented and sustained until the outbreak is controlled or a vaccine becomes available (Ferguson et al., 2020).

In Pakistan, the initial COVID-19 disease model was developed by Shah et al. (2020), who utilized the generalized SIR method to accurately predict the spread of the virus, including the rates of infections, recoveries, and deaths. Subsequently, Ahmed et al. (2020) built on this model by incorporating additional compartments and adopting the SEIR framework. Naik et al. (2020) introduced a more complex model with eight compartments, called SEQAIPTR, which includes Susceptible, Exposed, Quarantine, Incubated, Infected, Symptomatic Infectious Population, Negative Test Result Population, and Recovered. While this model provides a more detailed understanding of COVID-19 dynamics, the availability of data for all required variables continues to be a significant challenge.

1.3 Problem Statement

In literature, many studies have been reported to analyse and predict the Behavior of COVID-19 in Pakistan. However, comprehensive models present a drawback as their identification is challenging, particularly during the initial outbreak when prompt decisions must be made. The Gill et al. (2020) STEQIR model has provided fascinating results to predict the spread of COVID-19 in Malaysia. However, the control interventions incorporating Non-pharmaceutical interventions (NPI) measures for the current scenario in Pakistan, which include vaccination compartments, have not yet been identified. Therefore, there is a need for such a model that covers the mentioned factors and may be obtained by modifying the STEQIR with SVEIR (Susceptible, Vaccinated, Exposed, Infected, and Recovered). This is the primary motivation for adopting a minimal SVEIR model to describe COVID-19 transmission.

1.4 Objectives

The main objective of this research is to develop a mathematical model for Pakistan that incorporates the vaccine factor to analyze COVID-19 trends in the country. The specific research objectives are as follows:

- i. To develop an SVEIR compartmental model that incorporates vaccination as a control intervention to stimulate COVID-19 transmission dynamics.
- ii. To derive both analytical and numerical solutions for the SVEIR model and apply it to COVID-19 data from Pakistan.
- iii. To validate the model by fitting it to actual COVID-19 case data from Pakistan and assess its predictive capability.

1.5 Scope of the Study

Mathematical modelling of COVID-19 cases in Pakistan provides critical insights into transmission dynamics, healthcare resource needs, and the impact of disease control interventions. These models also evaluate the effectiveness of public health measures, such as lockdowns and vaccinations, helping guide decisions on when and how to implement interventions to reduce transmission and minimize the burden on the healthcare system. Therefore, the scope of this study is limited to investigating a COVID-19 mathematical model that incorporates control interventions, including the vaccine factor, to simulate the Susceptible, Vaccinated, Exposed, Infected, and Recovered populations. Additionally, data on COVID-19 cases in Pakistan, covering the period from March 18, 2020, to April 2022, has been obtained from reliable sources and reputable organizations, including the National Disaster Management Authority (NDMA), the Ministry of National Health Services,

Regulations and Coordination, and the official website of the Pakistan Bureau of Statistics. Other parameters within the model will be predicted based on relevant resources and scientific literature.

1.6 Significance of the Study

The proposed COVID-19 mathematical modelling study in Pakistan is expected to provide valuable insights into the trajectory of the pandemic within the country. The outcomes and findings of this study will be crucial for policymakers and public health officials in making informed decisions and formulating effective strategies to control and manage the spread of COVID-19. The knowledge gained from this research may guide targeted strategies, promote efficient resource allocation, and contribute to ongoing efforts to mitigate and control the COVID-19 pandemic in Pakistan.

1.7 Thesis Structure

This thesis is organized into five chapters. Chapter 1 begins with an introduction to the history and global impact of COVID-19, followed by the motivation for proposing a model for Pakistan. Chapter 2 presents a detailed literature review, highlighting the socio-economic impact of COVID-19 and various materials and methods used to combat the pandemic. In Chapter 3, the methodology is concisely outlined, with a specific focus on the formulation and analysis of the SVEIR model, which is discussed and explained in detail. Chapter 4 presents the analysis and discussion of the results obtained from the proposed COVID-19 model for Pakistan, as well as a comparison and evaluation of the model's performance and sensitivity analysis. Finally, Chapter 5 concludes the study by summarizing the findings and outcomes and suggesting potential future directions for research.

1.8 Summary

Chapter 1 provides an overview of COVID-19 and its global impact. It emphasizes the importance of mathematical modelling in understanding the dynamics of the pandemic and identifying effective control strategies. This chapter also discusses the specific context of Pakistan, including the initial cases and the impact of COVID-19 on the healthcare system. The need for investigating an appropriate mathematical model to analyse the impact of interventions, such as the incorporation of vaccination, is highlighted in the problem statement. The objectives of the study are outlined, and the scope and significance of the research are also discussed in this chapter. Chapter 2 will present a related literature review to provide a better understanding of the state of the art and to focus on the aim of this study.

CHAPTER 2

LITERATURE REVIEW

2.1 Overview

This chapter provides an overview of COVID-19 and is divided into five sections. Section 2.2 presents the background of the COVID-19 disease, while Section 2.3 describes the situation of COVID-19 in Pakistan. Subsection 2.3.1 discusses the facilitation measures taken by the Government of Pakistan against COVID-19. Subsection 2.3.2 presents a province-wise overview of hospitals with isolation wards for COVID-19, and Subsection 2.3.3 outlines province-wise quarantine facilities in Pakistan. Subsection 2.3.4 discusses the vaccination efforts in Pakistan, with subsections as follows: Subsection 2.3.4.1 covers the Sinopharm vaccine, Subsection 2.3.4.2 discusses the AstraZeneca vaccine, and Subsection 2.3.4.3 presents the Pfizer vaccine. Subsection 2.3.5 highlights vaccination efficacy. Section 2.4 provides an overview of the mathematical modelling of COVID-19. Finally, Section 2.5 presents the chapter summary.

2.2 Background of the COVID-19 Disease

COVID-19 (Coronavirus) disease is caused by the novel coronavirus SARS-CoV-2, which is part of the larger coronavirus family known to cause illnesses ranging from the common cold to more severe diseases like MERS (Middle East Respiratory Syndrome) and SARS (Severe Acute Respiratory Syndrome). The virus was first identified in December 2019 in the city of Wuhan, located in Hubei province, China. Initial cases were linked to a seafood market that also sold live wild animals, suggesting that the virus may have been transmitted from animals to humans. It has spread rapidly across the globe, causing widespread illness, death, and economic disruption. It has caused a global pandemic with

devastating effects on public health, society, and the economy. Since the disease outbreak occurs, the pathogen attacks the human immune system, leading to the spread of the disease in the population. The impact of COVID-19 has been felt virtually in every corner of the world, and the efforts to stop its spread have remained a top priority for governments, public health officials, and individuals (WHO, 2019). The spread of COVID-19 has affected countries worldwide, particularly in Asia. The COVID-19 pandemic has affected Asian countries in different ways. Some countries, such as China and South Korea, have implemented aggressive measures such as lockdowns and widespread testing to control the spread of the virus.

In contrast, others, such as India and Indonesia, have struggled with high cases and deaths (Organization for Economic Co-operation and Development, 2021). Malaysia and Singapore used strict measures and accelerated vaccination efforts to control the virus, whereas the Philippines faced healthcare capacity and logistical issues. The pandemic disrupted economies across Asia, affecting tourism, manufacturing, and services, leading to various fiscal and monetary support measures from governments.

2.3 COVID-19 in Pakistan

Pakistan is a developing country struggling to manage the COVID-19 pandemic. Compared to other countries, it has needed help keeping up with the challenges presented by the pandemic. The situation of COVID-19 in Pakistan highlights the importance of understanding the Behavior of individuals in the population regarding vaccination decisions. With the ongoing vaccination campaign in the country, it is crucial to encourage individuals to get vaccinated to help control the spread of the virus (Abbas et al., 2021). The decision-making process can be modelled using game theory, which can provide insights into how

individuals weigh the costs and benefits of vaccination (Parveen et al., 2022). As of September 2021, Pakistan has 154 districts (Waris et al., 2020). However, it is essential to note that the number of communities in Pakistan can change over time due to administrative and political reasons (Wu et al., 2020). The first cases of COVID-19 in Pakistan were detected in the district of Karachi, in the southern province of Sindh (Siddiqui et al., 2020). The first two cases were reported on February 26, 2020, in a statement by the Sindh Health Department. Since then, the virus has spread throughout the country, affecting all provinces and major cities (Ali et al., 2020).

Within fifteen days, the range of confirmed cases (COVID-19 Positive) reached twenty (20) out of 471 suspected cases, with the highest numbers in the Sindh province, accompanied by Gilgit Baltistan (Fawwad et al., 2022). The confirmed cases had recent travel records from Iran, Syria, and London (Memon et al., 2021). These cases escalate with excessive fees, and the situation worsens (Waris et al., 2020).

Pakistani authorities have taken different steps against the COVID-19 outbreak. The Pakistani government has implemented various measures to control the spread of the virus, including lockdowns, the use of face masks, and social distancing. In addition to this, other arrangements, such as designated hospitals, quarantine centres, isolation facilities, treatments, public attention, and the response of the local community towards the COVID-19 outbreak, have been implemented on time. As of September 2021, Pakistan had recorded over 1.2 million confirmed cases of COVID-19 and over 27,000 deaths (WHO, 2021). The highest number of cases was reported in the province of Sindh, followed by the Punjab and Khyber Pakhtunkhwa (Daniyal et al., 2020). The country has also witnessed a surge in cases during the pandemic, with a peak of over 7,000 cases per day in June 2021 (WHO, 2021).

To prevent the COVID-19 disease in Pakistan, various steps were implemented in different provinces over time, as shown in Table 2.1.

Table 2.1: Current mandate implementation 2022.

	Primary school closure	Secondary school closure	Higher school closure	Entry restrictions for some non-residents	Entry restrictions for all non-residents	Individuals movements restricted	Curfew for businesses	Individual curfew	Gathering limit: 6 indoor, 10 outdoor	Gathering limit: 10 indoor, 25 outdoor	Gathering limit: 25 indoor, 50 outdoor	Gathering limit: 50 indoor, 100 outdoor	Gathering limit: 100 indoor, 250 outdoor	Restaurants closed	Bars closed	Restaurants/bars closed	Restaurants/bars curbside only	Gyms, pools, and other leisure closed	Non-essential retail closed	Non-essential retail curbside only	Non-essential workplaces closed	Stay home order	Stay home fine	Mask mandate	Mask mandate fine
Azad Jammu & Kashmir																									
Baluchistan																									
Gilgit-Baltistan																									
Islamabad																									
Khyber Pakhunkhwa																									
Punjab																									
Sindh																									

Source: Institute for Health Metrics and Evaluation, 2022(covid19.healthdata.org)

	Mandate in place		No mandate
	Mandate in place (imposed this week)		No mandate (lifted this week)
	Mandate in place (updated from previous reporting)		No mandate (updated from previous reporting)

2.3.1 Facilitation by the Government of Pakistan against COVID-19

The government of Pakistan is taking all necessary measures to address COVID-19 and fulfill its obligations to its citizens. Following the confirmation of the first case in Sindh, the government has taken utmost measures to ensure the safety of lives, utilizing COVID-19 mitigation techniques in its efforts. Measures such as early case detection and tracing, monitoring of contacts, risk communication, social distancing, quarantine, and isolation are crucial to avoid the spread of COVID-19 (Saqlain et al., 2020).

In the preparations to combat COVID-19, many hospitals have been working to contain the lethal epidemic of COVID-19 in the country. An overview of such hospitals specific to COVID-19 treatment is exhibited in Figure 2.1.

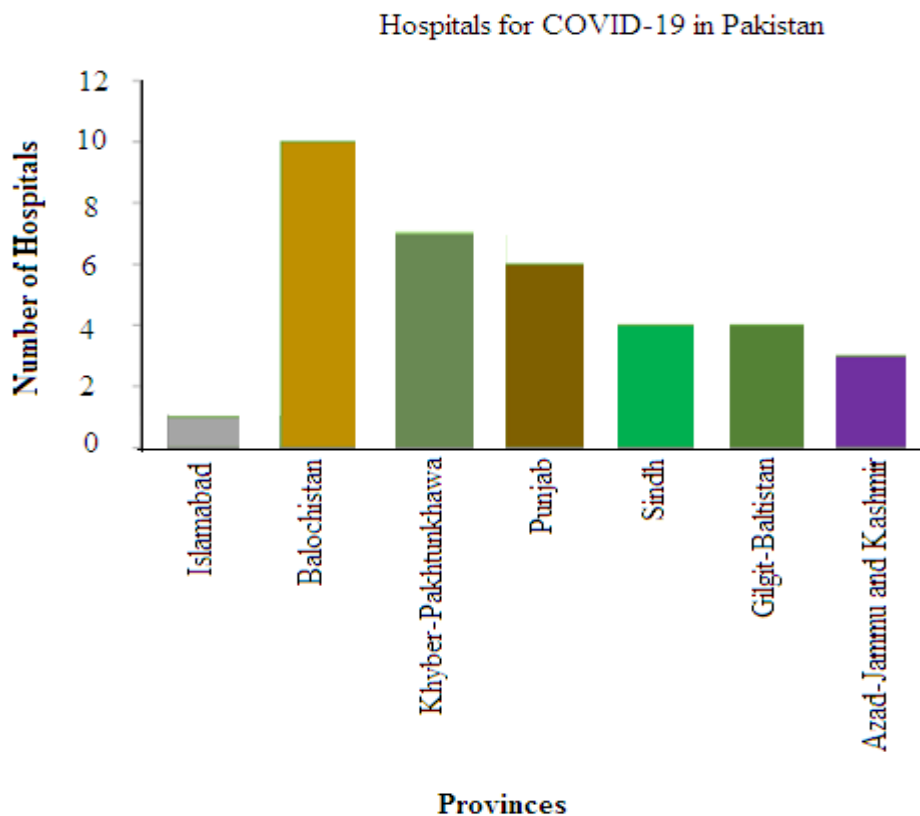


Figure 2.1: Number of hospitals for COVID-19 in Pakistan (Waris et al., 2020)

2.3.2 Province-wise hospitals with isolation wards for COVID-19 in Pakistan

Isolation, unlike quarantine, separates a sick or infected person from others to prevent the spread of infection or contamination. Hospitals used to isolate COVID-19 patients have been disrupted mainly in the provinces, evoking the excellent posture used to control the COVID-19 outbreak in Pakistan under such circumstances—the distribution of hospitals used for regional essential isolation (Khan et al., 2020). An overview of the number of medical facilities with the number of beds is revealed in Figure 2.2.

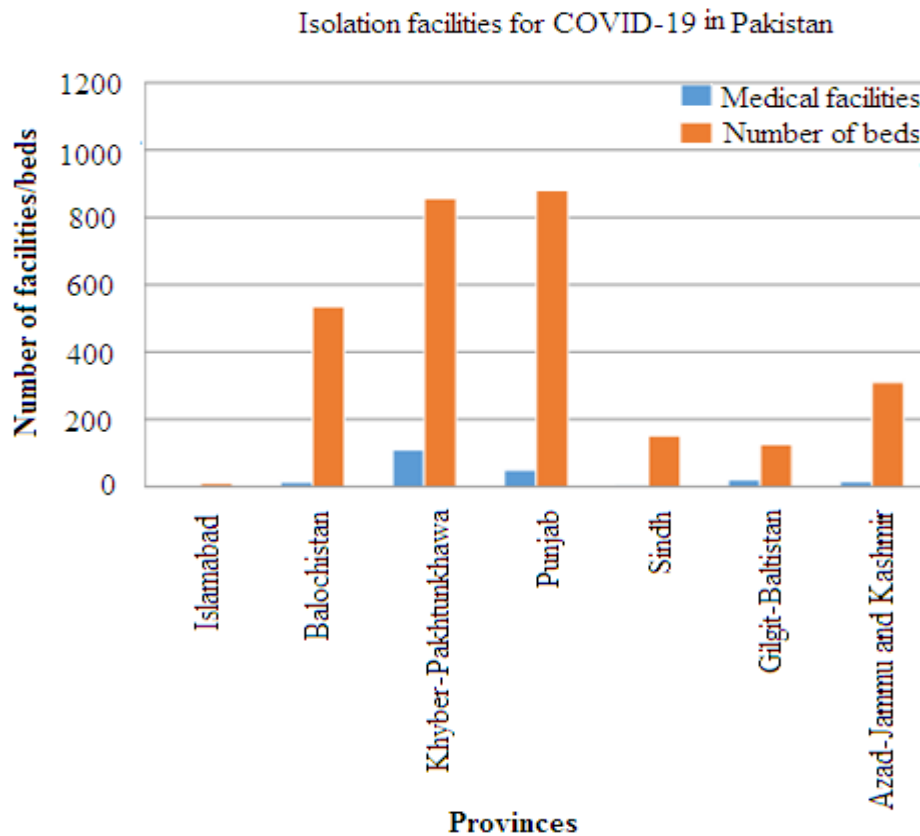


Figure 2.2: Hospitals with isolation wards Province-wise for COVID-19 in Pakistan
(Waris et al., 2020, Khan et al., 2020)

2.3.3 Province-wise quarantine Facilities for COVID-19 in Pakistan

Quarantine is used to limit the movement of people (in a non-healthcare facility) who are not yet sick but may have been exposed to COVID-19 to monitor symptoms and early

detection of cases. Facilities used by provinces to isolate people with COVID-19 have been extensively disrupted. A total of 23,557 quarantine measures have been implemented in 139 districts of Pakistan, reflecting the collective efforts across the country to control the COVID-19 outbreak. An overview of the number of quarantine facilities with the number of beds is revealed in Figure 2.3.

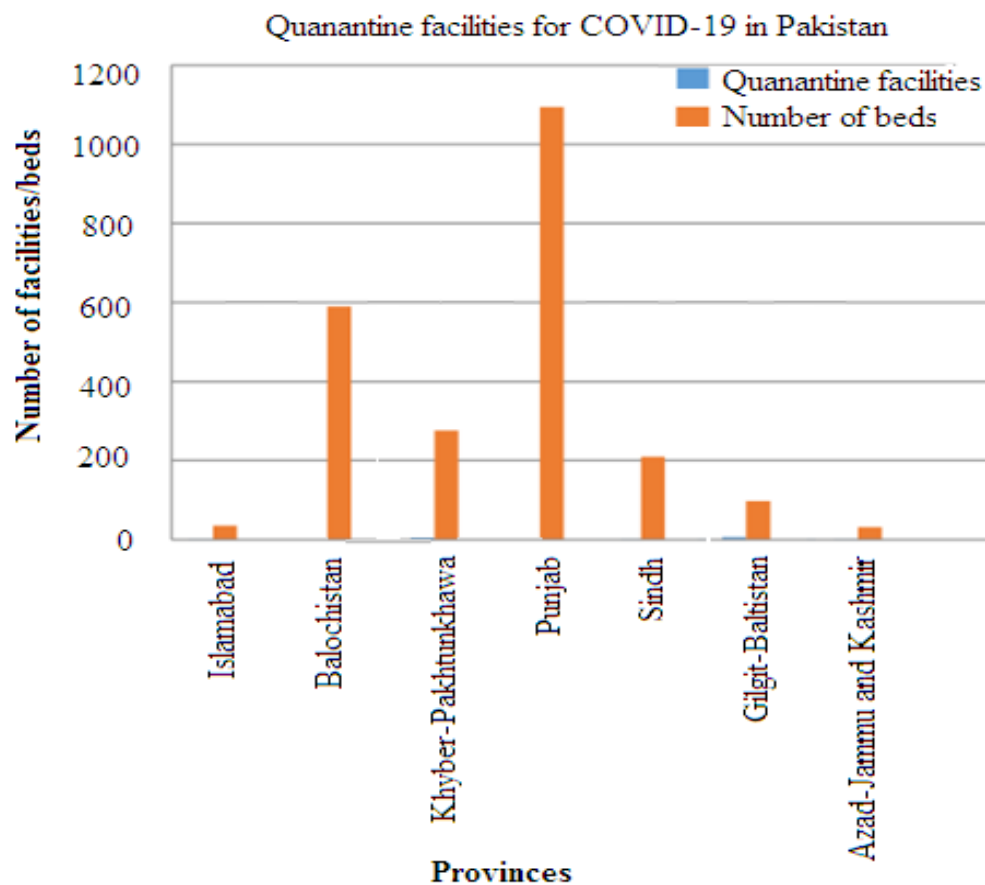


Figure 2.3: Quarantine Facilities Province-wise for COVID-19 in Pakistan (Waris et al., 2020; Khan et al., 2020)

2.3.4 Vaccination in Pakistan

Following the global rollout of vaccines from companies like Sinopharm, AstraZeneca, Pfizer, and Sinovac, as well as Moderna and Cansino, the number of active

cases and deaths decreased steadily. Pakistan used only three vaccines: Sinopharm, AstraZeneca, and Pfizer. The description of the vaccines that are used in Pakistan is given below.

2.3.4.1 Sinopharm Vaccine

The Sinopharm vaccine, also known as BBIBP-CorV, was developed by the China National Pharmaceutical Group (Sinopharm) in early 2020. This vaccine became a crucial part of Pakistan's COVID-19 vaccination campaign, with doses donated by China. Since February 2021, an initial 500,000 doses were administered, prioritizing frontline healthcare workers, followed by the elderly and other vulnerable populations in the country. The vaccine requires two doses per individual and has demonstrated an efficacy rate of nearly 79% in preventing symptomatic COVID-19 infections. Despite initial concerns about data transparency, the Sinopharm vaccine gained widespread acceptance as an essential tool in the fight against the pandemic. The rollout encountered challenges, including vaccine hesitancy and logistical issues. However, the availability of Sinopharm significantly enhanced Pakistan's efforts to lower severe cases and fatalities, playing a vital role in the country's public health response (Iftikhar et al., 2023).

2.3.4.2 AstraZeneca Vaccine

The AstraZeneca COVID-19 vaccine, also known as AZD1222, was developed by the University of Oxford in collaboration with AstraZeneca, a British-Swedish pharmaceutical company. The vaccine was first developed for use against COVID-19 in the United Kingdom. The development process began in early 2020. Pakistan initiated the AstraZeneca COVID-19 vaccine, locally known as Covishield, as part of its vaccination campaign in early 2021. Whereas, this vaccine reached Pakistan through COVAX, which

aims to provide equal access to COVID-19 vaccines worldwide. The introduction of the AstraZeneca vaccine in Pakistan marked a significant step in the country's efforts to combat the COVID-19 pandemic, complementing other vaccines like Sinopharm in the national immunization strategy (Hasan et al., 2023).

2.3.4.3 Pfizer Vaccine

The Pfizer-BioNTech COVID-19 vaccine was developed through a collaboration between Pfizer, an American pharmaceutical company, and BioNTech, a German biotechnology firm. BioNTech played a crucial role in the clinical trials for this vaccine. Pakistan began administering the Pfizer-BioNTech vaccine as part of its vaccination campaign in early 2021. Additionally, vaccines were provided to Pakistan through the COVAX initiative, which aims to ensure equitable access to COVID-19 vaccines globally. The introduction of the Pfizer-BioNTech vaccine in Pakistan marked a significant milestone in the country's efforts to combat the COVID-19 pandemic, complementing other vaccines like Sinopharm and AstraZeneca (Haider et al., 2023). By September 2021, over 65 million vaccine doses had been administered in Pakistan, with about 15% of the population fully vaccinated (Bukhari et al., 2022). As of December 2022, no provinces or territories had achieved a vaccination rate of 70% or higher for at least one dose, with 59% of the population fully vaccinated.

2.3.5 Vaccination Efficacy

The degree to which a vaccine offers protection against a particular illness or infection is referred to as vaccination effectiveness. It is an important measure that indicates how well a vaccine can prevent disease, reduce the severity of symptoms, and potentially prevent transmission of the pathogen. Effectiveness is typically determined through

meticulous clinical studies, where vaccinated individuals are alternative-treated controls. The vaccine's effectiveness percentage (%) is then determined by looking at the decrease in illness incidence or severity among the group that received the vaccination (Self et al., 2021).

To achieve effective population-level immunity and to stop the spread of infectious illnesses, high vaccination efficiency is necessary. It is important to remember that vaccination effectiveness might change depending on a person's age, health, and the availability of novel pathogen strains. Although a vaccine's effectiveness may be reduced against specific types, it can still provide significant protection and help minimize the risk of fatalities, serious outcomes, and hospitalizations. Continuous monitoring and research are essential in order to maintain and improve vaccination regimens' efficacy, especially in light of changing pathogens and new variations (Embi et al., 2021).

The vaccine uptake rate, also known as the vaccination rate, is calculated using the following formula (CDC Works 24/7, 2024).

$$\text{Vaccine Rate } (\omega) = \frac{\text{Number of vaccinated individuals}}{\text{Total population}} \times 100 \quad \text{Equation 2.1}$$

2.4 Overview of Mathematical Modelling of COVID-19

Similar to the modelling of other infectious diseases, mathematical modelling to predict the COVID-19 disease has also gained much attention—mathematical models designed to reflect the infection paths and predict how a specific disease will progress in time. Mathematical modelling is vital for COVID-19 for several reasons. Firstly, it can help policymakers and healthcare professionals make informed decisions about how to manage the pandemic. Secondly, by using mathematical models, one can predict how the virus might spread under different scenarios and determine the most effective interventions to prevent its spread.

According to (Kermack et al., 1927), the original mathematical description of the spread of infectious diseases in a population is the SIR model, which separates the whole population into three parts: Susceptible (S), Infected (I), and Removed (R) compartments. However, this model is only suitable for diseases against which people can obtain permanent immunity after a short period of infection and only for short durations of the latent stage. In the much more complicated case of COVID-19, the SEIR (Susceptible, Exposed, Infected, and Removed) model is assumed to be more appropriate. To further increase the model's fidelity, the STEQIR Model has been proposed (Gill et al., 2020). Here, T represents the population of traced close contacts with negative test results, and Q represents the population of traced exposed close contacts with positive test results who are undergoing quarantine and are isolated. This model advances the previous one by categorizing people into more detailed compartments to analyse complex situations. This study found that the Gill model effectively predicted the COVID-19 outbreak in Malaysia, which is similar to the practice in Pakistan.

According to the literature on Pakistan, there is no mathematical model in place; it appears that there is currently no single model that incorporates all the relevant factors related to COVID-19, such as the use of face masks, social distancing, and vaccination status (Rao et al., 2019). Additionally, they suggested the need for more models that effectively incorporate quarantine compartments to manipulate the challenges and factors of the COVID-19 disease.

Time series models, such as the Autoregressive Integrated Moving Average (ARIMA) and Seasonal Autoregressive Integrated Moving Average (SARIMA), have been widely used to statistically model time series data. The researchers have been using such models to forecast infectious disease trends (Allard et al., 1998). The ARIMA model is

preferred in this context because it is suitable for investigating the short-term effects of acute infectious diseases and fitting several trajectories (Wiley et al., 2002).

In addition, the ARIMA model is a practical and straightforward method that can produce reliable forecasts in situations with limited data. On the other hand, models like SIR (susceptible, infected, and recovered) and SEIR (susceptible, exposed, infected, and recovered) models tried to describe the dynamics of the evolution of COVID-19. Hangping Yao et al. (2020) developed a mathematical model that incorporates the stability theory of differential equations. The model is used to investigate the recent coronavirus disease (COVID-19) outbreak from 01 July 2020 to 14 August 2020 in Pakistan.

Ahmad et al. (2021) established a modified population model of susceptible and infected (SI) compartments to predict the spread of COVID-19 in Pakistan.

Fan et al. (2022) modelled COVID-19 infection using hospitalization, isolation, and quarantine compartments to present the cases of COVID-19 in the Pakistani population. Based on their simulations, they estimated the submerged parameters of the COVID-19 model with nonlinear least squares. The study suggests that without quarantine and hospitalization, the disease scenario in Pakistan was significantly worse, and the number of infected cases was rising rapidly.

Koufi et al. (2022) presented a stochastic-based differential equations SEIAR (Susceptible, Exposed, Infected, Asymptomatic Infected, and Recovered) model to study the dynamics of COVID-19 in Pakistan. The confirmed power of randomness to reduce the number of infected people with COVID-19 by comparing the results with the analogous deterministic model.

A mechanism for the timely and equitable distribution of COVID-19 vaccination among the various communities in Pakistan has been explored. The results show that "hesitancy" and "inequality" are two fundamental challenges that hinder the successful delivery of COVID-19 vaccination in Pakistan (Dhama et al., 2020, and Perveen et al., 2022).

The investigation of the spread of coronavirus in Pakistan is done by developing a SEIR time fractional model with the newly developed fractional operator of Atangana–Baleanu (AB) Azeem et al. (2021) considered short-term data retrieved from WHO from 19 March 2020 to 31 March 2020 and calculated the primary reproduction number to be $R_0=2.30748$ which shows that the virus was spreading rapidly during that period. Similarly, many other studies (Bushey et al., 2023; Ansari et al., 2023; Swadling et al., 2022; Uzair Ali et al., 2022) can be found that focus on various aspects of modelling COVID-19.

Various mathematical models have been employed to understand the dynamics of COVID-19 transmission in Pakistan, drawing insights from multiple studies and initiating the exploration using the SIR model, followed by (Ahmad et al. 2020), who introduced the SEIR fractional model, providing a more enhanced perspective on the epidemic. Subsequently, (Peter et al. 2021) expanded upon these foundations by developing a new mathematical model based on actual data from Pakistan, contributing to a deeper understanding of the local epidemiological situation. Naik et al. (2020) further enhanced the modeling framework by integrating the treatment dynamics using fractional derivatives, offering valuable insights into the impact of interventions. Li et al. (2021) contributed to the discourse with a dynamic study focusing on the third wave of the pandemic, enriching the understanding of temporal patterns. (Bhattacharjee et al. 2023) undertook a comparative analysis of various epidemiological models, providing valuable insights into their respective strengths and limitations. Gomez et al. (2023) introduced a model by incorporating migration

dynamics and a nonlinear incidence function, representing a significant advancement in epidemic modeling methodologies. These diverse studies collectively contribute to a comprehensive understanding of COVID-19 transmission dynamics, informing effective disease control and mitigation strategies in Pakistan and beyond.

A comprehensive literature review summary is presented in the following Table 2.2, which enlists the report's findings of studies that looked at human behavior, effects of lockdowns, social distancing, face masks, and other factors of COVID-19 data. Moreover, Table 2.2 also reviews the different aspects of the mathematical modelling of COVID-19 disease in Pakistan. The discussion focuses on the effects of vaccination compartments used in mathematical modelling by various researchers to mitigate the risk of COVID-19 cases in Pakistan.

Table 2.2: List of the reviews of the mathematical modelling of COVID-19.

No.	Year	Author	Title	Remarks
1	2020	(Ndairou et al., 2020).	Mathematical modelling of COVID-19 transmission dynamics with a case study of Wuhan.	SEIPAHRF model fits the current scenario using Wuhan data from March 26 to April 8, 2020.
2	2020	(Gill et al., 2020)	Modelling the Effectiveness of Epidemic Control Measures in Preventing the Transmission of COVID-19 in Malaysia.	MCO measures reduce peak COVID-19 cases by 99.1% using Malaysian data from January 25 to March 17, 2020.
3	2020	(Zeb et al., 2020)	Mathematical Model for Coronavirus Disease 2019 (COVID-19) Containing Isolation Class.	The SEIQR model shows that isolating infected individuals reduces COVID-19 spread, using US data from February 10 to April 2020.
4	2020	(Khoshnaw et al., 2020)	Mathematical modelling for coronavirus disease (COVID-19) in predicting future Behavior's and sensitivity analysis.	Reducing infected cases and preventing the wider spread of coronavirus using Iraq data from January to March 2020.

Table 2.2 continued

5	2020	(Naik, et al., 2020)	Modelling and analysis of COVID-19 epidemics with treatment in Fractional derivatives using real data from Pakistan.	Best-fitted parameter values were achieved using Pakistan data from January 10 to February 17, 2020.
6	2020	(Dhama et al., 2020)	COVID-19, an emerging coronavirus infection: advances and prospects in designing and developing vaccines, immunotherapeutic and therapeutics.	No effective vaccines or antivirals for COVID-19; robust preventive measures needed due to nosocomial infection risk.
7	2020	(Ilyas et al., 2020)	COVID-19 Pandemic in Pakistan.	Low literacy and awareness lead to non-compliance with social distancing and hand hygiene, based on Pakistan data from June-July 2020.
8	2020	(Shah et al., 2020)	Predicting COVID-19 Spread in Pakistan using the SIR Model.	Pakistan's 22 million population is at risk, with a predicted COVID-19 recovery rate of up to 98%, based on data from January 20 to February 9, 2020.
9	2020	(Ahmed et al., 2020)	A report on the COVID-19 epidemic in Pakistan using SEIR fractional model.	The SEIR model indicates a high COVID-19 spread in Pakistan compared to the initial days, with $\alpha=1$, based on data from March 19 to 31, 2020.
10	2020	(Li et al., 2020)	A dynamical study of SARS-COV-2: A study of third wave.	SEIARD model: Parameters δ and ψ can reduce third-wave infections in Pakistan (March 6 to April 30, 2021).

Table 2.2 continued

11	2021	(Peter et al., 2021)	A new mathematical model of COVID-19 using real data from Pakistan. SEIQR model best-fits parameters μ , δ , and σ using Pakistan data from July 1 to August 14, 2020.	
12	2021	(Dashtbali et al., 2021)	A compartmental model that predicts the effect of social distancing and vaccination on controlling COVID-19.	Social distancing and vaccine coverage effectiveness were analysed using data from Japan, Italy, Belgium, Germany, Nigeria, and Egypt (January 22 to June 23, 2020).
13	2021	(Arfan et al., 2021)	Investigation of Fractal-Fractional order model of COVID-19 in Pakistan under Atangana-Baleanu Caputo (ABC) derivative	Following WHO SOPs, such as wearing masks and maintaining social distancing, can help curb COVID-19 spread, as evidenced by Pakistan's data from March 1, 2020, to July 2021.
14	2021	(Oud et al., 2021)	A fractional-order mathematical model for COVID-19 dynamics with quarantine, isolation, and environmental viral load.	Reducing viral release lowers disease burden, as evidenced by Pakistan data from March 1 to June 30, 2020.
15	2021	(Babbar et al., 2022)	Response of educational institutions to COVID-19 pandemic: An inter-country comparison.	Explore global education modes and government measures during crises, based on Pakistan data from March 1 to June 30, 2020.
16	2022	(Babbar et al., 2022)	Stochastic differential equation model of COVID-19: A case study of Pakistan.	Investigate white noise and stochastic models with random effects of COVID-19, using Pakistan data from October 12, 2021, to December 2022.

Table 2.2 continued

17	2022	(Parveen et al., 2022)	Vaccination-hesitancy and Vaccination-inequality as challenges in Pakistan's COVID-19 response.	"Hesitancy" and "inequality" hinder COVID-19 vaccination in Pakistan; community mobilization and social distancing are needed (December 14, 2020, to January 27, 2021).
18	2022	(Taimoor et al., 2022)	COVID-19 pandemic data modelling in Pakistan using time-series SIR.	Only respiratory cases are considered; the SIR model shows comparable data, while the pSIR model (uniform distribution) is unreliable; the 14-day assumption is unsuitable for Pakistan.
19	2023	(Ahmad,et al., 2023)	COVID-19 in Pakistan: A national analysis of five pandemic waves.	In Pakistan (April 3, 2020, to February 23, 2022), a 1% increase in vaccinations reduced deaths by 0.38% (95% CI: -0.67, -0.08) in wave 5, with statistical significance.
20	2023	(Kubra & Ali, 2023)	Modeling and analysis of novel COVID-19 outbreak under fractal-fractional derivative in Caputo sense with power-law: a case study of Pakistan.	Examined COVID-19 using a fractal fractional derivative model with a power law kernel, based on Pakistan data from June 1, 2020, to March 8, 2021.
21	2023	(Naeem et al., 2023)	Soft computing techniques for forecasting of COVID-19 in Pakistan.	ANN, KF, LSTM, and SVM models applied to COVID-19 data in Pakistan (January 22, 2020, to August 18, 2021) showed increasing cases.
22	2024	(Zia et al., 2024)	Elucidating Severity of Waves of COVID-19 in Pakistan.	Analysis of four waves shows a strong correlation between reported cases, deaths, and testing capacity, emphasizing the need for vaccination.

Table 2.3: List of reviews of the mathematical modelling with vaccination of COVID-19.

No.	Year	Author	Title	Remarks
1	2021	(Yavuz et al., 2021)	A new mathematical modelling of the COVID-19 pandemic including the vaccination campaign.	Examined vaccination effectiveness and aspects, including biological feasibility and solution boundedness, using data from January 10 to February 17, 2020.
2	2022	(Haq et al., 2022)	A new mathematical model of COVID-19 with quarantine and vaccination.	Graphical analysis shows vaccination and quarantine significantly reduced infections; without these measures, infections increased rapidly.
3	2022	(Ali et al., 2022)	The impact of vaccination on the modelling of COVID-19 dynamics: a fractional order model.	A study shows reducing contact rate (up to 30%) and increasing vaccination (up to 50%) significantly cut new infection cases, based on data from March 1 to July 31, 2020.
4	2022	(Khan et al., 2022)	Optimal control analysis of COVID-19 vaccine epidemic model: a case study.	The model, using data from March 1 to June 30, 2021, simulates vaccination strategies and control measures' impact on COVID-19 eradication in Pakistan.
5	2023	(Sun et al., 2023)	Mathematical modelling of COVID-19 with vaccination using fractional derivative: a case study.	The study finds vaccination an effective control measure, with higher rates and efficacy leading to reduced future cases.
6	2023	(Bhatter et al., 2023)	A new fractional mathematical model to study the impact of vaccination on COVID-19 outbreaks.	Study (August 1, 2021 - July 21, 2022) shows increasing vaccine uptake is key to controlling disease, reducing transmission, and improving treatment.
7	2024	(Mustapha et al., 2024)	Mathematical Modelling of COVID-19 with Vaccination, Quarantine and Non-Pharmaceutical Interventions.	Effective vaccination and non-pharmaceutical interventions are crucial to preventing or curtailing COVID-19.

From the review of previous studies; it could be deduced that the mathematical modeling emerged as a vital tool for policymakers, providing insights into potential outbreak trajectories, evaluating the effectiveness of non-pharmaceutical interventions (NPIs), and planning resource allocation. The models applied in Pakistan largely mirror global trends but are adapted to the local context. The utility of these models was severely constrained by several interconnected limitations such as; effectiveness of early lockdowns in flattening the curve and delaying the first peak, the smart lockdown strategy that caused imbalance in public health and economic needs, high Impact of Non-Pharmaceutical Interventions (NPIs) that highlighted that a combination of NPI and vaccination rollout since the later models focused on vaccination, demonstrating that the speed and coverage of the rollout were more critical than the specific vaccine efficacy in preventing deaths and overwhelming hospitals. Moreover, the utility of COVID-19 models was severely constrained by several interconnected limitations such as, the data quality and availability that remained a primary constraint for the COVID-19 modeling efforts in Pakistan. Among the many other limitations of COVID-19 modeling the homogeneity assumptions, static parameters, lack of economic integration, operational and policy challenges were also remained the barrier in the COVID-19 modeling in Pakistan.

The literature also reveals that numerous studies have been conducted to analyze and predict the behavior of COVID-19 in Pakistan. However, adopting sophisticated models presents a drawback in that their identification is challenging, particularly during the initial outbreak when prompt decisions must be made. For instances, incomplete and inaccurate data limitations that may change under the testing policies; assumptions and simplification of COVID-19 model parameters; uncertainty and sensitivity of model parameters can lead to significant deviations; dynamic and evolving nature of the pandemic that can disrupt

model projections, model complexity may fit past data well but future data may difficult to interpret; finally, human behavior may affect the COVID-19 models reliability. That is the primary motivation for adopting a minimal model to describe COVID-19 transmission in Pakistan specifically by elaborating the effect of vaccination factor. Such a model can be achieved by making some modifications to Gill et al. (2020), specifically by introducing the Vaccination compartment and adjusting a few interaction parameters. The problem can be formulated based on a time-varying SVEIR model, which facilitates the reproduction of the disease's dynamic evolution with fewer parameters and accounts for the continually changing suppression measures employed by the Pakistani government. To maintain mathematical simplicity in formulation, the significant epidemiological factors that arise over extended periods, such as the loss of immunity following recovery, reinfection, the impact of vaccinations, and virus variations, may be incorporated.

2.5 Summary

This Chapter has provided the history of the COVID-19 disease and its global impact. It highlighted the significance of disease modelling in understanding and controlling the spread of COVID-19. The Chapter mainly discusses the current scenario of COVID-19 in Pakistan, which includes the range of confirmed cases and deaths. Diverse mathematical models and techniques used to examine COVID-19 in Pakistan are reviewed. The need for a comprehensive model incorporating vaccination and control interventions is highlighted. Chapter 3 will attempt to present and demonstrate the methodology to achieve the objectives of this thesis.

CHAPTER 3

RESEARCH METHODOLOGY

3.1 Overview

In this chapter, a concise methodology is presented to achieve the aim and objectives of the proposed research. An organized methodological process is followed. To propose and formulate a new model, an existing analogous model known as STEqIqIR or STEQIR (Gill et al., 2020) will first be evaluated. Based on this evaluation, and through the use of compartmental analysis and the incorporation of a control intervention (vaccination), the SVEIR model will be developed. Key properties relevant to the proposed model will also be discussed. The interpretation of various parameters involved in the model will be presented simultaneously. The possibility of obtaining an analytical solution for the proposed model will be explored, followed by the presentation of a numerical solution strategy.

To derive a realistic solution, parameter values will be calibrated or estimated using available data and literature. Finally, performance metrics and the model's goodness of fit will be defined. The proposed model will be validated by comparing its results for the Pakistan scenario with those obtained from the existing STEQIR model (Gill et al., 2020). A summary of the chapter will be provided at the end.

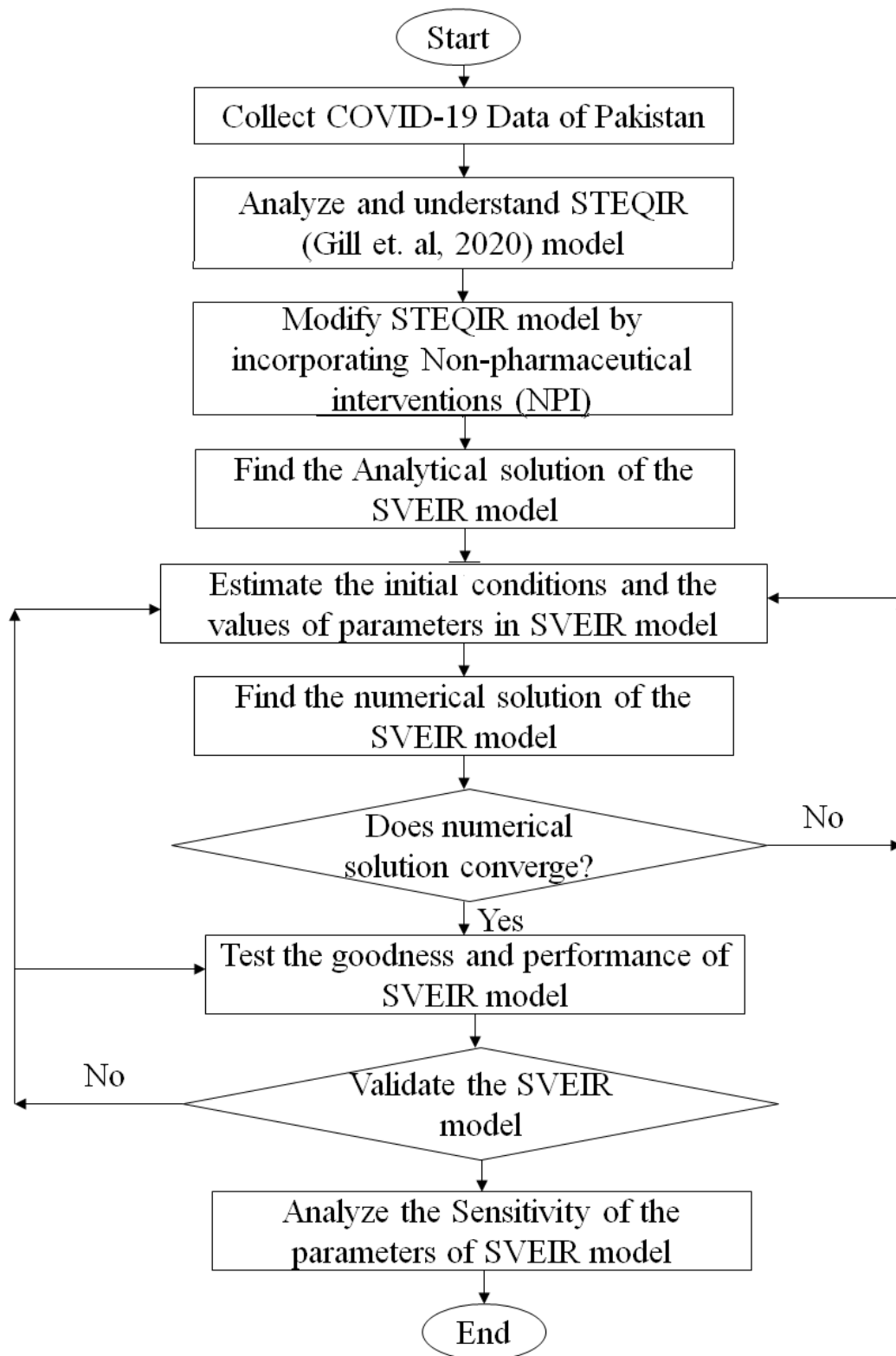


Figure 3.1: The research methodology process flow chart

3.2 Evaluation of the Gill Model

The model proposed by Gill et al. (2020) is highly relevant and serves as a suitable example for understanding disease dynamics. Moreover, the Gill et al. (2020) model incorporates essential factors such as quarantine, isolation, and social distancing measures strategies actively employed by health authorities in Pakistan and other countries around the world. This model has demonstrated its reliability and applicability in previous research on infectious diseases, making it a valuable tool for exploring the complexities of COVID-19, particularly in contexts similar to Pakistan. Its potential to generate insights into key parameters, such as the basic reproduction number (R_0) and disease outcomes, supports its use in guiding public health policies and interventions.

The model by Gill et al. (2020), which is based on Malaysian data, serves as our base model. The interactions among the different dependent variables S, T, E, E_q , I_q , I, and R are illustrated through a compartmental diagram, as shown in Figure 3.2 below.

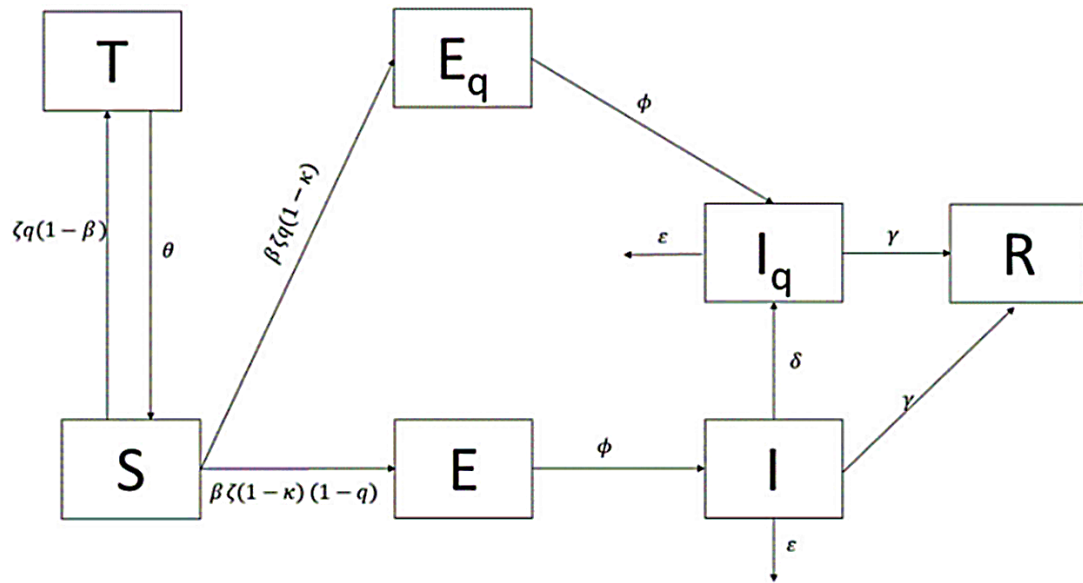


Figure 3.2: The (Gill et al., 2020) model for COVID19 disease considered for Malaysia

Similarly, the interactions among the dependent variables can be expressed mathematically as a system of non-linear ordinary differential equations (Equations 3.1-3.7) as follows,

$$\frac{dS}{dt} = \theta T - \frac{\beta \xi q(1-\kappa)SI}{N} - \frac{\beta \xi(1-q)(1-\kappa)SI}{N} - \frac{\xi q(1-\beta)SI}{N}, \quad \text{Equation 3.1}$$

$$\frac{dT}{dt} = \frac{\xi q(1-\beta)SI}{N} - \theta T, \quad \text{Equation 3.2}$$

$$\frac{dE}{dt} = \frac{\beta \xi(1-q)(1-\kappa)SI}{N} - \phi E, \quad \text{Equation 3.3}$$

$$\frac{dI}{dt} = \phi E - \varepsilon I - \delta I - \gamma I, \quad \text{Equation 3.4}$$

$$\frac{dE_q}{dt} = \frac{\beta \xi q(1-\kappa)SI}{N} - \phi E, \quad \text{Equation 3.5}$$

$$\frac{dI_q}{dt} = \phi E_q + \delta I - \gamma I_q - SI_q, \quad \text{Equation 3.6}$$

$$\frac{dR}{dt} = \gamma I + I_q, \quad \text{Equation 3.7}$$

where S is the susceptible population, T is the negative test result population, E is the exposed population, and I is the infected population, E_q is the positive test result population undergoing quarantine, I_q is the infected isolated population, and R is the recovered population. Moreover, the description of other auxiliary parameters is given in Table 3.1:

Table 3.1: List of the parameters used in Equation 3.1-3.7 and their description

Parameters	Description
N	Total human population in Pakistan
$1/\phi$	Incubation Period
β	The probability of susceptibility becoming infectious per contact
$1/\gamma$	Infectious period
ε	The death rate due to COVID-19
ξ	The average number of contacts per day per case
q	The proportion of close contact traced per day
δ	The mean daily rate at which infectious cases are isolated
θ	The duration of quarantine
κ	The proportion of exposed persons who performed effective precautions

In light of the ongoing pandemic, the development of a suitable mathematical model for predicting the spread of COVID-19 has become increasingly important. Previous studies have explored various factors affecting transmission rates and the number of infected individuals. In this study, an improved mathematical model that considers five variables, viz. Susceptible (S), Vaccination (V), Exposed (E), Infected (I), and Recovered (R) are proposed.

3.3 Formulation of SVEIR Model

Since the main objective of this study was to propose a mathematical model by incorporating the control intervention or using the vaccine compartment. Therefore, this study introduces an innovative mathematical model for COVID-19 by considering the five variables: Susceptible (S), Vaccinated (V), Exposed (E), Infected (I) and Recovered (R); in short (the SVEIR model). The compartmental diagram of the proposed model, which is based on the COVID-19 data of Pakistan. The transition from the Susceptible (S) compartment to the Vaccinated (V) compartment is modulated by τ , which signifies people in the vulnerable group who start receiving a vaccination rate, and ω indicates the vaccine wane rate. Conversely, it is an individual's transition from the Vaccinated (V) that moves towards the Susceptible (S) compartment. The shifting from Susceptible (S) towards Exposed (E) involves β , which represents the probability of susceptibility becoming infectious per contact, as well as the average number of contacts per day per contact which is denoted by ξ . Progression from the Exposed (E) towards the Infected (I) compartment is denoted by ϕ . That indicates the incubation period. The recovered (R) compartment emerges from the Infected (I) compartment due to γ that shows the infectious period. At the same time, ε and δ contribute to individuals exiting the Infected chamber (I), signifying the recovery rate and the rate at which infectious cases are isolated, respectively. These parameters collectively dictate the dynamics of individuals within and transitioning between compartments in the compartmental model.

Additionally, μ plays a pivotal role in various transitions, accounting for natural deaths among different groups. When modelling mortality (deaths), μ is often used in conjunction with other parameters or as a part of the equation to determine the rate at which individuals transition from compartments like I (Infected) or R (Recovered) compartments.

The specific usage of μ this model depends on the mortality component of this model's equations. Furthermore, the numerical values of parameters can be obtained by using Equations 3.9-3.14 with the help of R-studio on the basis of information obtained from the Pakistan Bureau of Statistics (PBS), Ministry of National Health Services, Regulation and Coordination (MoNHSRC).

After observing the appropriate fit parameter values, there is a need to formulate an improved mathematical model that focuses on Pakistan's current scenario. This research replaces the traced close-contact and a negative test result population (T) compartment with the Vaccinated (V) compartment, as shown in Figure 3.3.

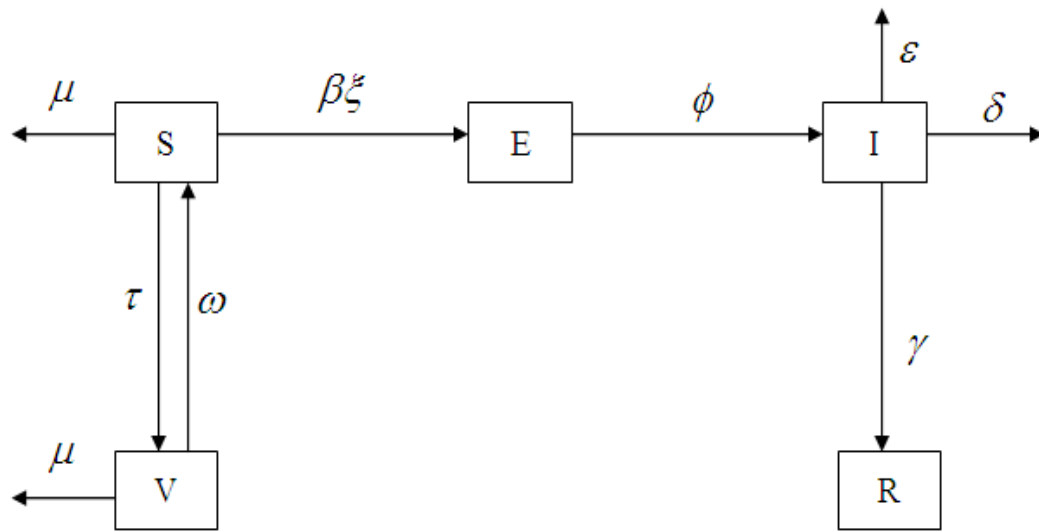


Figure 3.3: The extended Susceptible (S), Vaccinated (V), Infected (I), Exposed (E), and Recovered (R) model depicts the control measures taken in Pakistan

By comparing the above compartment model and the Gill et al. 2020 model, the scenario can be represented as a system of non-linear ordinary differential equations as follows,

$$\frac{dS}{dt} = (\mu + \omega)V - \frac{\beta\xi SI}{N} - \tau S, \quad \text{Equation 3.8}$$

$$\frac{dV}{dt} = \tau S - (\mu + \omega)V, \quad \text{Equation 3.9}$$

$$\frac{dE}{dt} = \frac{\beta\xi SI}{N} - \varphi E, \quad \text{Equation 3.10}$$

$$\frac{dI}{dt} = \varphi E - \varepsilon I - \delta I - \gamma I, \quad \text{Equation 3.11}$$

$$\frac{dR}{dt} = \gamma I. \quad \text{Equation 3.12}$$

The description of the different interaction parameters involved in the above SVEIR model is listed in Table 3.2.

Table 3.2: List of the parameters and their description

Parameters	Description
N	Total human population in Pakistan
$1/\phi$	Incubation Period
β	The probability of susceptibility becoming infectious per contact
$1/\gamma$	Infectious period
ε	The death rate due to COVID-19
ξ	The average number of contacts per day per case
τ	People in the vulnerable groups receiving vaccination rates
μ	Natural death rate (constant for all classes)
ω	Vaccine wane rate
δ	The mean daily rate at which infectious cases are isolated

In the above formulated SVEIR model Equations (3.8-3.12), the vaccination acts as a control lever that can be adjusted to reduce the spread of the virus. In the model, it does several key things, for example, it moves individuals from Susceptible to a Protected Group. A certain number of people from the S compartment are moved directly into the V compartment at a rate determined by the vaccination campaign's speed and coverage. In this way, the outcome of vaccine intervention will lead to lower peak prevalence, delay and flatten the epidemic curve, reduce total attack rate, and herd immunity threshold.

3.3.1 Estimation of the Values of the Parameters

The selection of parameters in COVID-19 models is a crucial step because it determines how well the model reflects reality. Parameters are typically chosen or estimated through a combination of theory, clinical/epidemiological evidence, and data fitting. However, in this study, the estimation of the parameters involves one of the many techniques; in a simple case, the values can be directly obtained from the population data and relevant COVID-19 data. The data should be valid for the target demographic and period. The estimation can also be based on the body of current literature or professional expertise for the model parameters. The process of estimating the parameters will begin with these first estimations.

Other methods, such as Maximum Likelihood Estimation (MLE), Least Squares Estimation (LSE), and iterative methods, are appropriately used depending on the model, data, and applications. For the case of Pakistan, Table 3.3 provides the estimated values of the parameters used in Equations 3.7-3.12.

Table 3.3: List of the parameters and their corresponding values used in the model simulation

Parameters	Description	Value	Source
N	Total human population in Pakistan	235,824,862	(PBS2022)
$1/\phi$	Incubation Period	0.1	Estimated using the data
β	The probability of susceptibility becoming infectious per contact	0.273	Calibrated using data
$1/\gamma$	Infectious period	1/6.5	Calibrated using data
ε	The death rate due to COVID-19	0.25	Estimated
ξ	The average number of contacts per day per case	30	Calibrated using data
τ	People in the vulnerable groups are receiving vaccination rates	1.0	Calibrated using data
μ	Natural death rate (constant for all classes)	0.8408	Calibrated using data
ω	Vaccine wane rate	1.0	Calibrated using data
δ	The mean daily rate at which infectious cases are isolated	0.039	Fitted using LSE

3.3.2 Analytical Solution of SVEIR Model

The above model (Equations 3.7 to 3.12) is based on the mathematical modeling theories for disease epidemics (Coccia, 2023), whereas, for the endemic equilibrium state, it must have $\frac{dS}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = 0$. Therefore, assuming initially that the population attains disease-free equilibrium as $(S(0), E(0), I(0), R(0)) = (N, 0, 0, 0)$, then $S/N=1$. For the disease to spread in the population, $I > 0$, resulting in $\beta S - (\delta + \gamma + \varepsilon) > 0$. Comparing the thin inequality with the definition of the basic reproductive number, R_0 , this can be defined as follows,

$$R_0 = \frac{\beta\xi}{(\delta + \gamma + \varepsilon)}. \quad \text{Equation 3.13}$$

Accordingly, the vaccinated reproductive number (R_{vac}) is obtained through the SVEIR Model using the Next Generation Matrix (NGM). The vaccination reproduction number represents the number of secondary cases that can arise from a single infected individual in a completely susceptible population, considering the effect of vaccination. The following Equation 3.14 gives the formula for calculating the (R_{vac}),

$$R_{vac} = \frac{\theta\beta(1-\psi\xi)}{(\theta + \mu)(\alpha I + \delta I + \lambda I + \mu)}(S^* + \omega V^*), \quad \text{Equation 3.14}$$

where θ is the duration of quarantine, ψ is vaccine efficacy, α is the effectiveness of the vaccine in reducing susceptibility, λ is the force of infection, S^* and V^* Are the endemic equilibrium points of Susceptible and Vaccinated, respectively. It is also noteworthy to mention that if $R_{vac} > 1$, the epidemic is likely to increase exponentially, indicating a higher transmission potential, and if $R_{vac} < 1$, the epidemic is expected to reduce over time.

The endemic equilibrium points for the dependent variables exist when $R_0 > 1$. Suppose that $X^* = (S^*, V^*, E^*, I^*, R^*)$ is the endemic equilibrium point of the model (Equations 3.7-3.12), then X^* can be computed by taking all derivatives of the equations and equating them to zero as described below:

$$(\mu + \omega)V^* - \frac{\beta\xi S^* I^*}{N} - \tau S^* = 0, \quad \text{Equation 3.15}$$

$$\tau S^* - (\mu + \omega)V^* = 0, \quad \text{Equation 3.16}$$

$$\frac{\beta\xi S^* I^*}{N} - \phi E^* = 0, \quad \text{Equation 3.17}$$

$$\phi E^* - \varepsilon I^* - \delta I^* - \gamma I^* = 0, \quad \text{Equation 3.18}$$

$$\gamma I^* = 0. \quad \text{Equation 3.19}$$

Solving the Equations 3.15 to 3.19, the following expressions for X^* are obtained,

$$S^* = \frac{N(\mu + \omega)V^* - \beta\xi I^* S^*}{N\tau} \quad \text{Equation 3.20}$$

$$V^* = \frac{\tau S^*}{(\mu + \omega)}, \quad \text{Equation 3.21}$$

$$E^* = \frac{\beta\xi S^* I^*}{\phi N}, \quad \text{Equation 3.22}$$

$$I^* = \frac{\phi E^* - \varepsilon I^* - \delta I^*}{\gamma}, \quad \text{Equation 3.23}$$

$$R^* = 0. \quad \text{Equation 3.24}$$

The SVEIR model (Equations 3.7 to 3.12) consists of a non-linear set of ordinary equations that appears to be highly difficult for analytical solution. However, an attempt was made to find a possible analytical solution using Maple software, a symbolic computer algebra system. However, the expressions computed by Maple do not make any sense. The following Equations 3.25 to 3.29 are the analytical expressions for the SVEIR model, where Equation 3.25 is an implicit relation for the S variable, and the other four variables are explicit relations for V, E, I, and R, respectively. It shows that, due to the implicit nature of the variable S, the other variables cannot be evaluated, particularly. Therefore, the analytical solution for the SVEIR is quite impractical.

$$\begin{aligned} & -\left(\frac{d}{dt}S(t)\right)\beta\xi S(t)^3\phi + {}_{C_3}e^{\tau iS(t)(\mu+\omega)}\mu\beta\xi S(t)^3\phi + {}_{C_3}e^{\tau iS(t)(\mu+\omega)}\omega\beta\xi S(t)^3\phi - \phi^2S(t)^4\beta\xi - \\ & \tau S(t)^4\beta\xi\phi + \left[N\varepsilon S(t)\left(\frac{d^2}{dt^2}S(t)\right) + N\left[\frac{d^2}{dt^2}S(t)\right]_{C_3}e^{\tau iS(t)(\mu+\omega)}\mu + N\left[\frac{d^2}{dt^2}S(t)\right]_{C_3}e^{\tau iS(t)(\mu+\omega)}\omega - \end{aligned}$$

$$\begin{aligned}
& N\varepsilon S(t) - C_3 \tau S(t)(\mu + \omega) e^{\tau i S(t)(\mu + \omega)} \mu - N\varepsilon S(t) - C_3 \tau S(t)(\mu + \omega) e^{\tau i S(t)(\mu + \omega)} \omega - \\
& N\delta S(t)_{C_3 \tau S(t)(\mu + \omega) e^{\tau i S(t)(\mu + \omega)} \mu} - N\delta S(t) - C_3 \tau S(t)(\mu + \omega) e^{\tau i S(t)(\mu + \omega)} \omega - \\
& N\gamma S(t)_{C_3 \tau S(t)(\mu + \omega) e^{\tau i S(t)(\mu + \omega)} \mu} - N\gamma S(t)_{C_3 \tau S(t)(\mu + \omega) e^{\tau i S(t)(\mu + \omega)} \omega} + 2N\varepsilon S(t) \tau \left(\frac{d}{dt} S(t) \right) + \\
& 2N\delta S(t) \tau \left(\frac{d}{dt} S(t) \right) + 2N\gamma S(t) \tau \left(\frac{d}{dt} S(t) \right) + N\varepsilon \left(\frac{d}{dt} S(t) \right)^2 + N\delta \left(\frac{d}{dt} S(t) \right)^2 + \\
& N\gamma \left(\frac{d}{dt} S(t) \right)^2 - N\varepsilon \left(\frac{d}{dt} S(t) \right)_{C_3 e^{\tau i S(t)(\mu + \omega)} \omega} - N\delta \left(\frac{d}{dt} S(t) \right)_{C_3 e^{\tau i S(t)(\mu + \omega)} \mu} - \\
& N\delta \left(\frac{d}{dt} S(t) \right)_{C_3 e^{\tau i S(t)(\mu + \omega)} \omega} - N\gamma \left(\frac{d}{dt} S(t) \right)_{C_3 e^{\tau i S(t)(\mu + \omega)} \mu} - \\
& N\gamma \left(\frac{d}{dt} S(t) \right)_{C_3 e^{\tau i S(t)(\mu + \omega)} \omega} + 2_{C_2 \beta \xi S(t) \phi} \left(\frac{d}{dt} S(t) \right) - \\
& N\varepsilon \left(\frac{d}{dt} S(t) \right)_{C_3 e^{\tau i S(t)(\mu + \omega)} \mu} - NS(t)_{C_3 \tau^2 S(t)(\mu + \omega)^2 e^{\tau i S(t)(\mu + \omega)} \mu} - \\
& NS(t)_{C_3 \tau^2 S(t)(\mu + \omega)^2 e^{\tau i S(t)(\mu + \omega)} \omega} - N \left(\frac{d}{dt} S(t) \right) \left(\frac{d^2}{dt^2} S(t) \right) + NS(t) \left(\frac{d^3}{dt^3} S(t) \right) + \\
& N\delta S(t) \left(\frac{d^2}{dt^2} S(t) \right) + N\gamma S(t) \left(\frac{d^2}{dt^2} S(t) \right) S(t) - 2(N\varepsilon S(t) \left(\frac{d}{dt} S(t) \right) + N\delta S(t) \left(\frac{d}{dt} S(t) \right) + \\
& N\gamma S(t) \left(\frac{d}{dt} S(t) \right) - N\varepsilon S(t)_{C_3 e^{\tau i S(t)(\mu + \omega)} \mu} - N\varepsilon S(t)_{C_3 e^{\tau i S(t)(\mu + \omega)} \omega} + N\varepsilon S(t)^2 \tau - \\
& N\delta S(t)_{C_3 e^{\tau i S(t)(\mu + \omega)} \mu} - N\delta S(t)_{C_3 e^{\tau i S(t)(\mu + \omega)} \omega} + N\delta S(t)^2 \tau - \\
& N\gamma S(t)_{C_3 e^{\tau i S(t)(\mu + \omega)} \mu} - N\gamma S(t)_{C_3 e^{\tau i S(t)(\mu + \omega)} \omega} + N\delta S(t)^2 \tau + NS(t) \left(\frac{d^2}{dt^2} S(t) \right) - \\
& NS(t)_{C_3 \tau S(t)(\mu + \omega) e^{\tau i S(t)(\mu + \omega)} \mu} - NS(t)_{C_3 \tau S(t)(\mu + \omega) e^{\tau i S(t)(\mu + \omega)} \omega} - \\
& N \left(\frac{d}{dt} S(t) \right)^2 + N \left(\frac{d}{dt} S(t) \right)_{C_3 e^{\tau i S(t)(\mu + \omega)} \mu} + N \left(\frac{d}{dt} S(t) \right)_{C_3 e^{\tau i S(t)(\mu + \omega)} \omega} + \\
& _{C_3 \beta \xi S(t)^2 \phi} \left(\frac{d}{dt} S(t) \right) = 0
\end{aligned}$$

Equation 3.25

$$V(t) = _{C_3 e^{\tau i S(t)(\mu + \omega)}}$$

Equation 3.26

$$E(t) = \int -\frac{1}{\tau S(t)(\mu + \omega)} \left(\frac{d}{dt} S(t) \right) \tau S(t)(\mu + \omega) - \left(\frac{d}{dt} V(t) \right) \mu - \left(\frac{d}{dt} V(t) \right) \omega + \tau S(t)(\mu + \omega) \phi S(t) + \tau^2 S(t) S(t)(\mu + \omega) dt + C_2, \quad \text{Equation 3.27}$$

$$II(t) = \frac{N \left(\frac{d}{dt} E(t) + \phi S(t) \right)}{\beta \xi S(t)}, \quad \text{Equation 3.28}$$

$$R(t) = \int \gamma II(t) dt + C_1, \quad \text{Equation 3.29}$$

3.3.3 Numerical Solution of SVEIR Model

As mentioned in the previous section, the analytical solution of the SVEIR was discussed, and it was pointed out that the analytical solution becomes impractical due to non-linearity. Therefore, the numerical solution can be more practical as it can be easily implemented on computers. From the practice, it is often found that the Runge-Kutta (RK) method is efficiently used for such types of non-linear systems. The different variants of the RK method have been used depending on the problems. In the case of the SVEIR model (Equations 3.8 to 3.12). After testing the different trials on R-studio software, it was revealed that the Runge-Kutta fourth and fifth order (RK45) method performs well and provides a stable solution of the SVEIR. Therefore, in this study, the RK45 method will be employed. The iterative formula of RK45 method for solving the system of non-linear ODEs (Equations 3.8 to 3.12) adopts a procedure to determine if the proper step size h is being used. At each step, two different approximations for the solution are made and compared. If the two answers are in close agreement, the approximation is accepted. If the two answers do not agree to a specified accuracy, the step size is reduced. If the answers agree to more significant digits than required, the step size is increased. Each step requires the use of the following six values:

$$k_1 = hf(t_k, y_k), \quad \text{Equation 3.30}$$

$$k_2 = hf(t_k + \frac{1}{4}h, y_k + \frac{1}{4}k_1), \quad \text{Equation 3.31}$$

$$k_3 = hf(t_k + \frac{3}{8}h, y_k + \frac{3}{32}k_1 + \frac{9}{32}k_2), \quad \text{Equation 3.32}$$

$$k_4 = hf(t_k + \frac{12}{8}h, y_k + \frac{1932}{2197}k_1 - \frac{7200}{2197}k_2 + \frac{7296}{2197}k_3), \quad \text{Equation 3.33}$$

$$k_5 = hf(t_k + h, y_k + \frac{439}{216}k_1 - 8k_2 + \frac{3680}{513}k_3 - \frac{845}{4104}k_4), \quad \text{Equation 3.34}$$

$$k_6 = hf(t_k + \frac{1}{2}h, y_k - \frac{8}{27}k_1 + 2k_2 - \frac{3544}{2565}k_3 + \frac{1859}{4104}k_4 - \frac{11}{40}k_5), \quad \text{Equation 3.35}$$

Then an approximation to the solution of the problem is made using a Runge-Kutta method of order 4 as follows,

$$y_{k+1} = y_k + \frac{25}{216}k_1 + \frac{1408}{2565}k_3 + \frac{2197}{4101}k_4 - \frac{1}{5}k_5. \quad \text{Equation 3.36}$$

A better value for the solution is determined using a Runge-Kutta method of order 5:

$$z_{k+1} = y_k + \frac{16}{135}k_1 + \frac{6656}{12825}k_3 + \frac{28561}{56430}k_4 - \frac{9}{50}k_5 + \frac{2}{55}k_6, \quad \text{Equation 3.37}$$

According to the generative formula in Runge-Kutta 4th & 5th order method, for S(t), V(t), E(t), I(t) and R(t) of SVEIR Model can be written as:

$$S_{k+1} = S_k + \frac{25}{216}k_1^S + \frac{1408}{2565}k_3^S + \frac{2197}{4101}k_4^S - \frac{1}{5}k_5^S. \quad \text{Equation 3.38}$$

$$S_{z_{k+1}} = S_k + \frac{16}{135}k_1^S + \frac{6656}{12825}k_3^S + \frac{28561}{56430}k_4^S - \frac{9}{50}k_5^S + \frac{2}{55}k_6^S, \quad \text{Equation 3.39}$$

$$V_{k+1} = V_k + \frac{25}{216}k_1^V + \frac{1408}{2565}k_3^V + \frac{2197}{4101}k_4^V - \frac{1}{5}k_5^V. \quad \text{Equation 3.40}$$

$$Vz_{k+1} = V_k + \frac{16}{135}k_1^V + \frac{6656}{12825}k_3^V + \frac{28561}{56430}k_4^V - \frac{9}{50}k_5^V + \frac{2}{55}k_6^V, \quad \text{Equation 3.41}$$

$$E_{k+1} = E_k + \frac{25}{216}k_1^E + \frac{1408}{2565}k_3^E + \frac{2197}{4101}k_4^E - \frac{1}{5}k_5^E, \quad \text{Equation 3.42}$$

$$Ez_{k+1} = E_k + \frac{16}{135}k_1^E + \frac{6656}{12825}k_3^E + \frac{28561}{56430}k_4^E - \frac{9}{50}k_5^E + \frac{2}{55}k_6^E, \quad \text{Equation 3.43}$$

$$I_{k+1} = I_k + \frac{25}{216}k_1^I + \frac{1408}{2565}k_3^I + \frac{2197}{4101}k_4^I - \frac{1}{5}k_5^I, \quad \text{Equation 3.44}$$

$$Iz_{k+1} = I_k + \frac{16}{135}k_1^I + \frac{6656}{12825}k_3^I + \frac{28561}{56430}k_4^I - \frac{9}{50}k_5^I + \frac{2}{55}k_6^I, \quad \text{Equation 3.45}$$

$$R_{k+1} = R_k + \frac{25}{216}k_1^R + \frac{1408}{2565}k_3^R + \frac{2197}{4101}k_4^R - \frac{1}{5}k_5^R, \quad \text{Equation 3.46}$$

$$Rz_{k+1} = R_k + \frac{16}{135}k_1^R + \frac{6656}{12825}k_3^R + \frac{28561}{56430}k_4^R - \frac{9}{50}k_5^R + \frac{2}{55}k_6^R. \quad \text{Equation 3.47}$$

The mentioned schemes of RK45 methods are put into Equations 3.8 to 3.12 and solved for all the k-values by imposing the given initial conditions, and the method is run iteratively until the numerical solution is achieved at the desired accuracy.

3.3.4 Model Simulation

The nonlinear system of ordinary equations (Equations 3.7 to 3.12) has been solved numerically by writing a user-defined code for the higher-order RK method on R software. The initial conditions applied were taken from the available data of Pakistan, and the values of the other parameters used in the model were chosen as mentioned in Table 3.3. The simulation was performed for various parameter values, and the Behavior of the S, V, E, I,

and R dependent variables was predicted, which will be presented and discussed in Chapter 4.

3.4 Performance Metrics to Measure the Goodness of Proposed SVEIR Model

For measuring and analyzing the goodness of the models, the following metrics have been used.

3.4.1 Root Mean Square Error (RMSE)

The RMSE is frequently used in analyzing the goodness of model fitting. If y_i is the original value and $\hat{y}_i$ is the estimated value using the model. The RMSE is obtained by taking the square root of the average of squared residuals between them and is defined by the following formula,

$$RMSE = \sqrt{\frac{1}{n} \sum_{i=1}^n (y_i - \hat{y}_i)^2}, \quad \text{Equation 3.48}$$

3.4.2 Sum of Squares of Error (SSE)

Just like the RMSE, the SSE is also an important goodness metric. It is a measure of the total squared discrepancy between the observed data and the estimation fitting model. Often, it is used as a comparative model selection criterion. A small value of SSE indicates that the fitted model is closely aligned with the observed data. The following formula obtains SSE,

$$SSE = \sum_{i=1}^n (y_i - y_i^*)^2. \quad \text{Equation 3.49}$$

3.4.3 Coefficient of Determination R-Square

The coefficient of determination, R-squared (R^2), measures the percentage of the best-fitting regression model to the observed data. For example, $R^2=0.7$ indicates that 70% of the data fit the regression model. Generally, a higher value of the coefficient of determination indicates a better fit for the model. The formulae to calculate the R^2 are given below:

$$R^2 = SSR / SST, \quad \text{Equation 3.50}$$

Where SSR is the sum of squared residuals and SST is the total variation in the observed data set.

3.4.4 Mean Absolute Percentage Error (MAPE)

The MAPE is used to analyse the percentage accuracy and is obtained by multiplying 100 by the Mean Absolute Error (MAE) as given below,

$$MAPE = 100 \times \frac{1}{n} \sum |y_i - y_i^*|, \quad \text{Equation 3.51}$$

3.4.5 Correlation

The correlation between two variables or among multiple variables is one of the most important statistical measures that determine the degree of association or interdependence among the variables. It also helps to decide the goodness of the various models when they are required to compare. The following formula is used to calculate the coefficient of correlation (Pearson's coefficient of correlation).

$$r_{yy^*} = \frac{n \sum y_i y_i^* - \sum y_i \sum y_i^*}{\sqrt{n \sum y_i^2 - (\sum y_i)^2} \sqrt{n \sum y_i^{*2} - (\sum y_i^*)^2}} \quad \text{Equation 3.52}$$

Where r is the coefficient of correlation, y and y^* are comparative variables. In this study, the correlation can be used to assess and compare the degree of association between the SVEIR model and the observed data of COVID-19 to assess the model's accuracy.

3.5 Model Validation

The numerical solution of the proposed SVEIR model will be validated by comparing it with the Gill et al. (2020) model using Pakistan data. Both models will be compared in terms of the goodness of fit using the data from Pakistan.

3.6 Sensitivity Analysis

To determine the effects of parameters on the model output, the sensitivity of the parameters will be analyzed. This will help in deciding which variable significantly affects the model's behavior and predictions. The variations in S , V , E , I , and R under the influence of some key parameters are listed in Table 3.3. The numerical solution for each dependent variable will be obtained for different trial values of a specific parameter while keeping other parameters fixed. The impact of parameter variations on each dependent variable will highlight the model's sensitivity.

3.7 Summary

In this chapter, the methodology to achieve the objectives of this study was demonstrated concisely. First, the Gill et al. (2020) model was analyzed for COVID-19, and then it was modified to propose the SVEIR model. The analytical and numerical solution strategy was also presented, and the performance metrics to evaluate the goodness of the model are also defined. Finally, the validation and sensitivity analysis for the proposed model have been discussed. Chapter 4 will present and discuss the results obtained by adopting the methodology discussed in this chapter.

CHAPTER 4

RESULTS AND DISCUSSION

4.1 Overview

This chapter is devoted to presenting and discussing the results obtained through the implementation of the proposed methodology. The numerical solution of the SVEIR model, based on data from Pakistan, will be presented for all five dependent variables. Specifically, the model will be validated by comparison with a related model, and the performance of the SVEIR model will also be evaluated. To assess the impact of the parameters involved in the SVEIR model, a sensitivity analysis will be conducted. Finally, a conclusive summary will be provided at the end of this chapter.

4.2 Formulation and Implementation of the SVEIR Model

The first objective of this study was to propose a mathematical model that incorporates control interventions, specifically through the inclusion of a vaccination compartment. The motivation for this research stemmed from the need to incorporate Non-Pharmaceutical Interventions (NPIs) into the modelling framework to reflect the current scenario in Pakistan. A model that addresses these factors was developed by modifying the Gill et al. (2020) model, resulting in the formulation of the SVEIR model (Susceptible, Vaccinated, Exposed, Infected, and Recovered). This new mathematical model for COVID-19 considers five key variables: Susceptible (S), Vaccinated (V), Exposed (E), Infected (I), and Recovered (R), collectively referred to as the SVEIR model, which has already been presented in Chapter 3 along with the corresponding compartmental diagram in Figure 3.3. The following section presents the numerical solution of the proposed SVEIR model.

4.3 Numerical Solution of the Proposed SVEIR Model

The COVID-19 data for Pakistan, covering the period from 18 March 2020 to April 2022, was obtained from reliable sources, including the National Disaster Management Authority (NDMA), the Ministry of National Health Services, Regulations and Coordination, and the official website of the Pakistan Bureau of Statistics. The data related to key variables—such as the number of active cases, deaths, quarantined individuals, vaccinated individuals, recovered individuals, and the exposed population—was processed for incorporation into the SVEIR model. The model analysis provides outbreak simulations, including the duration of the outbreak, the peak timing in months, and the number of peak active cases. These simulations were conducted under the assumption of no control or movement restriction measures. Additionally, the model evaluates the reduction in peak active cases under various control measures, which are described and analyzed.

For testing and implementation of the proposed model, the nonlinear system of ordinary differential equations was solved numerically using a user-defined code based on a higher-order Runge-Kutta (RK) method implemented in R software. The initial conditions were taken from the actual data, while the parameter values used in the model were sourced from Table 3.1. The numerical solution was computed for the period from 28 December 2021 to 7 April 2022.

Figure 4.1 illustrates the Behavior of the five dependent variables: Susceptible (S), Vaccinated (V), Exposed (E), Infected (I), and Recovered (R). It can be observed that the number of susceptible individuals increases initially, reaching a peak for a short period, and then gradually declines to an asymptotic value over time. The vaccination compartment plays a vital role in the interaction with other variables. The figure indicates that as the number of recovered individual's increases, the vaccinated population decreases. The

exposed and infected populations show similar trends, with the exposed population rising smoothly to a peak and then declining gradually.

In contrast, the infected population follows the same pattern but at a lower intensity. The recovered population interacts with both the exposed and infected populations. Following the introduction of the COVID-19 vaccination, the recovered population steadily increases and eventually stabilizes over time. In summary, the numerical simulation of all five variables effectively projects the outbreak trajectory over the coming months.

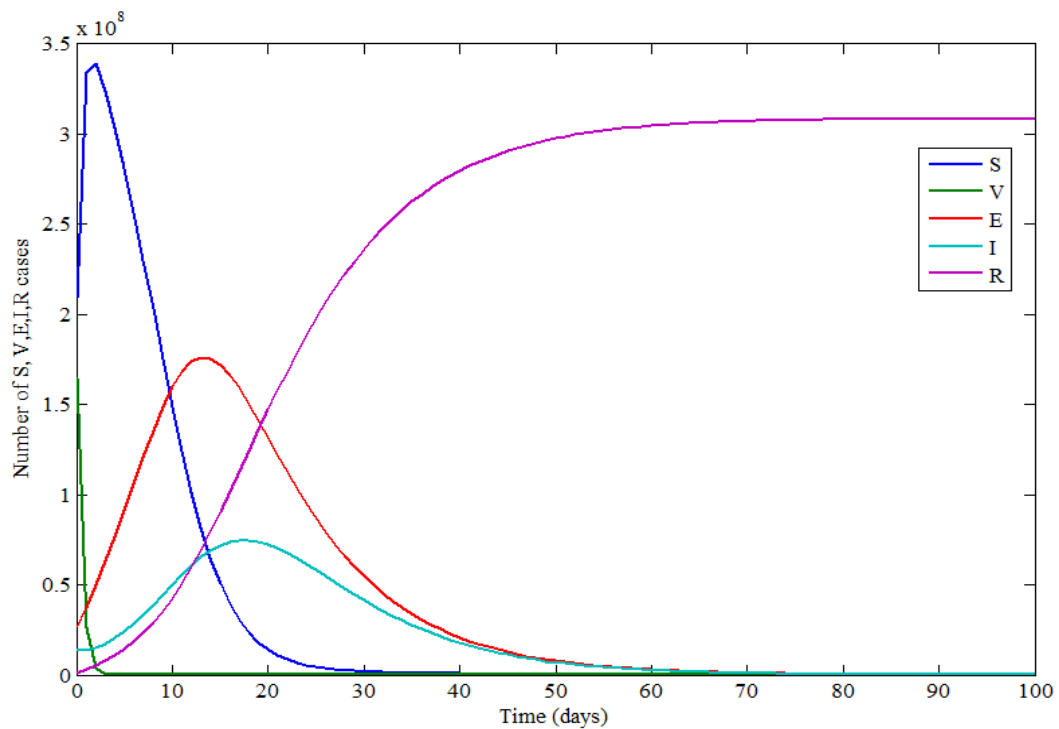


Figure 4.1: The solution of the SVEIR Model (with intervention) for COVID-19

4.4 Goodness and Performance Analysis of the SVEIR Model

Examination the actual data alongside the numerical outcomes produced by Pakistan's SVEIR model provides valuable insights into the complex dynamics of the COVID-19 pandemic within the country. The SVEIR Model, which incorporates factors such as vaccination rates, transmission dynamics, and disease progression, is a comprehensive tool

for simulating and understanding the spread of the virus. The graphical representation shows the observed data through circle markers, while the continuous line fitted through the points represents the model's predictions. The performance of the model can be estimated through the performance metrics mentioned in Chapter 3. This comparative analysis helps refine the SVEIR Model and enhances its predictive accuracy. Figures 4.2 to 4.6 compare the actual observed data and the fitted SVEIR model curves for S, V, E, I, and R compartments, respectively. The results show a good agreement of SVEIR results with the observed data.

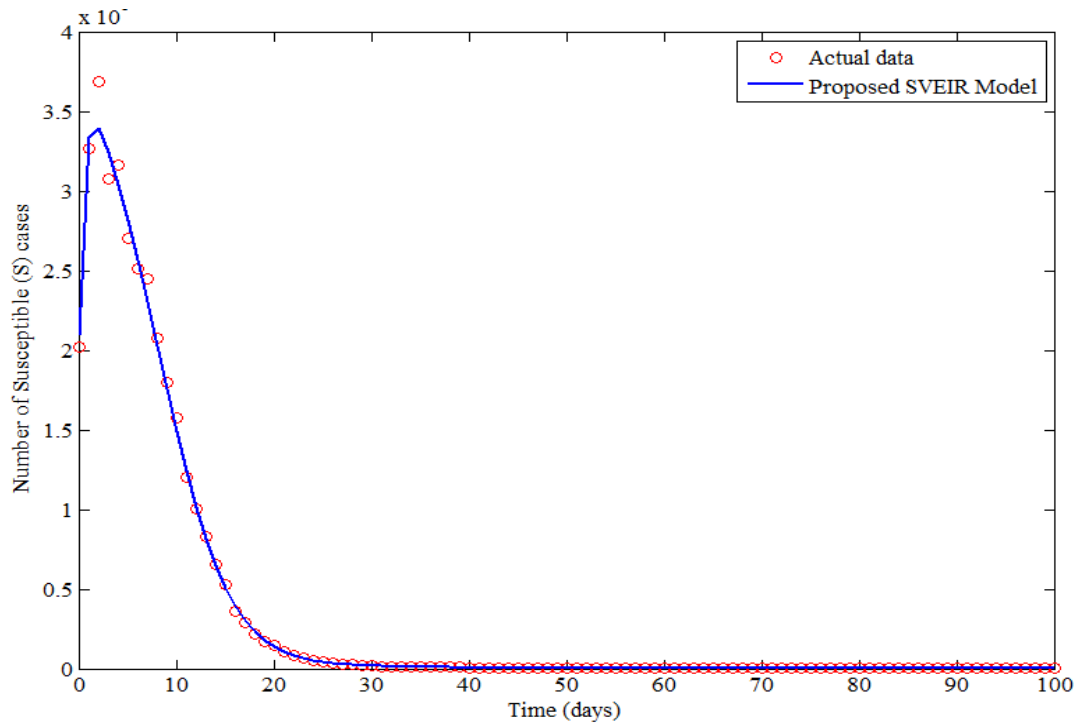


Figure 4.2: The comparison of Susceptible (S) values obtained by the SVEIR model with actual data

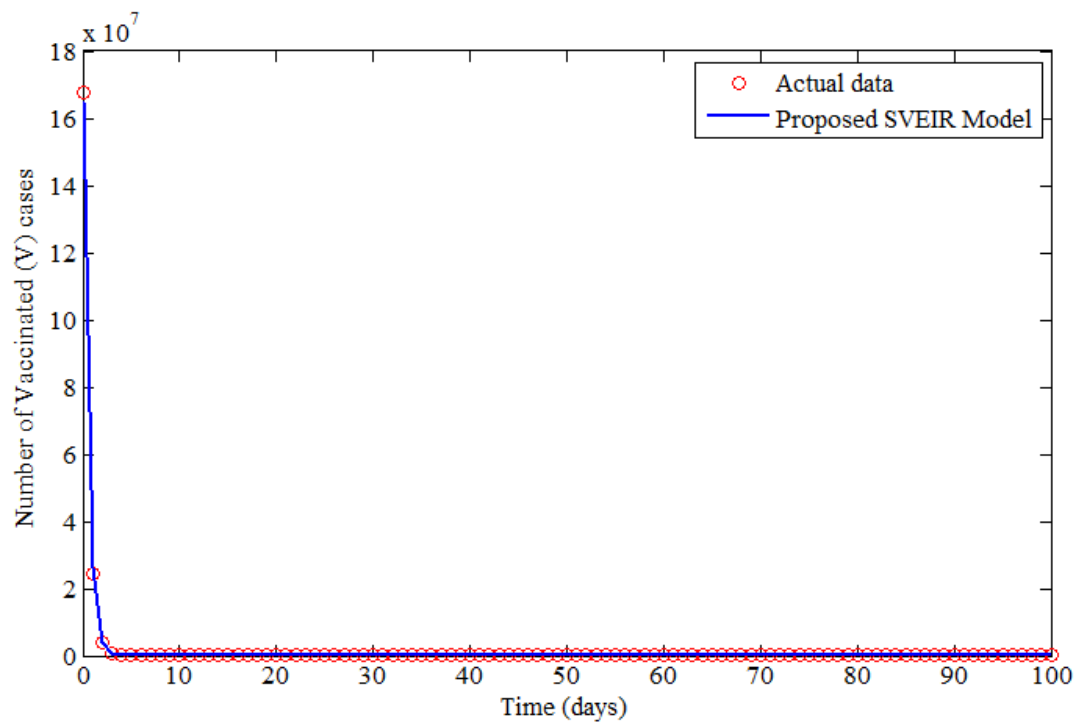


Figure 4.3: The comparison of Vaccinated (V) values obtained by the SVEIR model with actual data

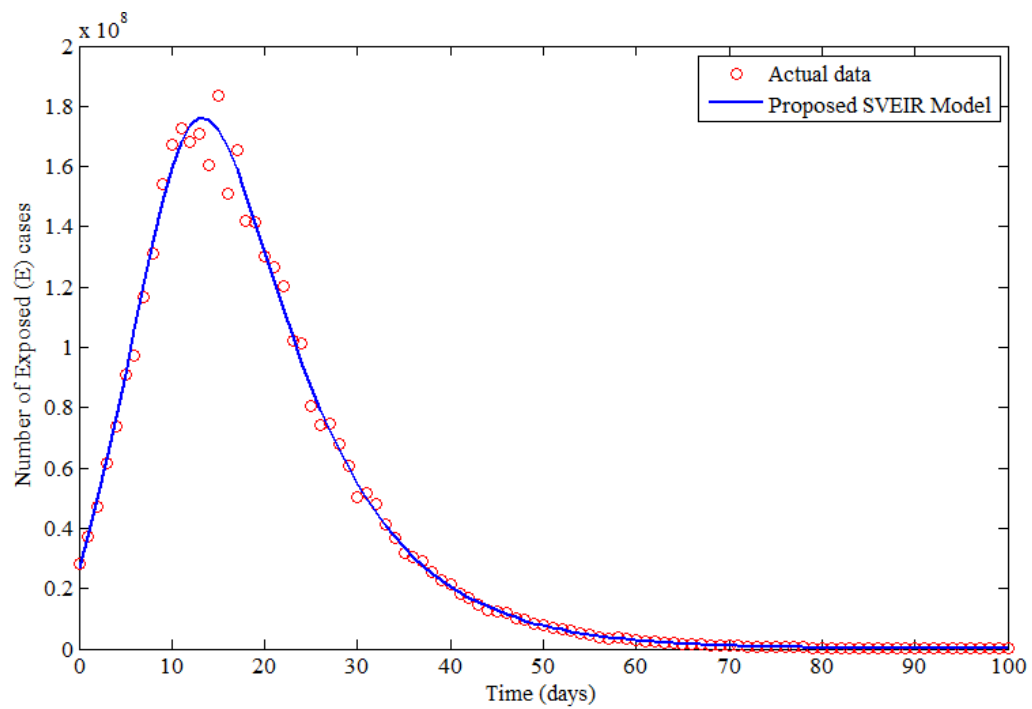


Figure 4.4: The comparison of Exposed E values obtained by the SVEIR model with actual data

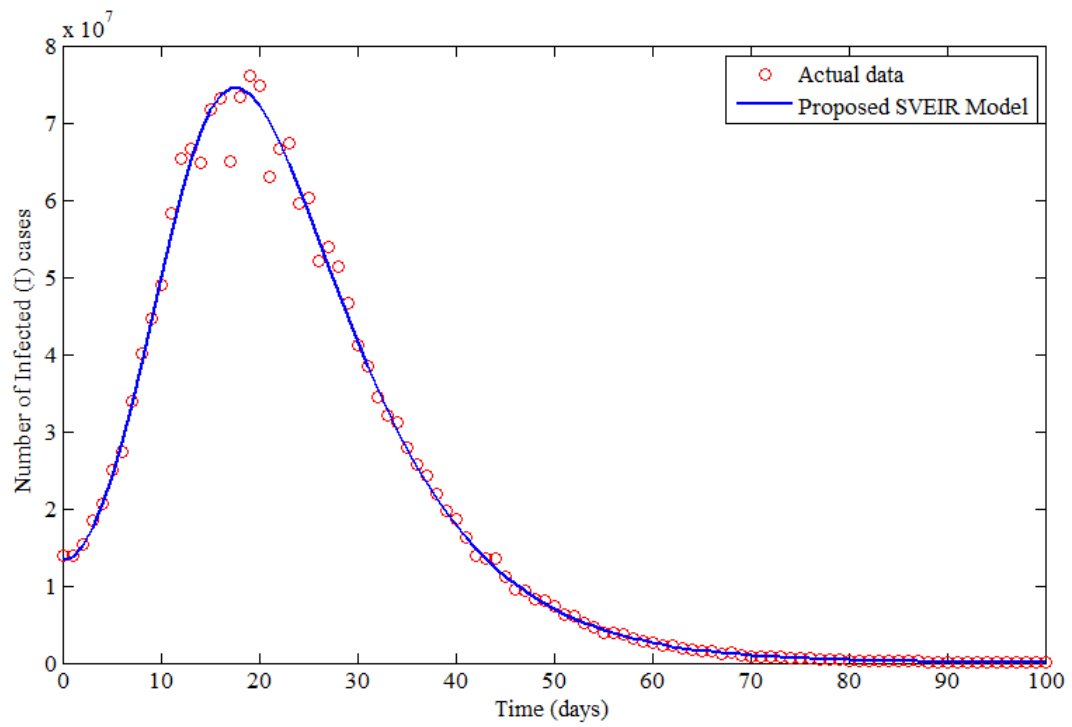


Figure 4.5: The comparison of Infected (I) values obtained by the SVEIR model with actual data

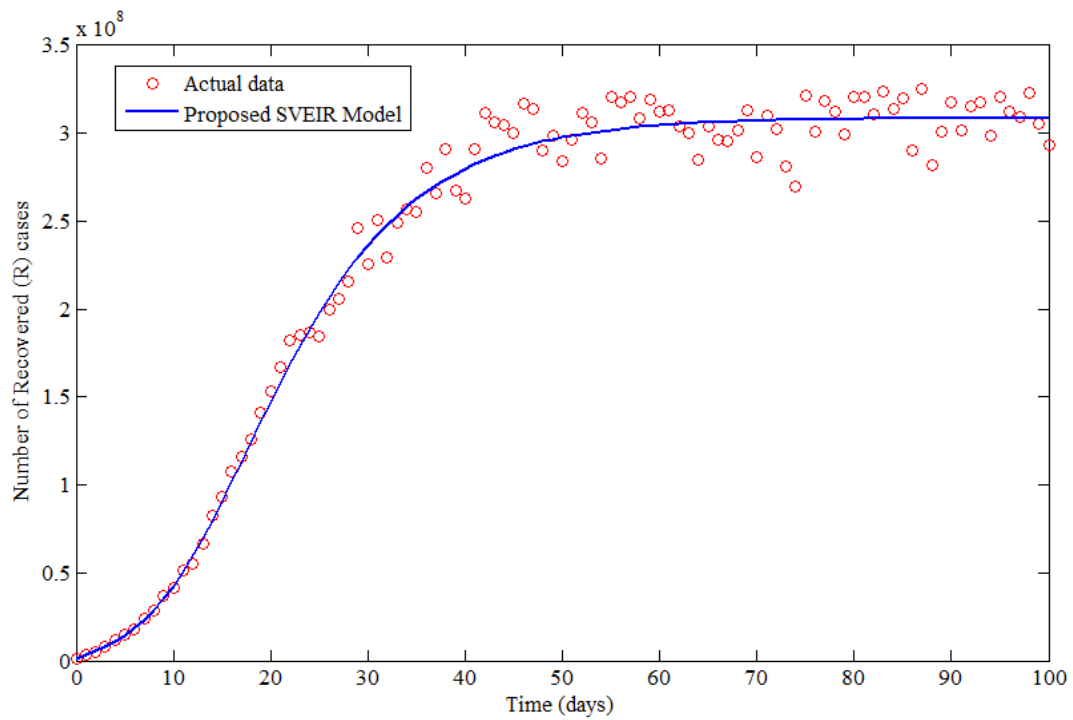


Figure 4.6: The comparison of Recovered (R) values obtained by the SVEIR model with actual data

In the above Figures 4.2 to 4.6, the actual data have been compared with the SVEIR model fitted curves. However, the output values are in millions of population due to Pakistan's large population. So, it is difficult to determine how good a model is or how many discrepancies there are. To assess the goodness of the model, the maximum absolute percentage error (MAPE), the root mean square error (RMSE), the sum of squares error (SSE), the coefficient of determination (R^2), and the coefficient of correlation (r) between the actual data and the SVEIR model curves have been calculated. The following Table 4.1 lists the performance values of the SVEIR model for each dependent variable against the actual data. It should be noteworthy that the values mentioned in Table 4.1 depend on the initial conditions and the values of the parameters involved in the model. Due to the large population of Pakistan, the errors in the SVEIR model prediction may also exhibit high errors. However, the performance values are strongly acceptable and may provide good forecasts.

Table 4.1: Analysis of performance metrics for the goodness of the model

Variable / Performance metric	MAPE	RMSE	SSE	R^2	r
S	15.14	4345.64	190702697.20	0.9091	0.924
V	9.72	328.73	10869477.98	0.9346	0.9502
E	14.46	3525.70	1255635250.70	0.9191	0.9386
I	13.15	1607.36	261147633.94	0.9254	0.9310
R	12.23	1169	1380312103	0.9397	0.9498

Figure 4.7 (a) shows that the MAPE for all five variables falls between 9.72 and 15.42. The Vaccinated (V) population exhibits a lower MAPE of 9.72 compared to other populations. Similarly, the RMSE and SSE are found to be lower in the Vaccinated (V) variable, as can be seen in Figures 4.7 (b)-(c). After the Vaccinated (V) variable, the Recovered (R) variable poses less maximum absolute percentage error MAPE, RMSE, and SSE. Typically, the coefficient of determination (R-square) must be higher, often close to 90%, 95%, or 99%. In the case of Pakistan data, it is not possible to achieve a value of R-squared of 99%. As shown in Figure 4.7 (d), the R-square values for all five variables in the SVEIR model are 0.9, indicating a 90% level of significance. This suggests that the model performs well and strongly determines its predictions. Figure 4.7 (e) exhibits the degree of association between the observed data and SVEIR prediction. The results indicate a strong correlation between the observed data and the SVEIR model, ranging from 92.4% to 95.02%. It verifies the good agreement between the SVEIR model results and the observed data.

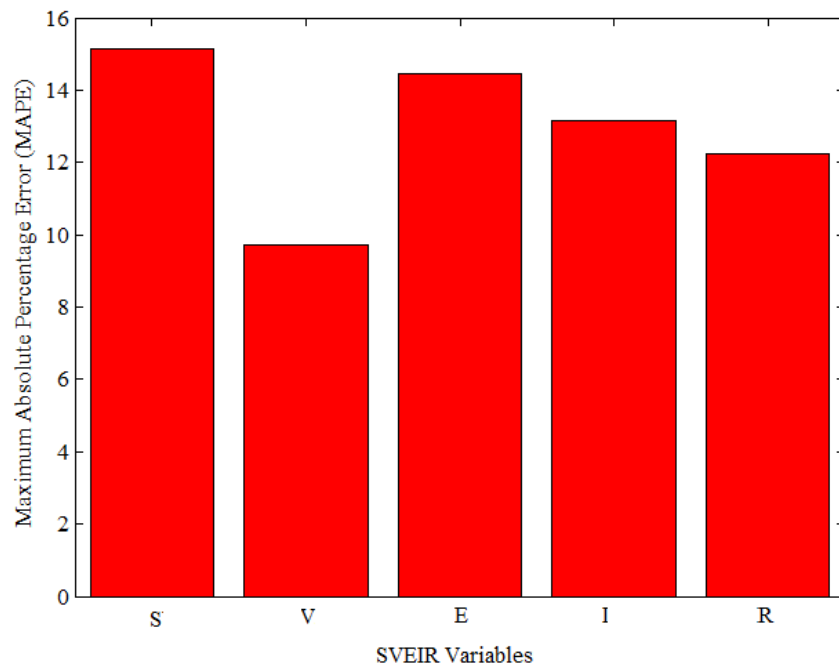


Figure 4.7(a): The comparison of MAPE for S, V, E, I, R variables

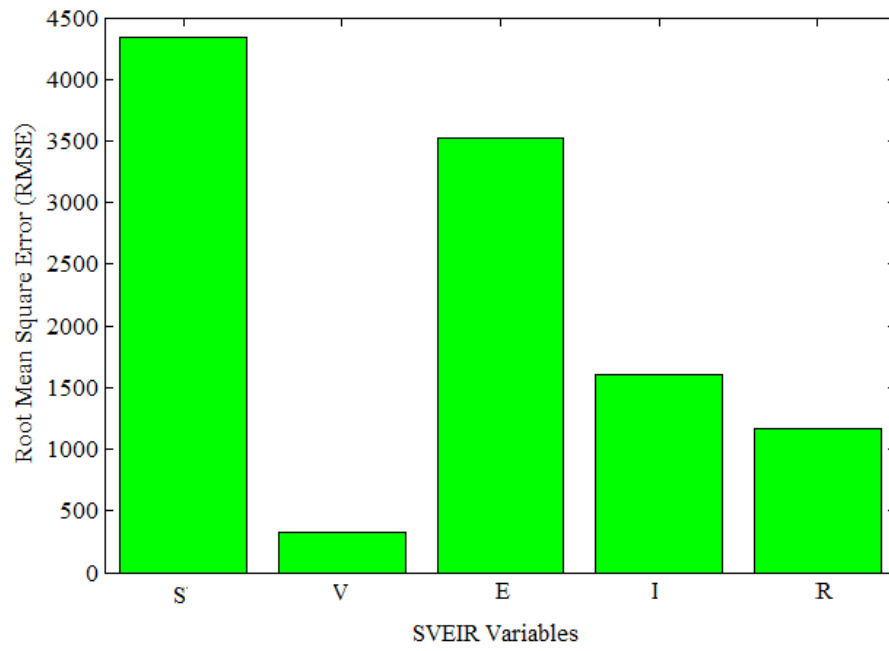


Figure 4.7(b): The comparison of RMSE for S, V, E, I, R variables

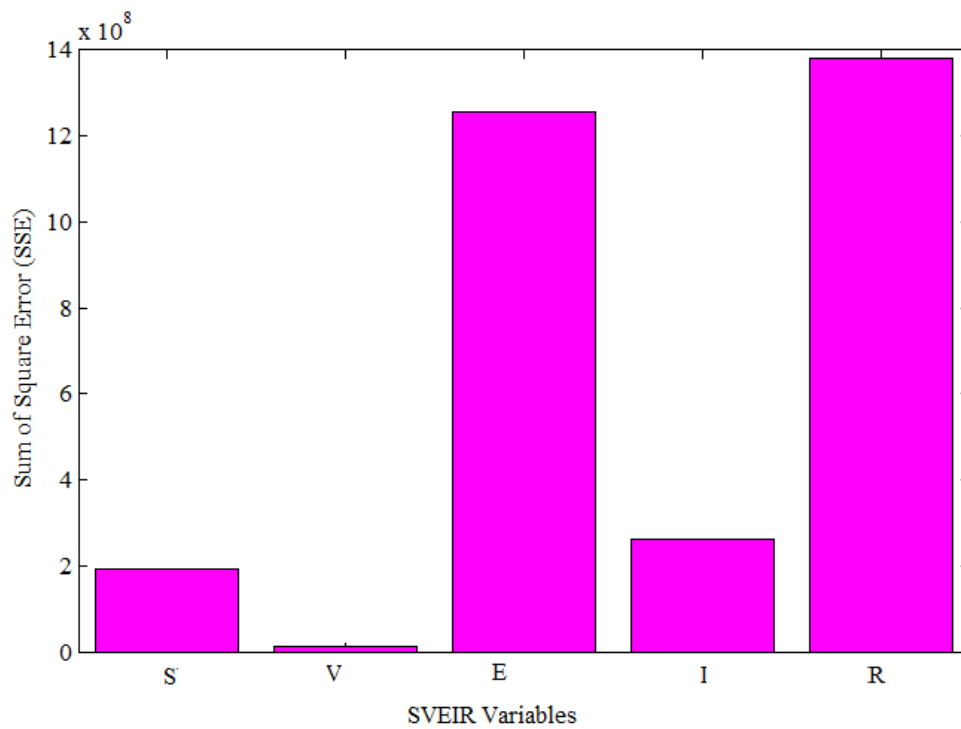


Figure 4.7(c): The comparison of SSE for S, V, E, I, R variables

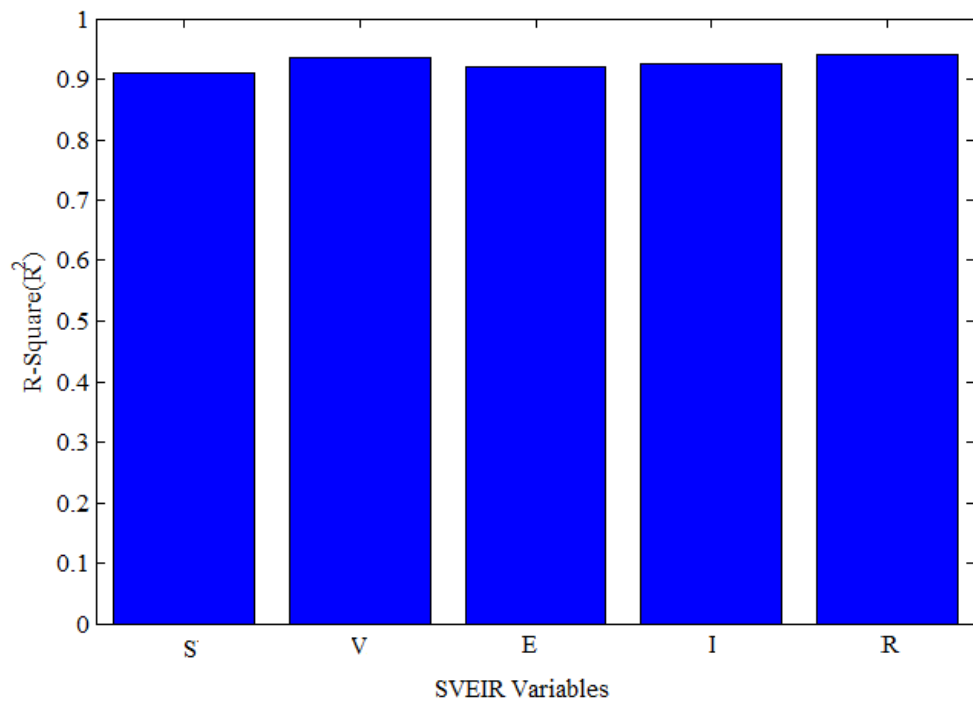


Figure 4.7(d): The comparison of R-squared for S, V, E, I, R variables

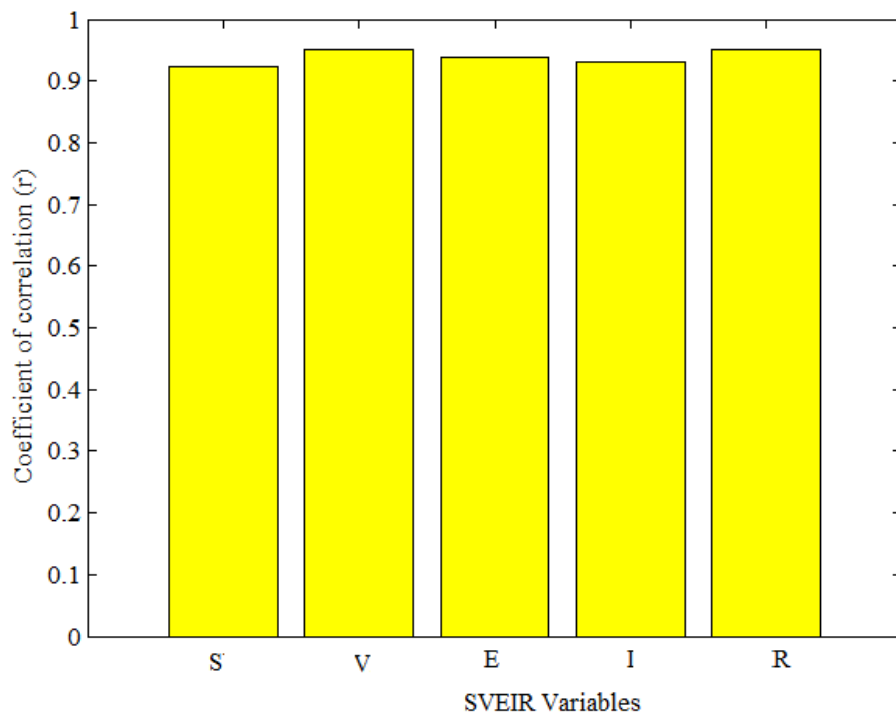


Figure 4.7(e): The comparison of Coefficient of correlation for S, V, E, I, R variables

4.5 Validation of the SVEIR Model

An essential component of an epidemiological model is its validation, specifically whether the proposed model aligns with other existing models. This improves the model's accuracy in understanding the transmission of the epidemic better and predicting the future directions of diseases. The Gill et al (2020) model was adopted for Pakistan COVID-19 data as it can be used as a benchmark due to its relevance with the SVEIR model. The following Figures 4.8 - 4.9 present the comparison of the S, E, I, and R variables obtained from the proposed SVEIR model and the Gill et al (2020) model. The results of both models are compared with the actual data. Whereas, the performance of both methods is evaluated using maximum absolute percentage error (MAPE) as shown in Table 4.2 and Figure 4.12. It can be seen that the percentage errors in the proposed SVEIR model results are less than the percentage errors of the results of Gill et al (2020). This shows that the SVEIR model performs better for the Pakistan COVID-19 data as compared to Gill et al. Hence, it also validates the results of the SVEIR model.

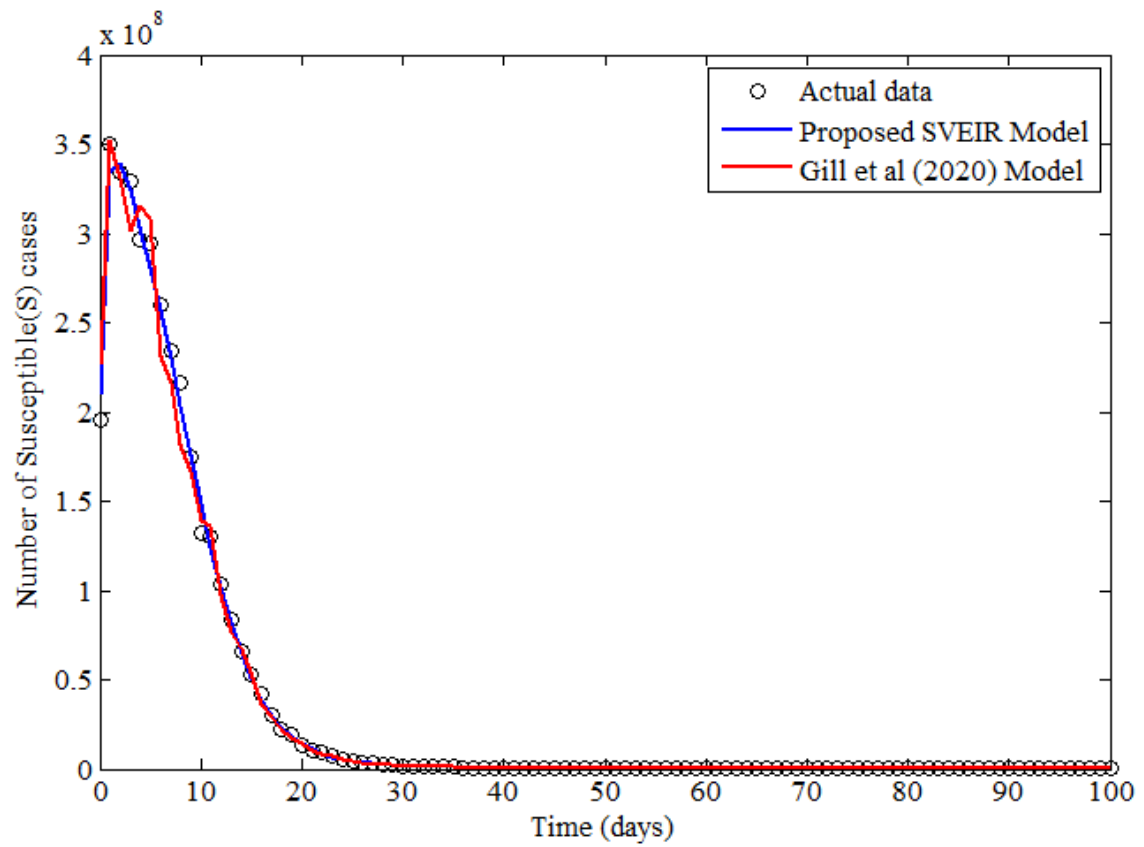


Figure 4.8: The comparison of Susceptible (S) values obtained by the SVEIR model with the Gill et al (2020) model

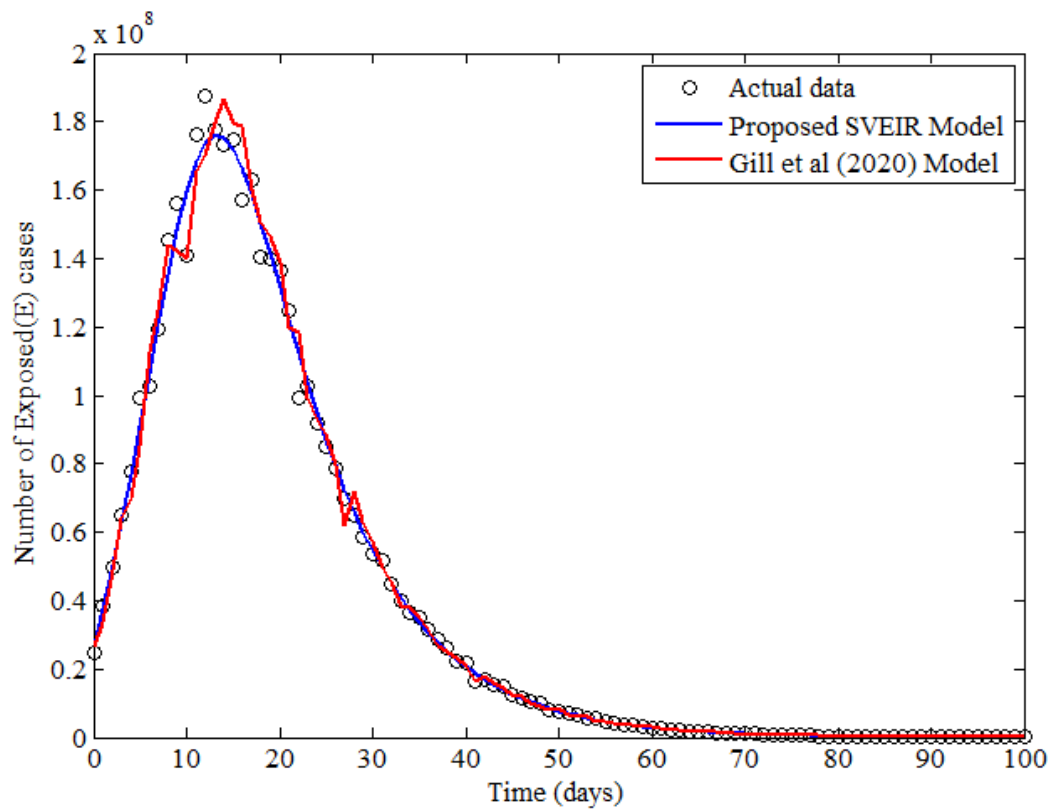


Figure 4.9: The comparison of Exposed (E) values obtained by SVEIR model Gill et al (2020) model

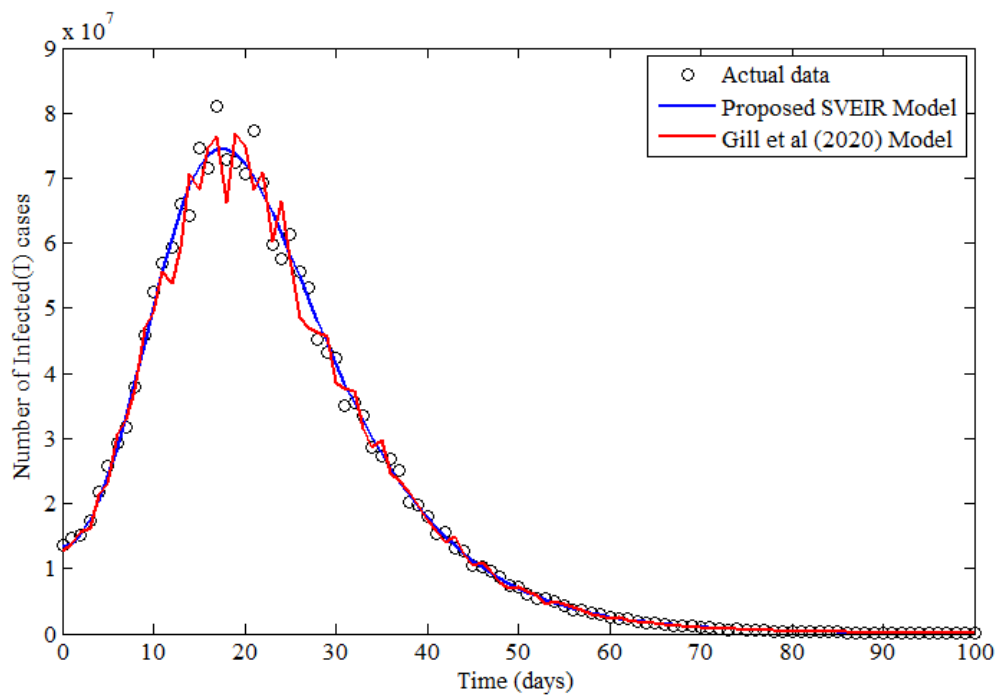


Figure 4.10: The comparison of Infected (I) values obtained by the SVEIR model, Gill et al (2020) model

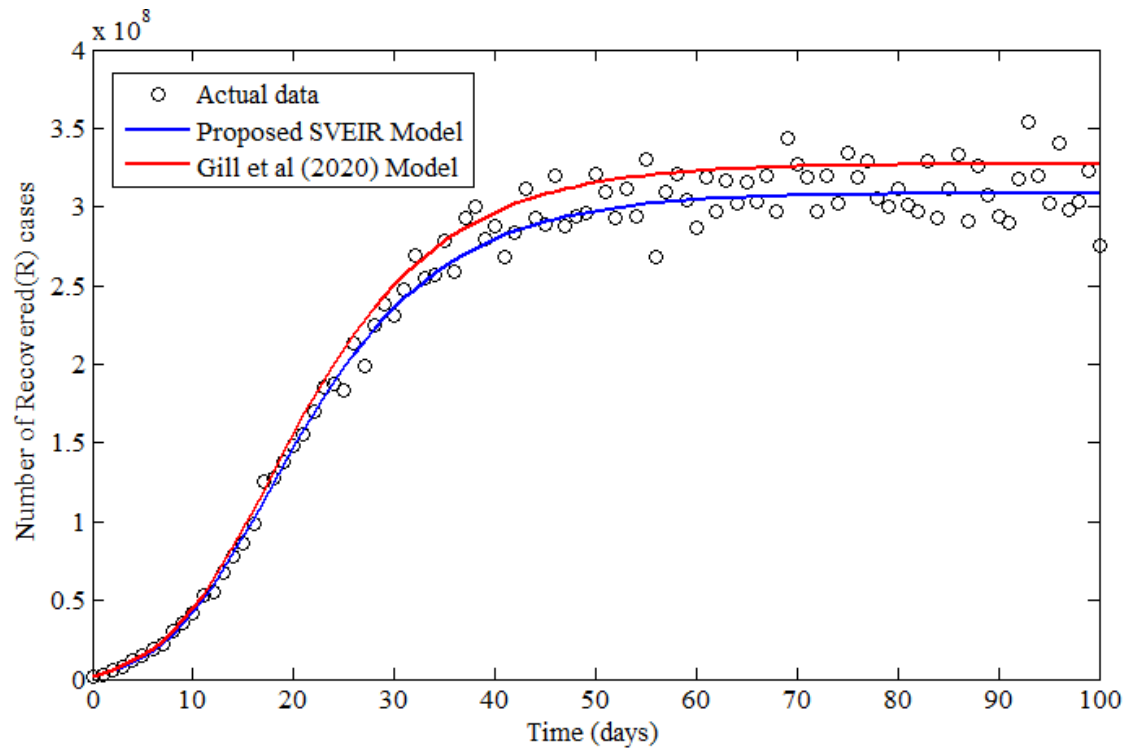


Figure 4.11: The comparison of Recovered (R) values obtained by the SVEIR model, Gill et al (2020) model

Table 4.2: Analysis of performance metrics for the goodness of the model

Variable	MAPE	
	SVEIR Model	Gill et al (2020) Model
S	15.14	20.31
E	14.46	16.29
I	13.15	16.70
R	12.23	16.25

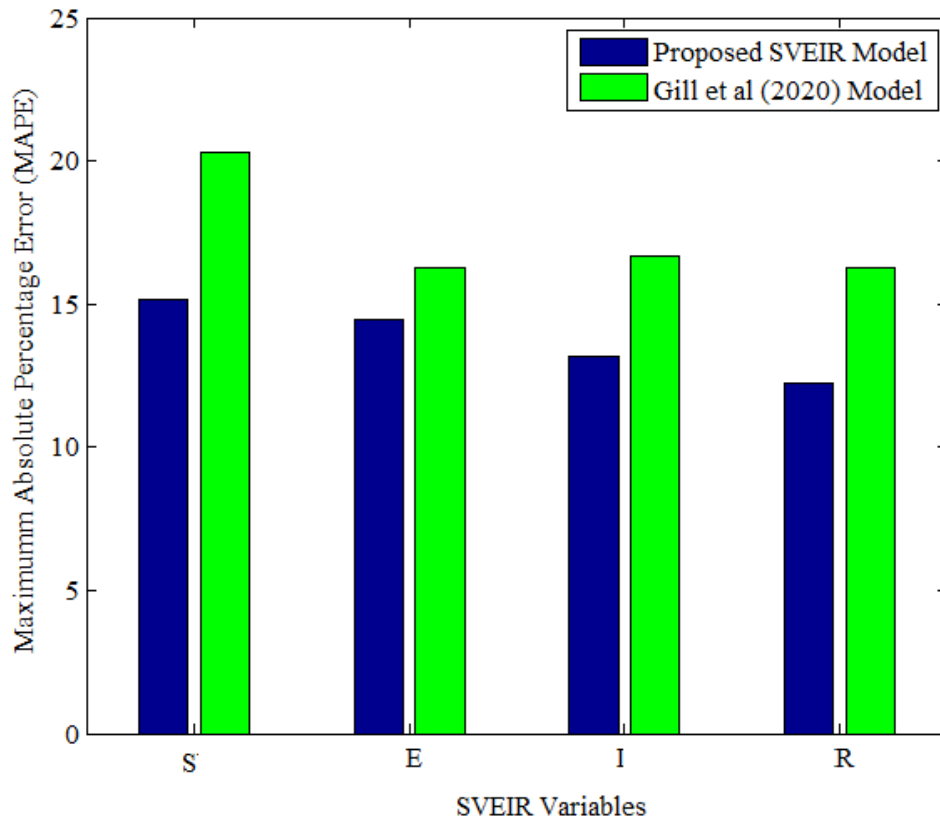


Figure 4.12: The comparison of MAPE for S, E, I, R variables Gill et al (2020) model

4.6 Sensitivity Analysis of the Parameters of the SVEIR Model

Sensitivity evaluation is a crucial tool in assessing the robustness and reliability of mathematical models, including those used to analyse COVID-19 dynamics. It entails systematically varying various parameters to recognize how changes in these inputs impact the model's consequences. Within the context of COVID-19 modelling in Pakistan, sensitivity evaluation permits researchers and policymakers to explore the model's sensitivity to variations in parameters like transmission rates, intervention effectiveness, and population characteristics. By analysing how alterations in those parameters affect the model's predictions, experts gain insights into the uncertainties and limitations of the version's effects. Sensitivity analysis aids in figuring out which parameters have the most

significant impact on the model's results and highlights regions where uncertainty may also exist. This approach provides comprehensive insight into the performance, enables the assessment of reliability in various scenarios, and aids decision-makers in developing effective strategies to manage and control the ongoing pandemic. The following Sections elaborate on the sensitivity of various parameters involved in the proposed SVEIR model.

4.6.1 Sensitivity Analysis of Transmission Rate (β)

In Figures 4.13 to 4.17 for β values, the time-dependent variation of the population of the disease compartments in susceptible, vaccinated, exposed, infected, and recovered individuals, respectively, has been displayed. In Figure 4.13, it is seen that, as the order of β In the long run, they are less susceptible. In Figures 4.14 and 4.15, it is observed that the number of vaccinated individuals and exposed individuals decreases over time, and there are fewer individuals. According to Figure 4.16, the peak in carrier individuals occurred between the time intervals 6 and 11 for the $\beta = 1$ value, while it occurred in earlier times for the importance of β . For example $\beta = 0.25$, infected individuals seem to have decreased asymptotically before the time $t=6$. It can be said that this is because the ordinary derivatives have a memory effect. In Figure 4.17, changes over time in recovered individuals are examined. As time passes, it is observed that the number of recovered individuals increases as the β increases. In contrast, in the long term, as the β rises, the number of recovered individuals increases.

The sensitivity of the SVEIR model with respect to changes in the transmission rate (β) highlights that slight variations in β significantly impact the long-term Behavior of susceptible, vaccinated, exposed, infected, and recovered populations. The model is exceptionally responsive to changes in the probability of susceptibility becoming infectious

per contact, emphasizing the importance of understanding and controlling transmission rates for effective pandemic management.

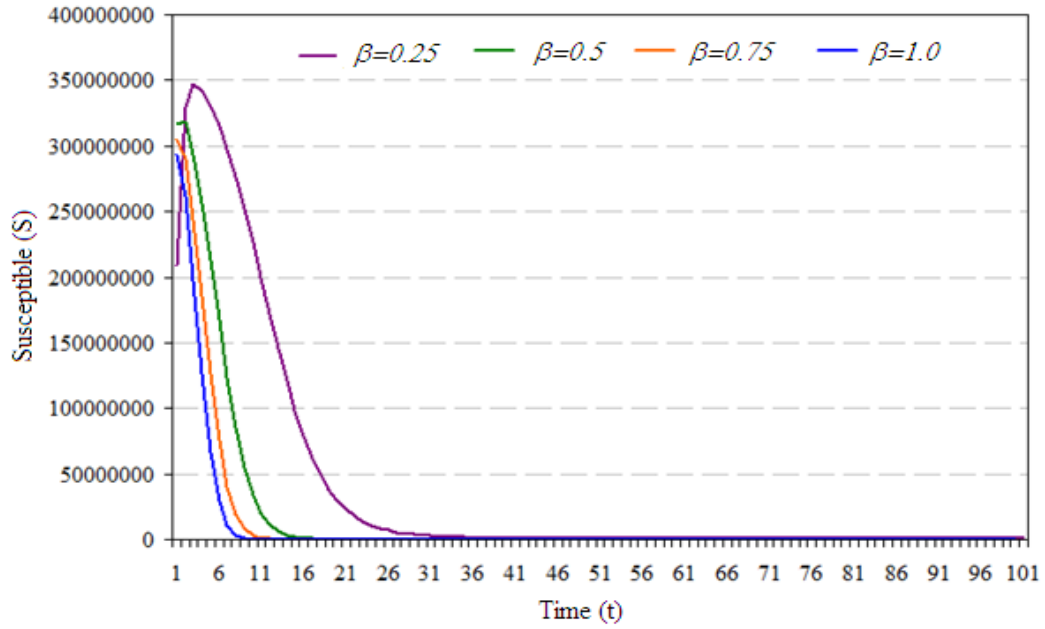


Figure 4.13: Behavior of Susceptible (S) class for different probabilities of susceptible becoming infectious per contact (β) values

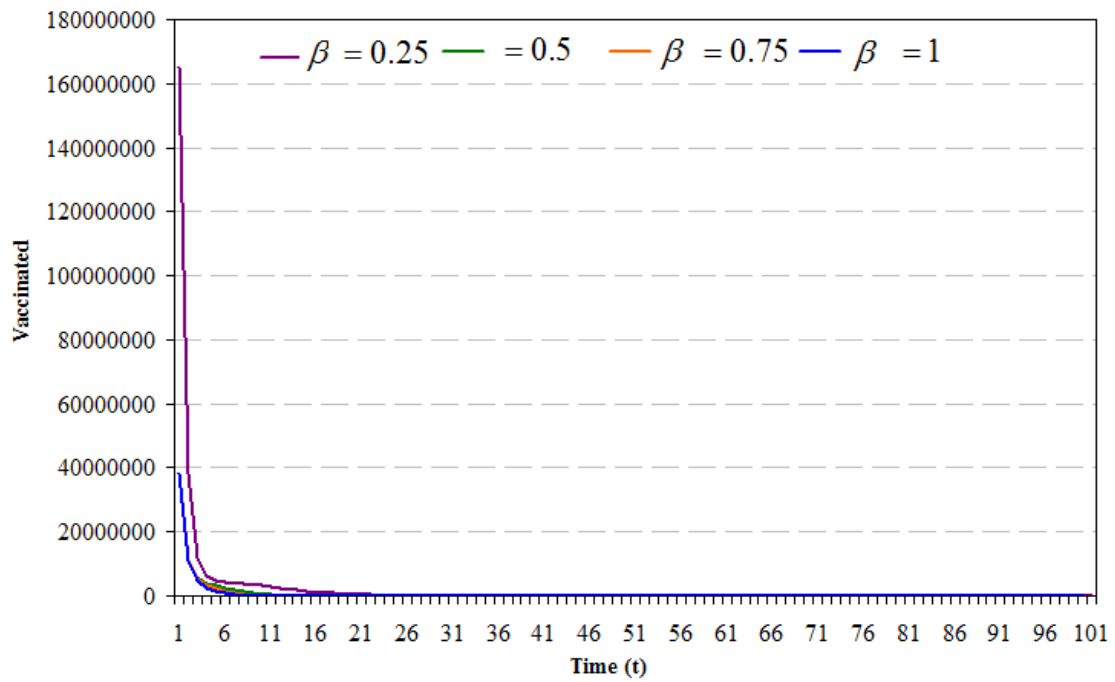


Figure 4.14: Behavior of Vaccinated (V) class for different Probability of susceptible become infectious per contact (β) values

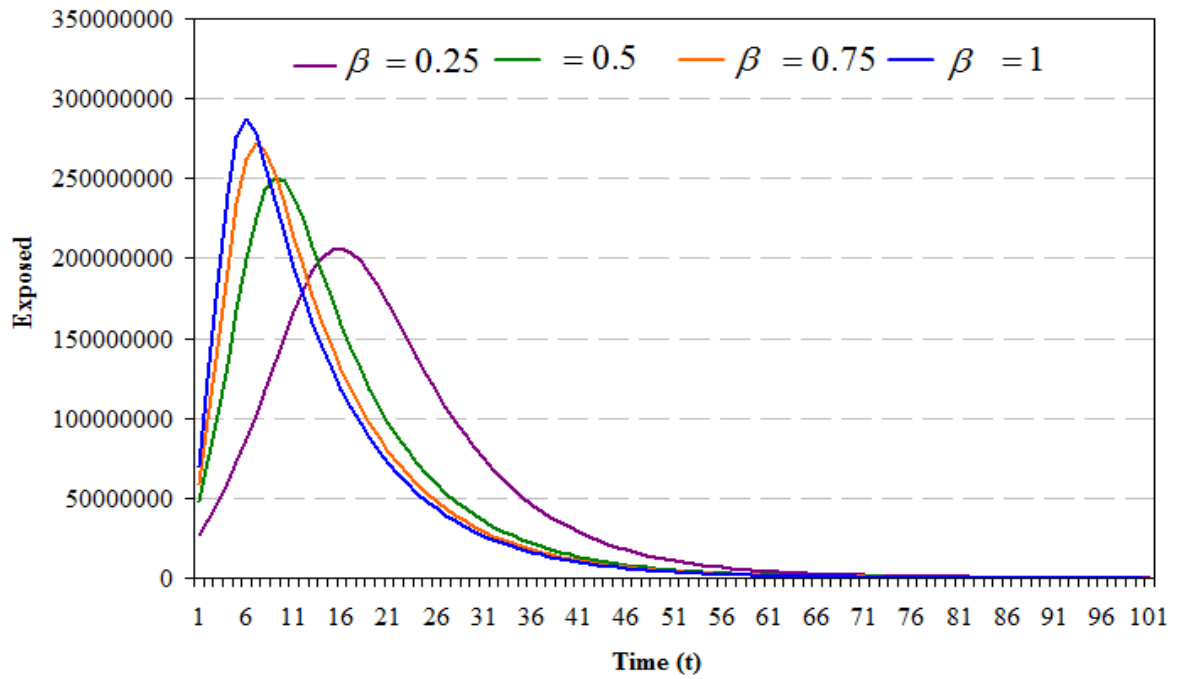


Figure 4.15: Behavior of Exposed (E) class for different Probability of susceptible become infectious per contact (β) values

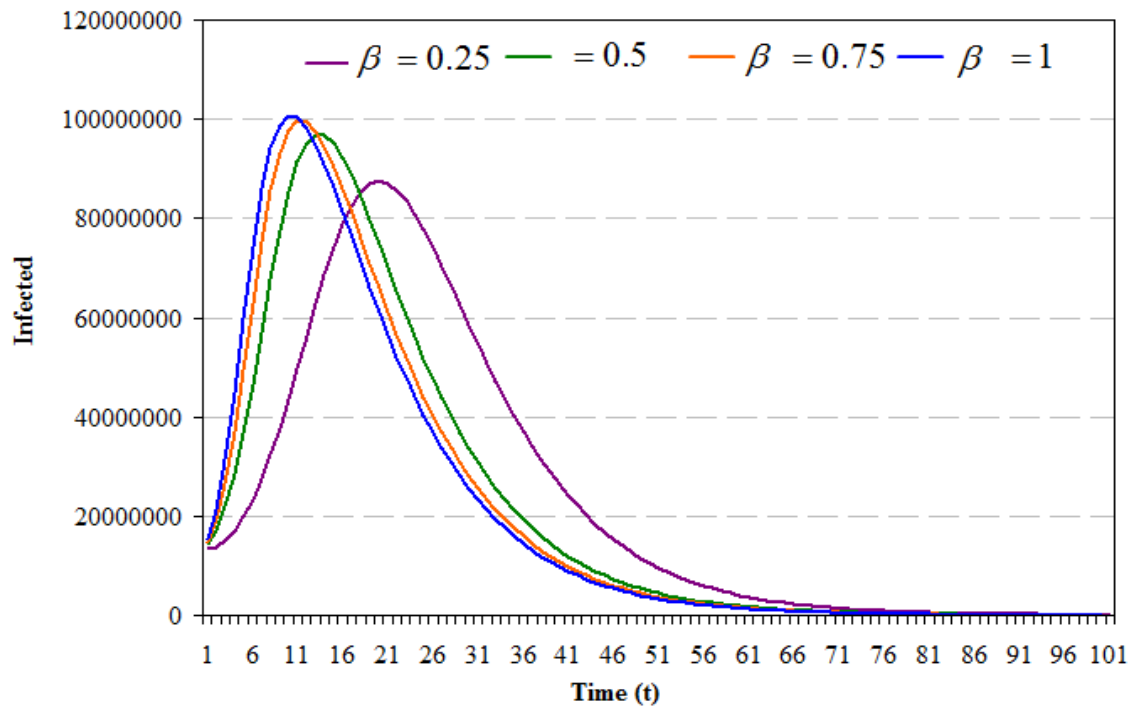


Figure 4.16: Behaviour of Infected (I) class for different Probability of susceptible becoming infectious per contact (β) values

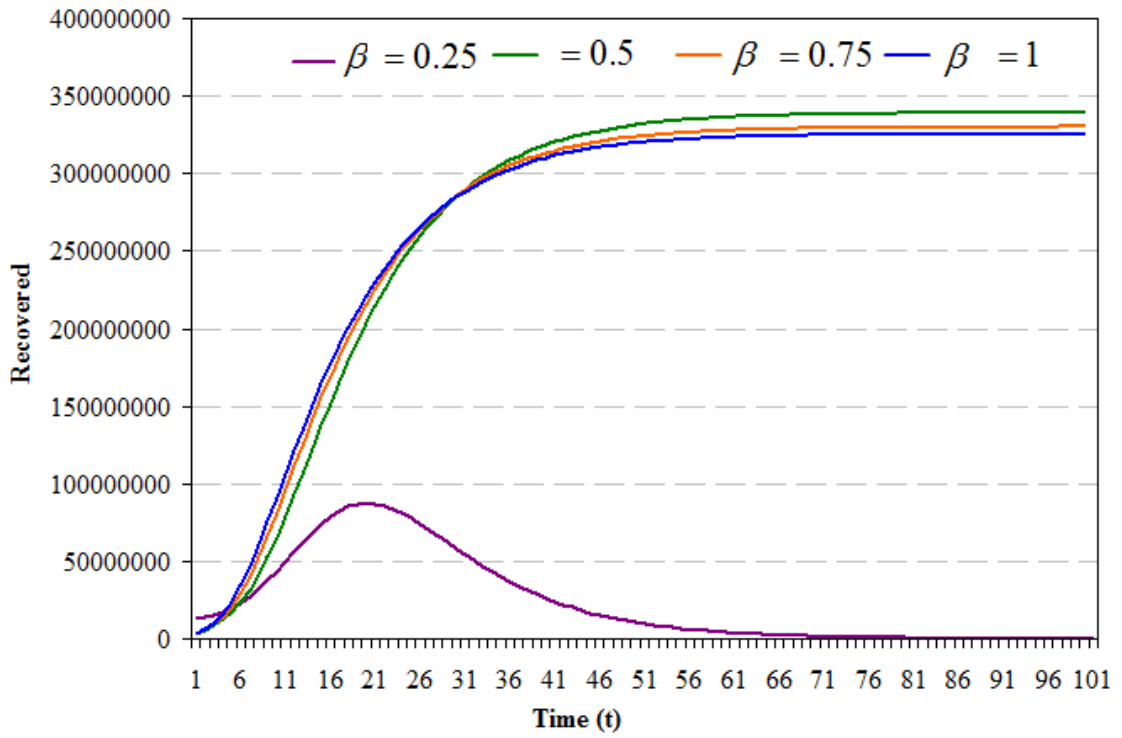


Figure 4.17: Behavior of the Recovered (R) class for different probabilities of susceptible becoming infectious per contact (β) values

4.6.2 Sensitivity Analysis of Infectious Period (γ)

In Figures 4.18 to 4.22 for different $\gamma = 0.1$, $\gamma = 0.2$, $\gamma = 0.3$, and $\gamma = 0.4$ values of γ , which is the transmission infectious coefficient of the disease, the time-dependent variation of the population in susceptible, vaccinated, exposed, infected, and recovered individuals has been examined, respectively. In Figure 4.18, the variation of the population of susceptible individuals over time has been investigated for the values of $\gamma = 0.1$, $\gamma = 0.2$, $\gamma = 0.3$, and $\gamma = 0.4$. Here, the most appropriate γ value for the actual data is calculated as $\gamma = 0.1$ by the parameter estimation method. According to this value, it is observed that the number of susceptible individuals increased over time as compared to other values of γ in the simulation. The estimated number of vaccinated individuals for the $\gamma = 0.1$ value obtained by the parameter estimation method is less than the estimated vaccinated

individuals for the $\gamma = 0.2$, $\gamma = 0.3$, $\gamma = 0.4$ values. Additionally, for the value $\gamma = 0.1$, the number of vaccinated individuals appears to be more stable than the others. It is observed that the number of infected individuals is also significantly less for the value of $\gamma = 0.1$ compared to other values and approaches to an asymptotic point at the end of the simulation period. Figure 4.22 shows that for the value of $\gamma = 0.4$, the recovered individuals are increasing as compared to the other decreasing γ values.

The impact of the recovery rate (γ) on different compartments is demonstrated in Figures 4.18 to 4.22. The sensitivity analysis shows how variations in γ influence the susceptible, vaccinated, exposed, infected, and recovered populations over time. Notably, the choice of γ plays a crucial role in determining the peak infection and duration of the infectious period, underlining its sensitivity and importance in modelling the dynamics of COVID-19.

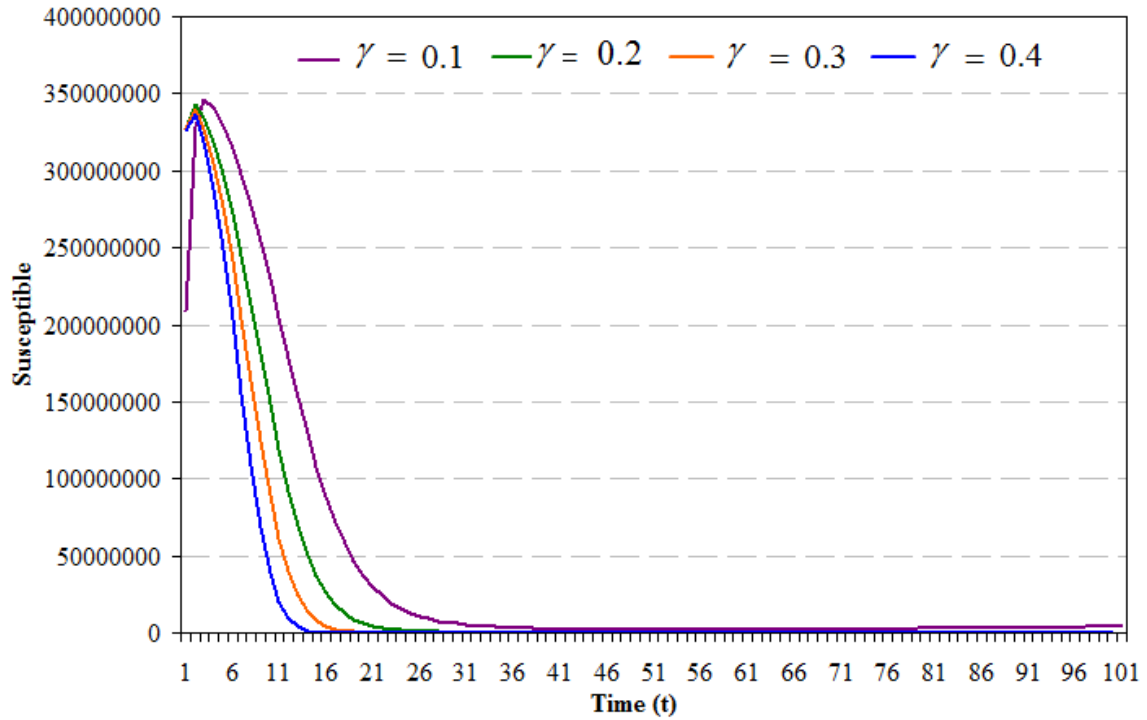


Figure 4.18: Behavior of Susceptible (S) class for different Infectious period (γ) values

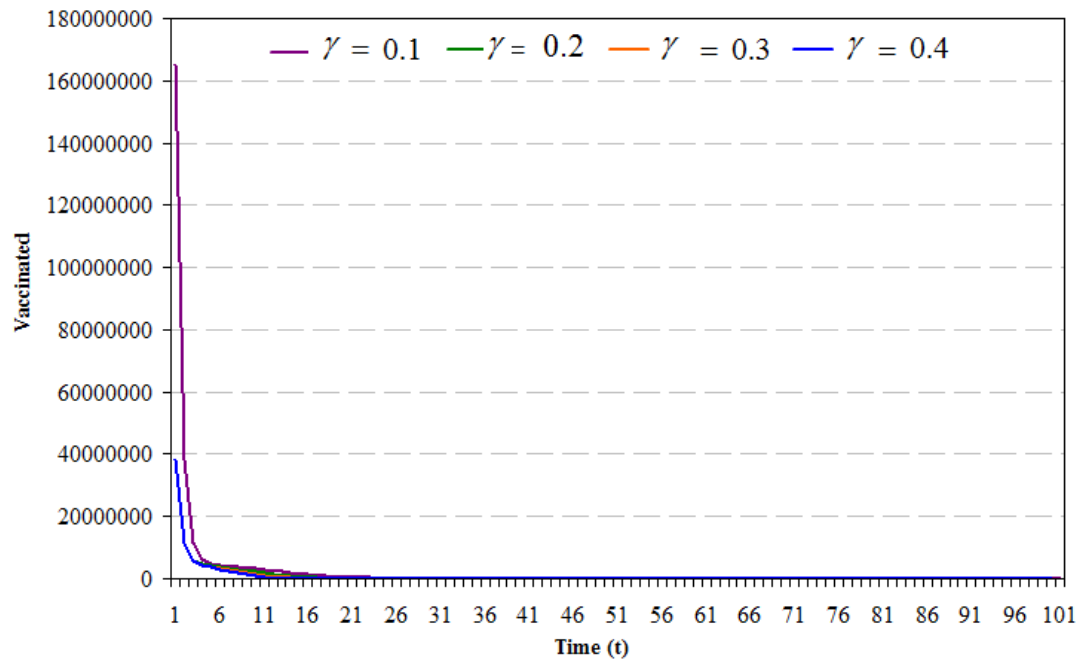


Figure 4.19: Behavior of Vaccinated (V) class for different Infectious periods (γ) values

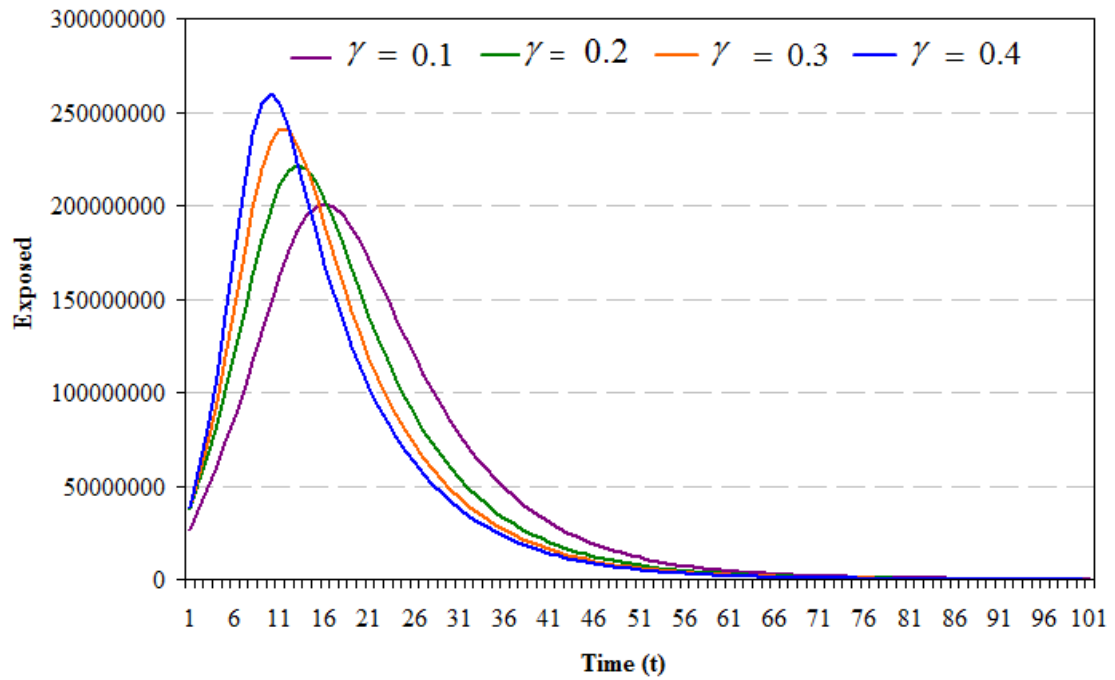


Figure 4.20: Behavior of Exposed (E) class for different Infectious period (γ) values

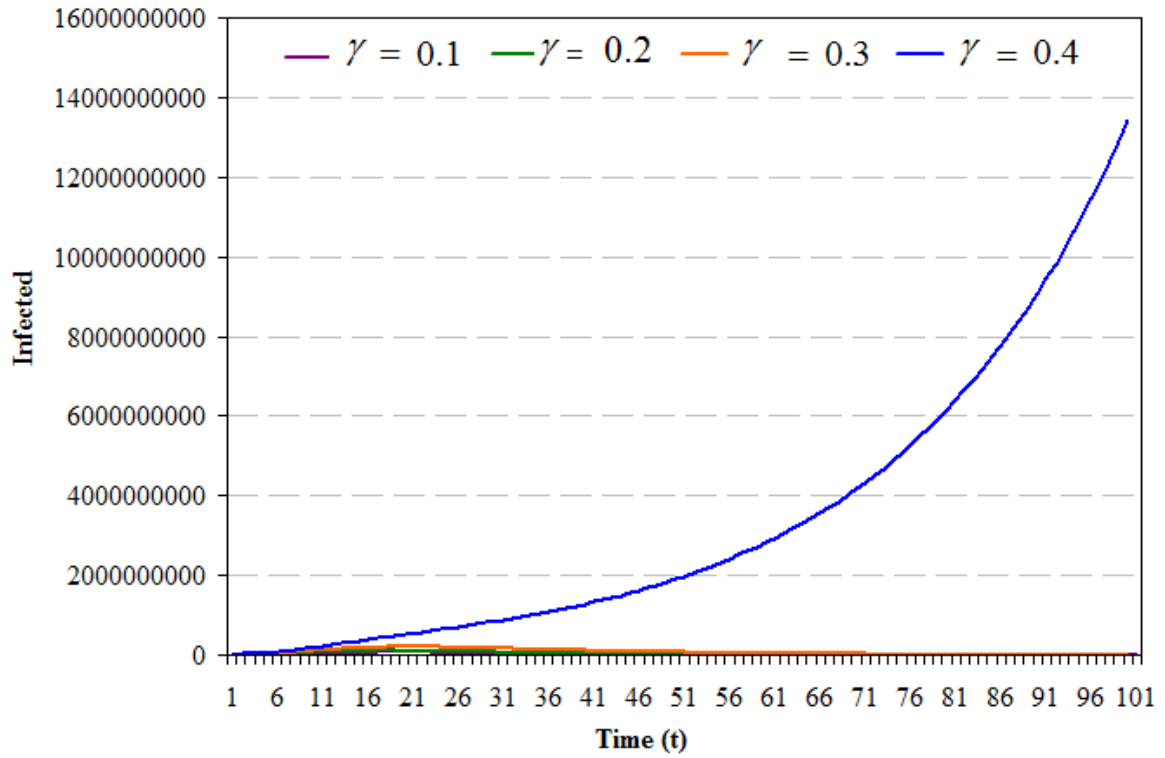


Figure 4.21: Behavior of Infected (I) class for different Infectious period (γ) values

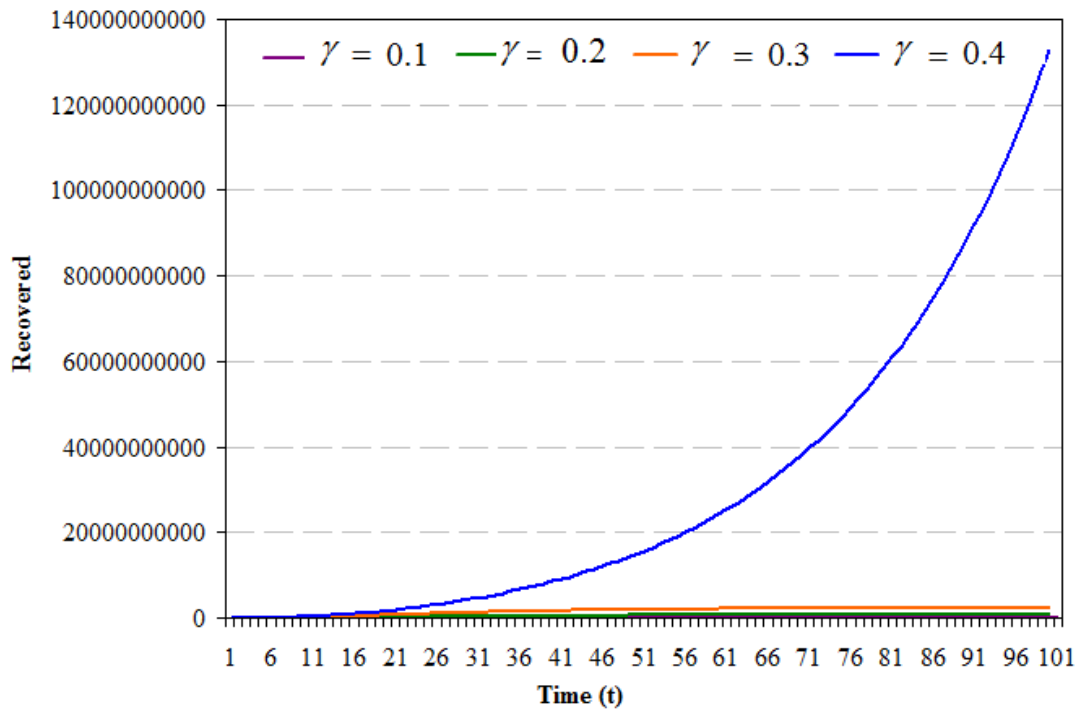


Figure 4.22: Behavior of Recovered (R) class for different Infectious period (γ) values

4.6.3 Sensitivity Analysis of Isolated Rate (δ)

The following Figures 4.23 to 4.27 exhibits the variations in the SVEIR model results caused by different values of δ ($\delta = 0.01$, $\delta = 0.1$, $\delta = 0.15$, and $\delta = 0.2$), which is the mean daily rate at which infectious cases are isolated. Here, it is observed that the number of sensitive individuals in the population for different δ values at the beginning is close to each other. As the δ value increases following time, the number of susceptible individuals in the population decreases. This situation can be interpreted as individuals who have never been isolated with the disease (sensitive) getting complete protection against the COVID-19 as a result of isolation.

Similarly, the variation of vaccination individuals in the population over time is investigated for different δ values in Figure 4.24. According to Figure 4.24, it is observed that when the value of δ increases, the effect is decreased on the vaccinated population. In Figure 4.25, the time-dependent variation of exposed individuals in the population for different δ values is examined. Here, it is seen that as the value of δ increases, the number of exposed individuals in the people also increases. Similarly, in Figures 4.26 and 4.27, when the value of δ is increased, the effect of infected individuals and the recovered population also increases.

The analysis underscores the role of isolation in affecting the susceptible, vaccinated, exposed, infected, and recovered individuals. Slight variations in δ lead to observable changes in the population dynamics, shedding light on the critical nature of effective isolation strategies in controlling the spread of the virus.

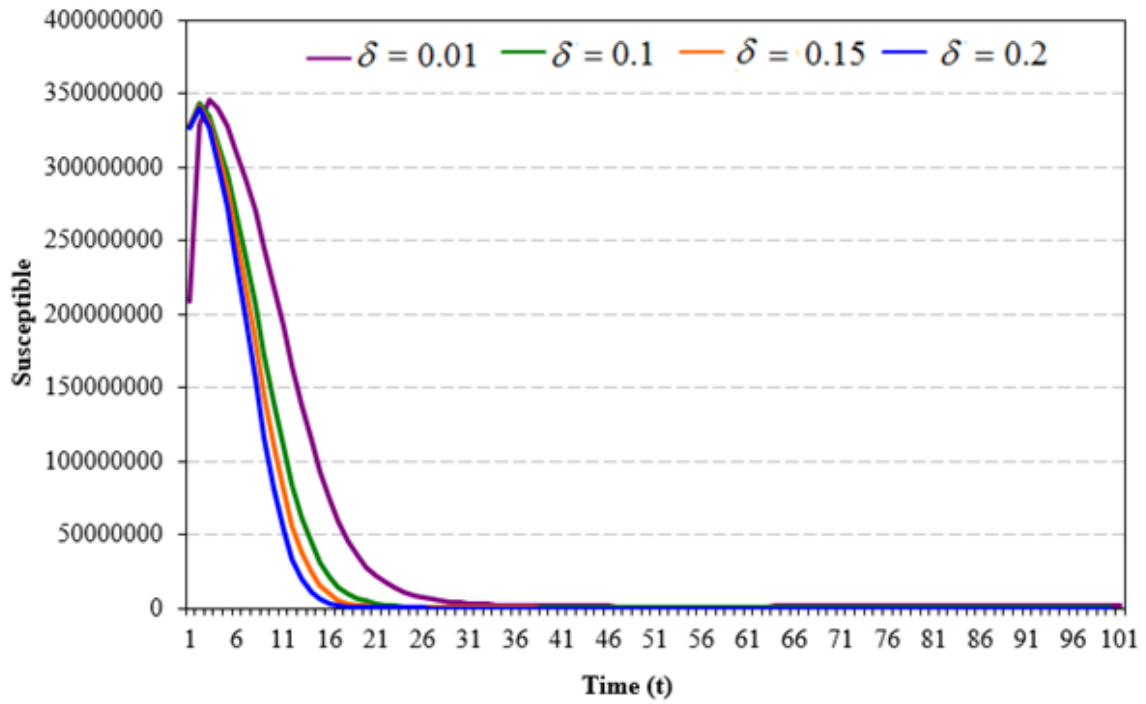


Figure 4.23: Behavior of Susceptible (S) class for different mean daily rates at which infectious cases are isolated (δ) values

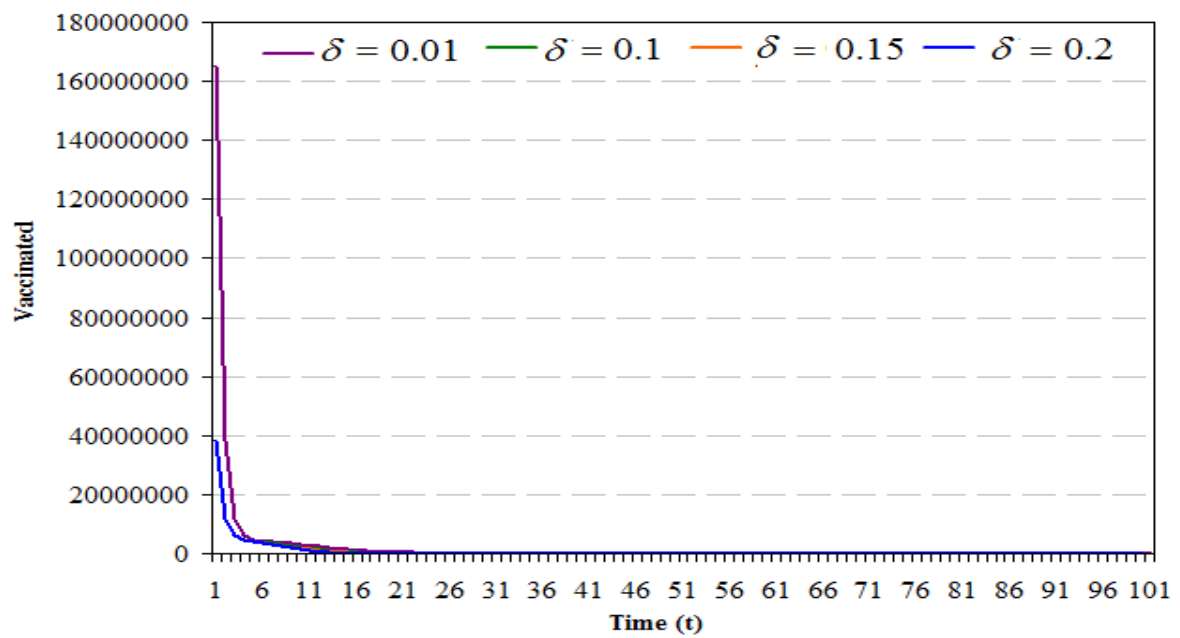


Figure 4.24: Behaviour of Vaccinated (V) class for different mean daily rates at which infectious cases are isolated (δ) values

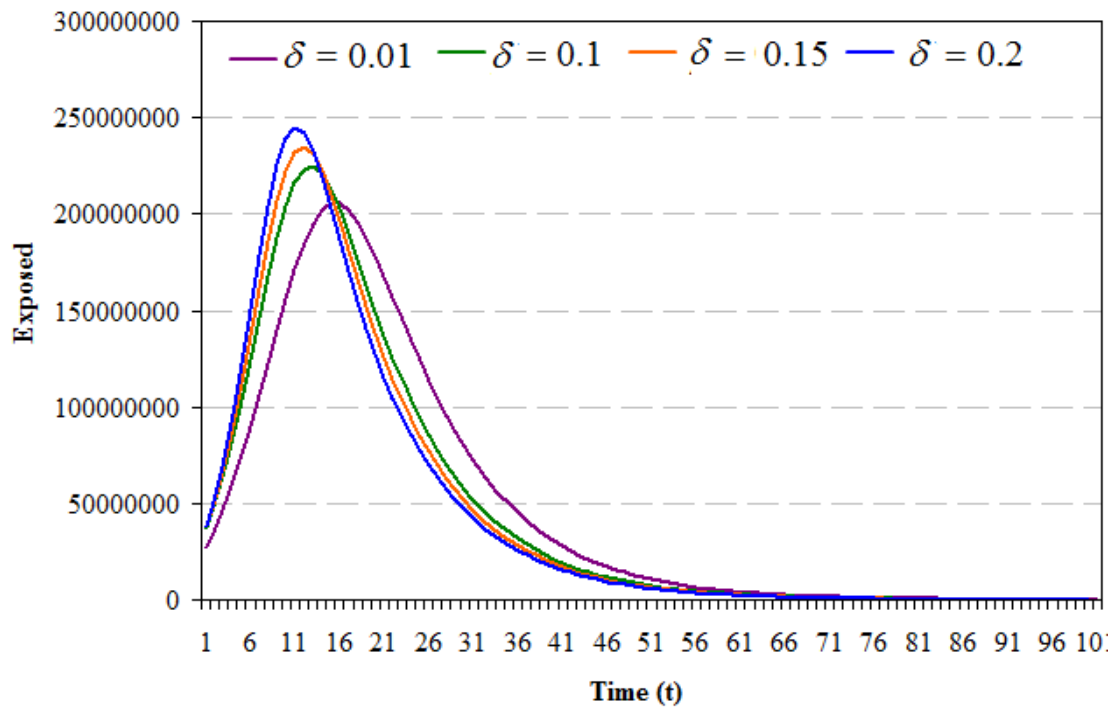


Figure 4.25: Behavior of Exposed (E) class for different mean daily rates at which infectious cases are isolated (δ) values

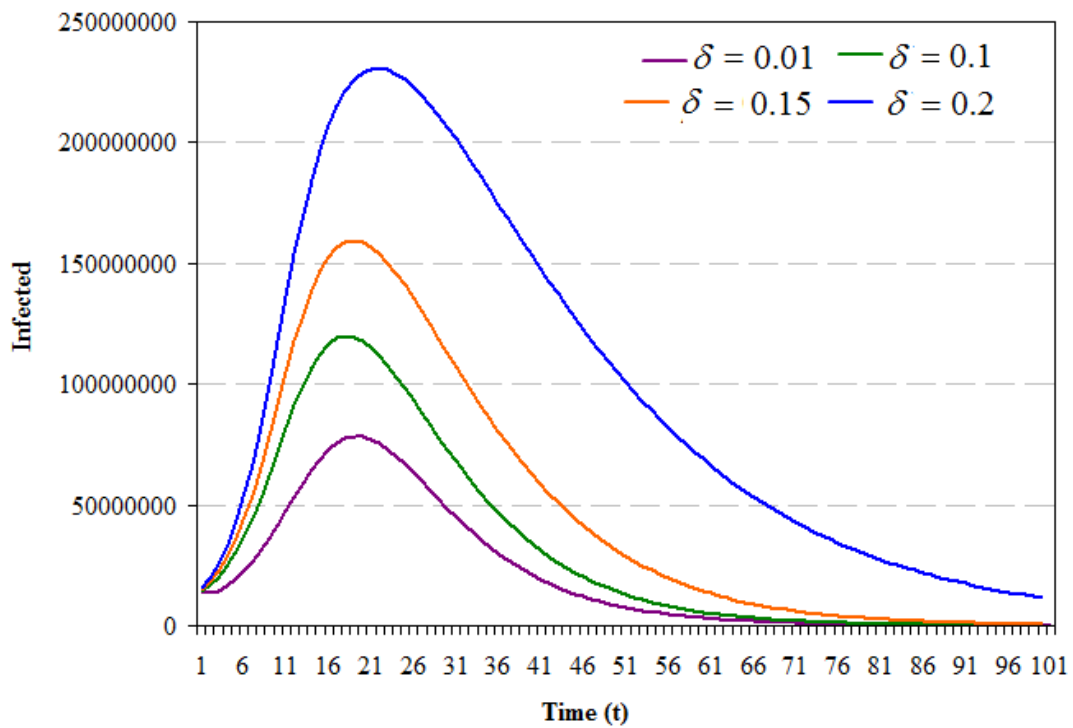


Figure 4.26: Behavior of Infected (I) class for different mean daily rates at which infectious cases are isolated (δ) values

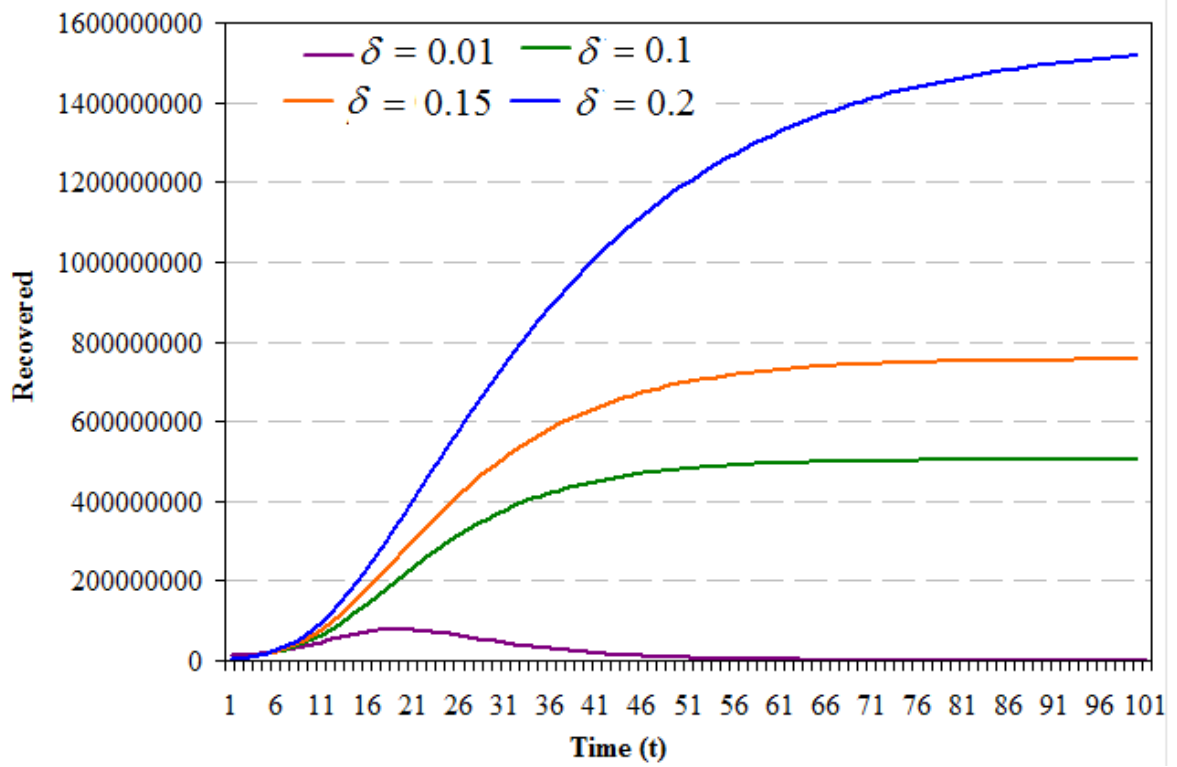


Figure 4.27: Behavior of Recovered (R) class for different mean daily rates at which infectious cases are isolated (δ) values

4.6.4 Sensitivity Analysis of death rate (ε)

Figures 4.28 to 4.32 exhibit the variations in S , V , E , I , and R under the influence of ε , respectively. The Behavior of the trends demonstrates that the S , E , I , and R pose more variations with respect to ε , while V is less as compared to other variables. Furthermore, increasing the values of ε , the trends of S , E , I and R also increased simultaneously. Figure 4.28 shows that the susceptible population (S) tends to decrease for the number of days to some extent and then marginally increase or asymptotically decrease for some fixed values of ε . It appears that the values of ε can control the Behavior of (S) significantly. In contrast, the vaccinated population (V) is not significantly affected by ε , as depicted in Figure 4.29. On the other hand, Figure 4.30 reveals that the exposed population (E) tends to behave like normally distributed data where the E shows the normal curves to the number of days. When

the ε is increased, the peak of the curves is reduced. In Figure 4.31, the infected population (I) also exhibits normal Behavior concerning time, but as the values of ε are reduced, the peak of the normal curves reaches an upward direction significantly increases. This suggests that to reduce the infection, the ε should be set to high values to reduce the infection. The Behavior of the recovered population (R) under the influence of ε is shown in Figure 4.32. It can be seen from the results that for the intermediate values of ε , more recovery is expected as compared to other smaller or larger values. The analysis presented in Figures 4.28 to 4.32 may help select any feasibility value of ε for which the infection can be put into any desired range. The analysis reveals how variations in ε impact the susceptible, vaccinated, exposed, infected, and recovered populations. Understanding the sensitivity of the model to mortality rates is crucial for policymakers in implementing strategies that mitigate the impact of the virus on public health and healthcare systems.

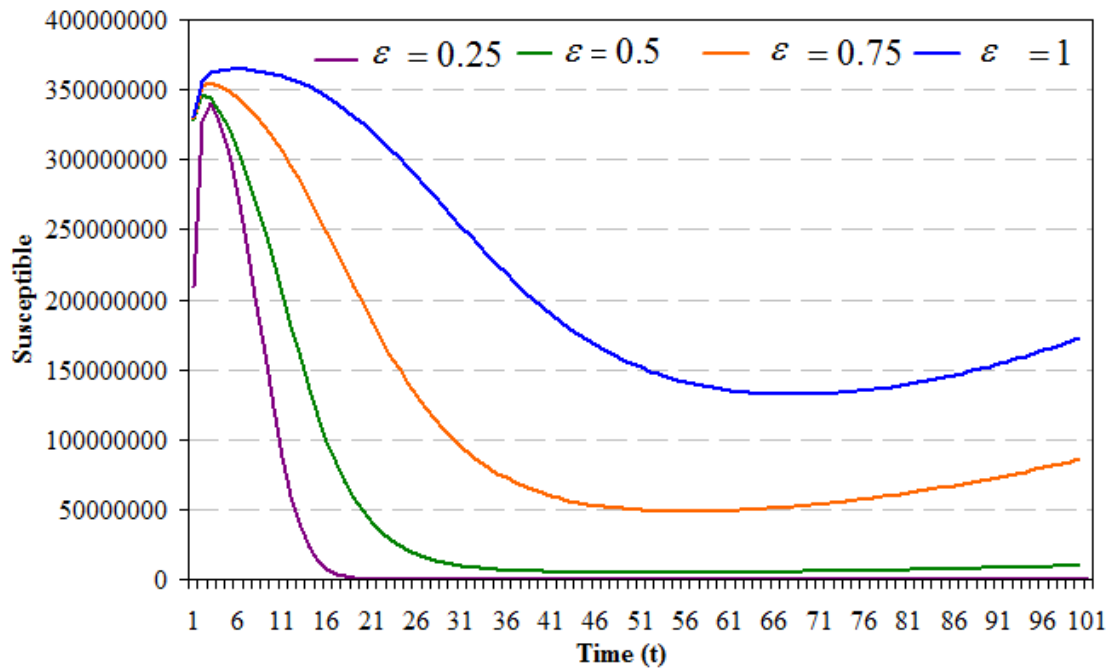


Figure 4.28: Behavior of Susceptible (S) class for different death rates due to COVID-19 (ε) values

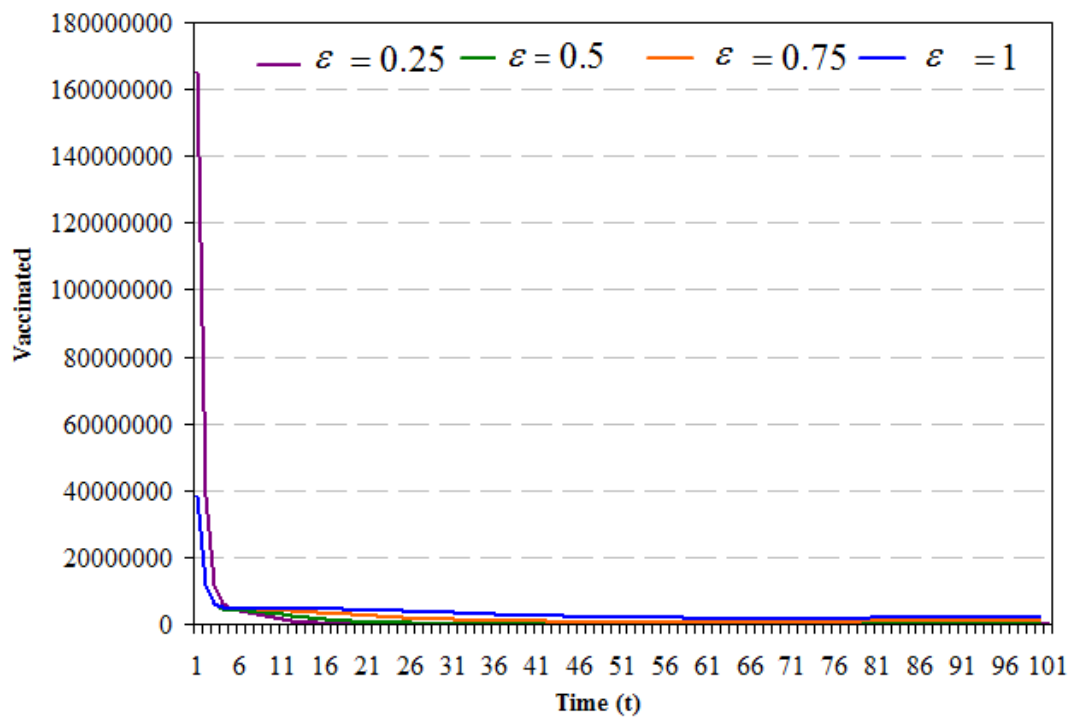


Figure 4.29: Behavior of Vaccinated (V) class for different death rates due to COVID-19 (ε) values

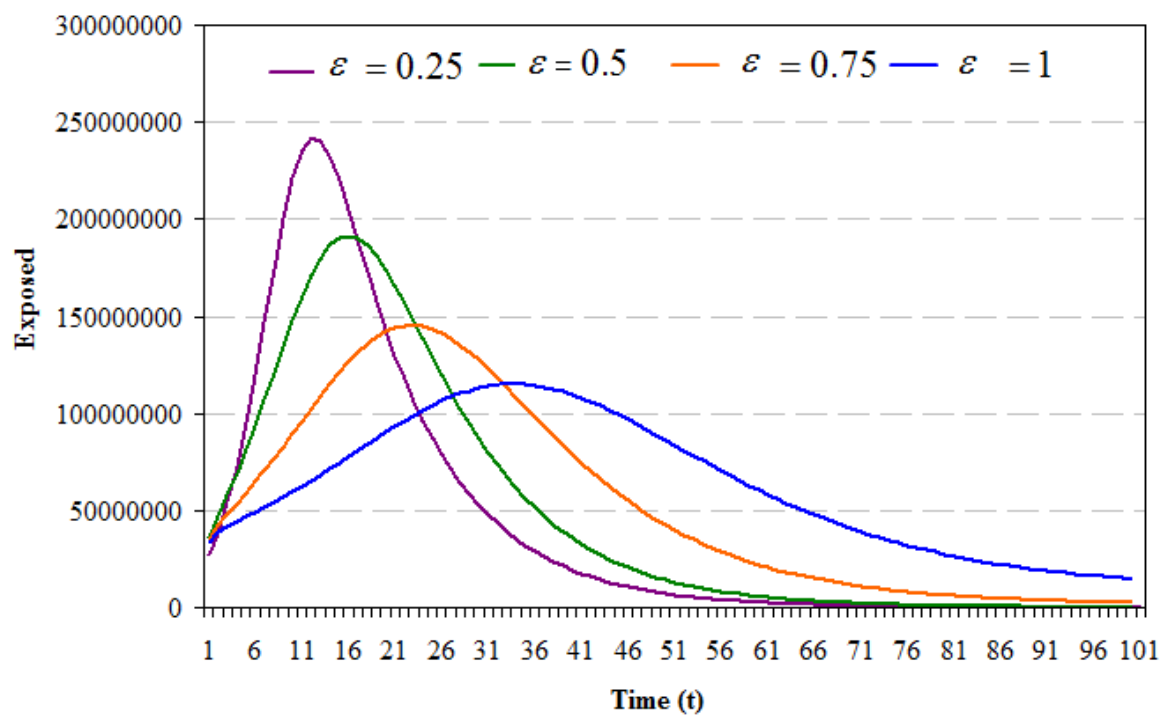


Figure 4.30: Behavior of Exposed (E) class for different death rates due to COVID-19 (ε) values

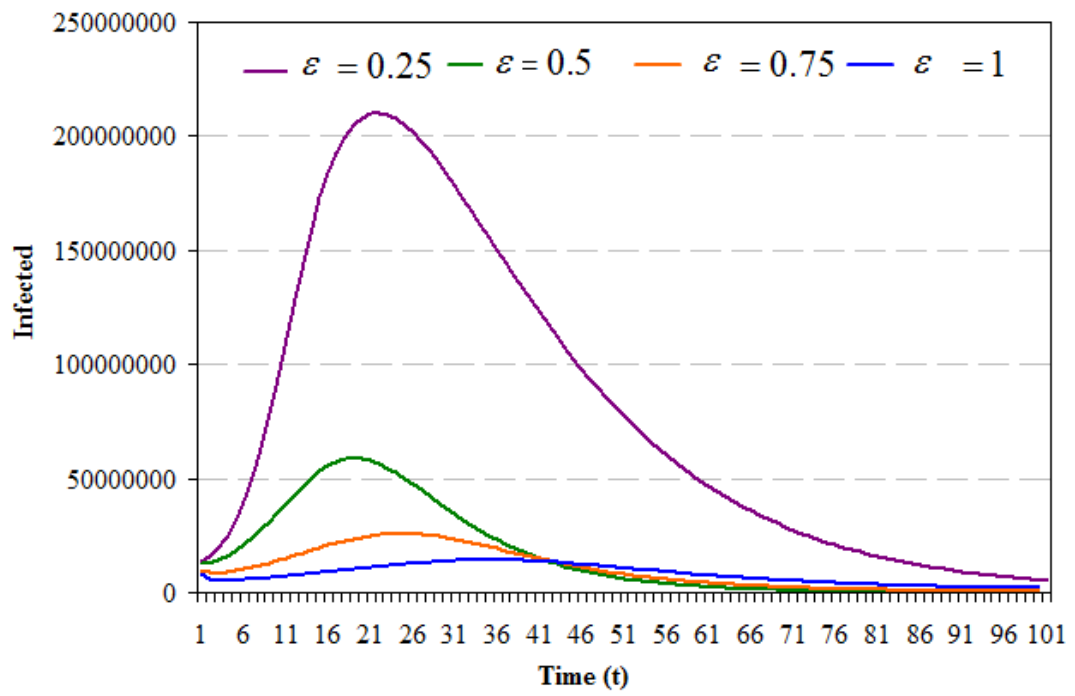


Figure 4.31: Behavior of Infected (I) class for different death rates due to COVID-19 (ε) values

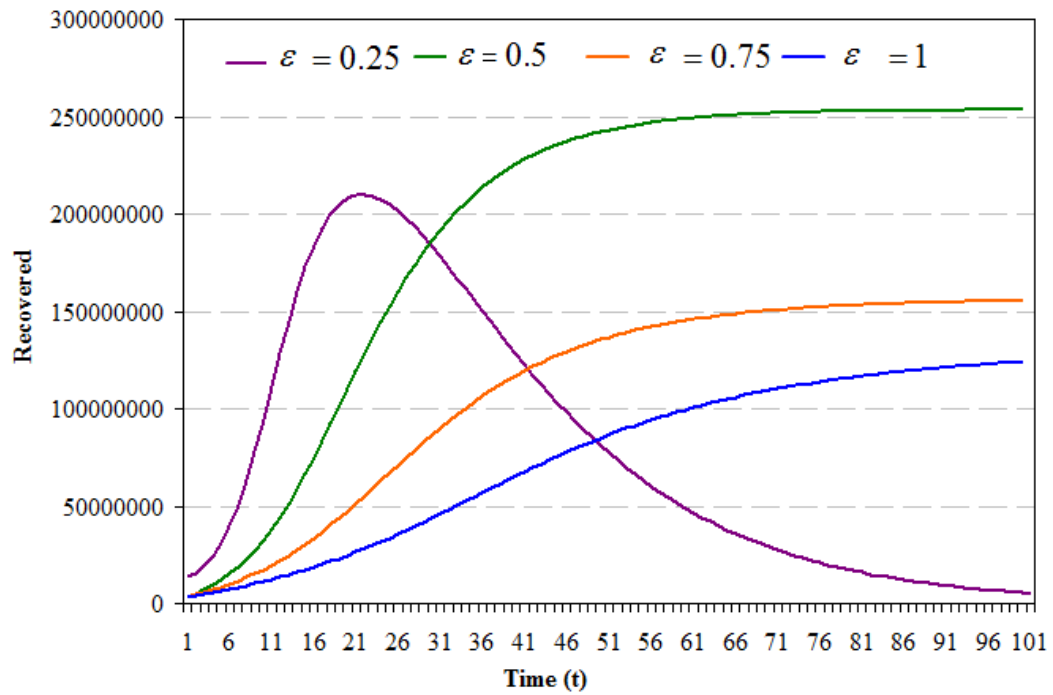


Figure 4.32: Behavior of Recovered (R) class for different death rates due to COVID-19 (ε) values

4.6.5 Sensitivity Analysis of Incubation Period(ϕ)

In Figures 4.33 to 4.37 for different values of ϕ which is the incubation period, $\phi = 0.25$, $\phi = 0.5$, $\phi = 0.75$, and $\phi = 0.1$, the variations on the S, V, E, I, and R individuals have been studied. Here, the most appropriate ϕ The value for the actual data is calculated as $\phi = 0.25$ by the parameter estimation method. According to Figure 4.33, it is observed that as the ϕ value increases, the number of susceptible individuals in the population decreases. Similarly, in Figure 4.34, the time variation of the number of vaccinated individuals for different ϕ values are examined. According to the simulation results, as ϕ As values increase over time, the number of exposed individuals decreases. Here, the opposite of the situation observed in Figure 4.35 is expected to occur. In other words, an increase in ϕ values (increasing the number of exposed individuals) will cause a decrease in the number of sensitive individuals and an increase in the number of susceptible individuals. According to Figure 4.36, the value ϕ increases, and then the effect of infected individuals also increases. Similarly, in Figure 4.37, when the value of ϕ decreased, the recovered individuals also decreased. On the other hand, when the value of ϕ is increased according to time, then the recovered individual's effect also increases.

The sensitivity of the model to changes in the incubation period (ϕ) is demonstrated in Figures 4.33 to 4.37. Variations in ϕ have discernible effects on the susceptible, vaccinated, exposed, infected, and recovered populations over time. This analysis highlights the significance of accurately estimating the incubation period for effective modeling and prediction of COVID-19 dynamics.

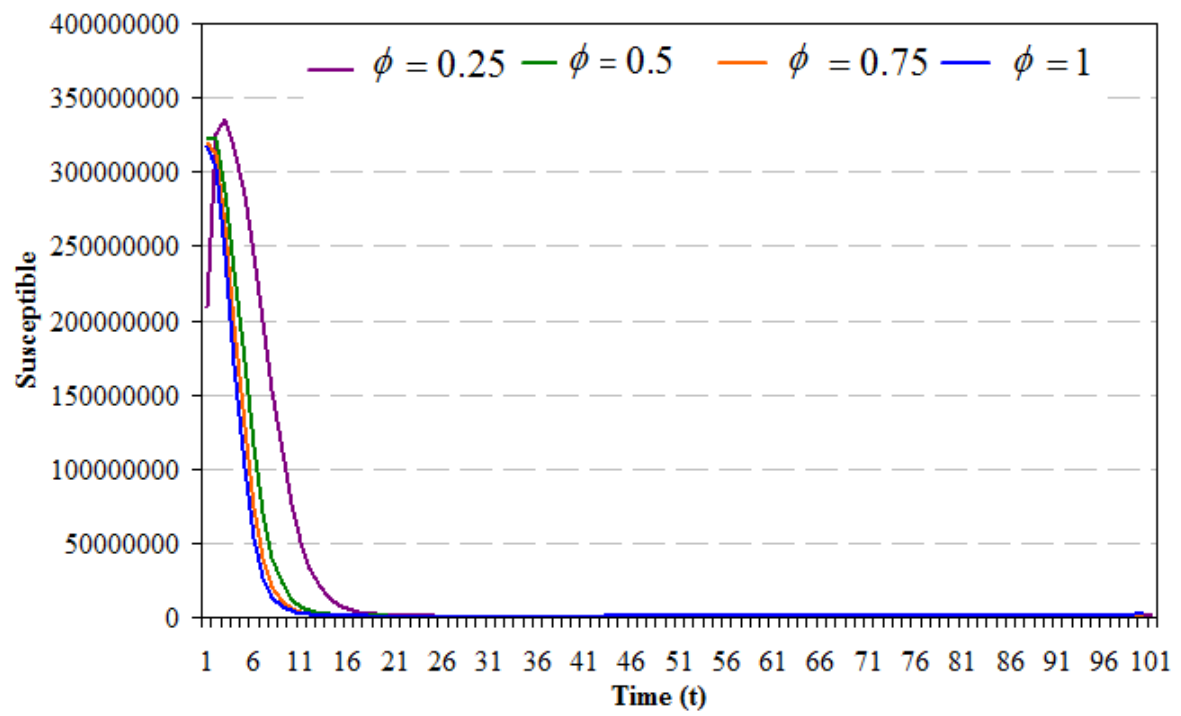


Figure 4.33: Behavior of Susceptible (S) class for different incubation periods (ϕ) values

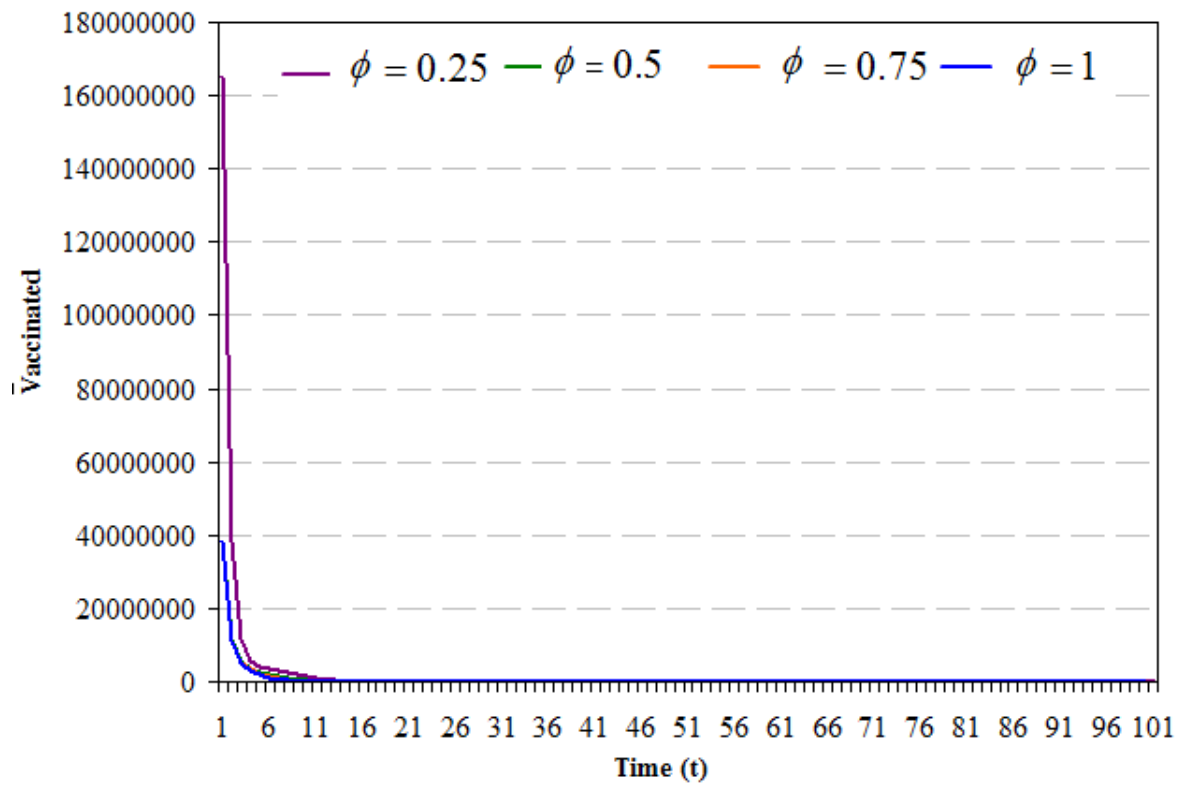


Figure 4.34: Behavior of Vaccinated (V) class for different incubation period (ϕ) values

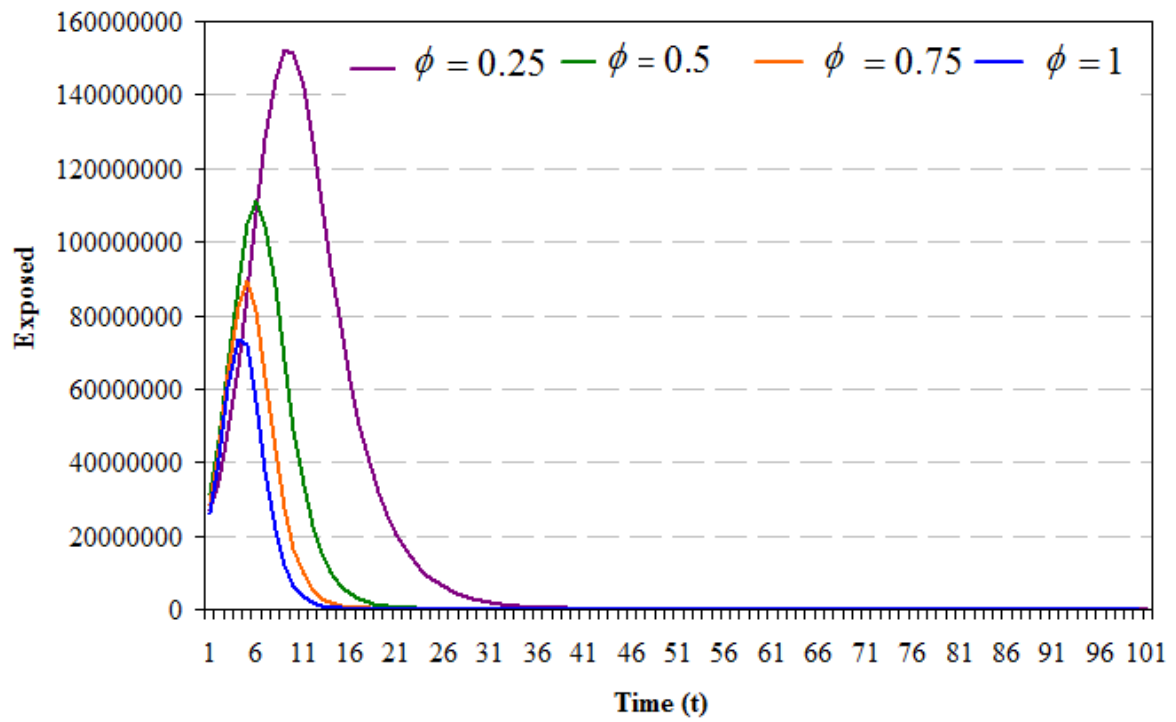


Figure 4.35: Behavior of Exposed (E) class for different incubation period (ϕ) values

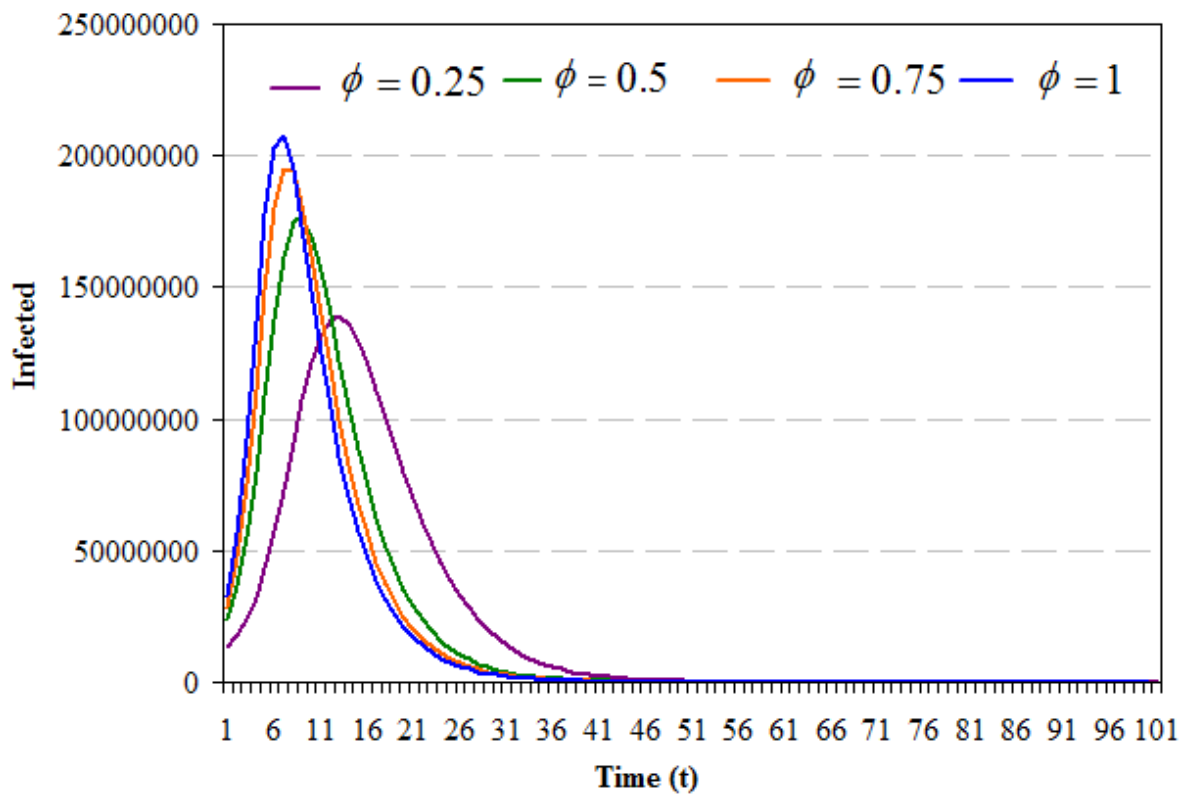


Figure 4.36: Behavior of Infected (I) class for different incubation period (ϕ) values

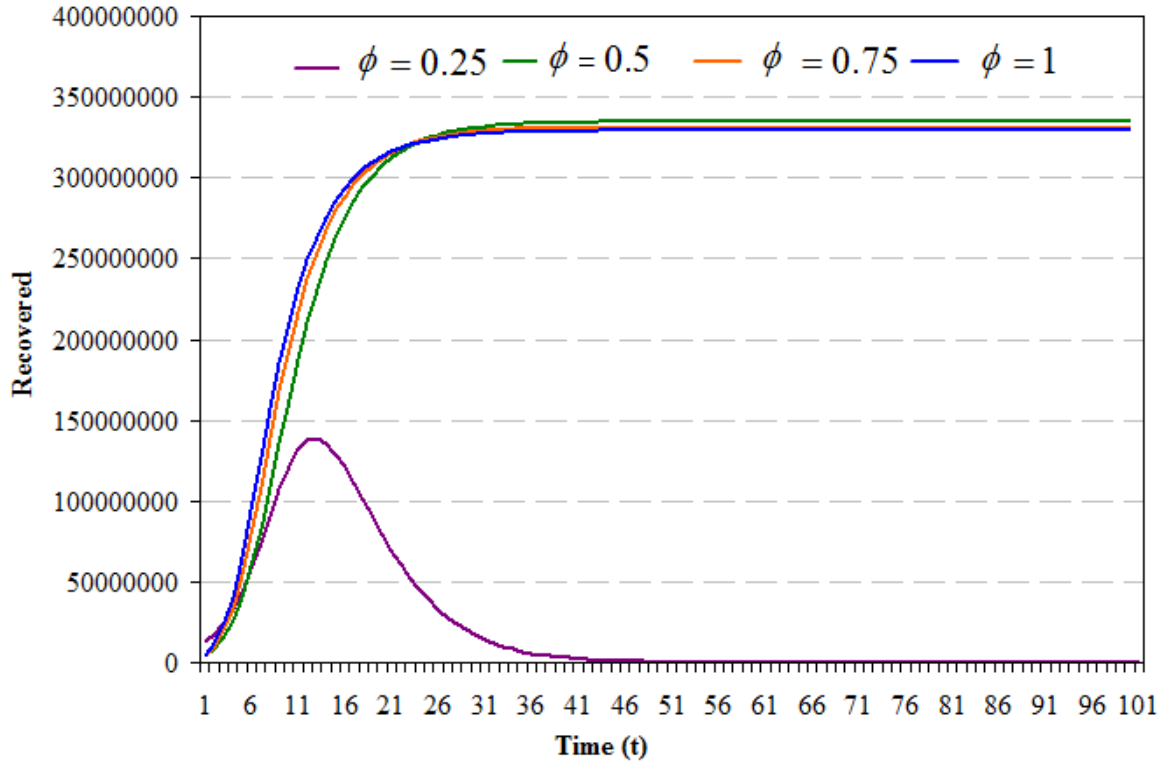


Figure 4.37: Behavior of Recovered (R) class for different incubation period (ϕ) values

4.6.6 Sensitivity Analysis of the average number of contacts per day per case (ξ)

In Figures 4.38 to 4.42, the variations caused by different values of ξ , which is the average number of contacts per day per case, $\xi = 0.25$, $\xi = 5$, $\xi = 10$, $\xi = 15$, and $\xi = 20$ have been exhibited. Here, the most appropriate ξ The value for the actual data is calculated. According to Figure 4.38, it is observed that as the ξ value increases, the number of susceptible individuals in the population decreases. Similarly, in Figures 4.39 the time variation of the number of sensitive vaccinated individuals for different ξ values is examined. According to the simulation results, as ξ values increase over time, the number vaccinated individual's decreases. In other words, an increase in ξ values (increasing the number of exposed and infected individuals) will cause an increase in the number of exposed and infected individuals. According to Figure 4.42, the value ξ decreases, and the effect of

recovered individuals also reduces. As time goes when, the value of ξ increases, the impact of recovered individuals also increases.

Figures 4.38 to 4.42 illustrate the sensitivity of the model to the average number of contacts per day per case (ξ). It is revealed that the small changes in ξ lead to significant alterations in the susceptible, vaccinated, exposed, infected, and recovered populations. Understanding how contact rates affect virus transmission is crucial for implementing targeted interventions and public health measures.

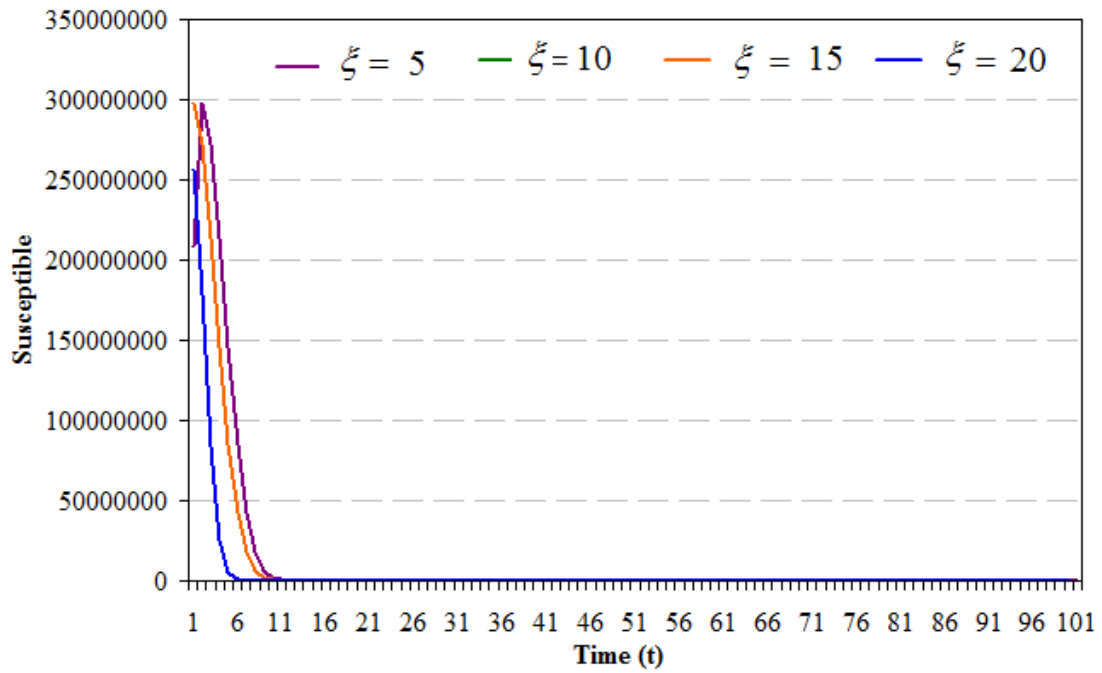


Figure 4.38: Behavior of Susceptible (S) class for different average number of contacts per day per case (ξ) values

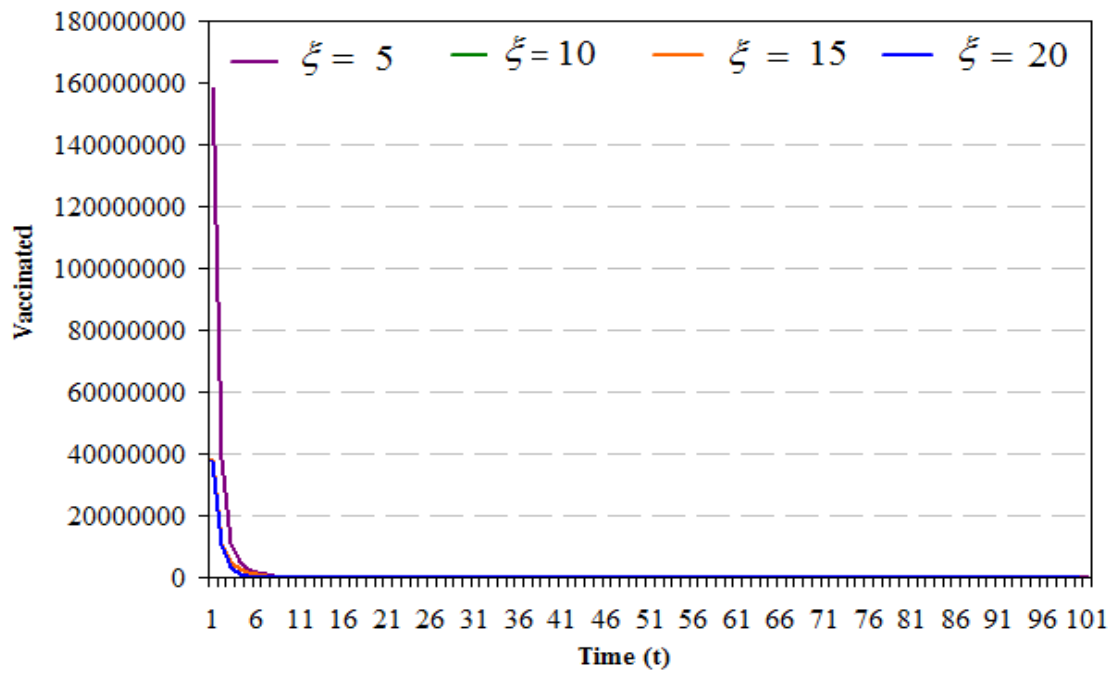


Figure 4.39: Behaviour of Vaccinated (V) class for different average number of contacts per day per case (ξ) values

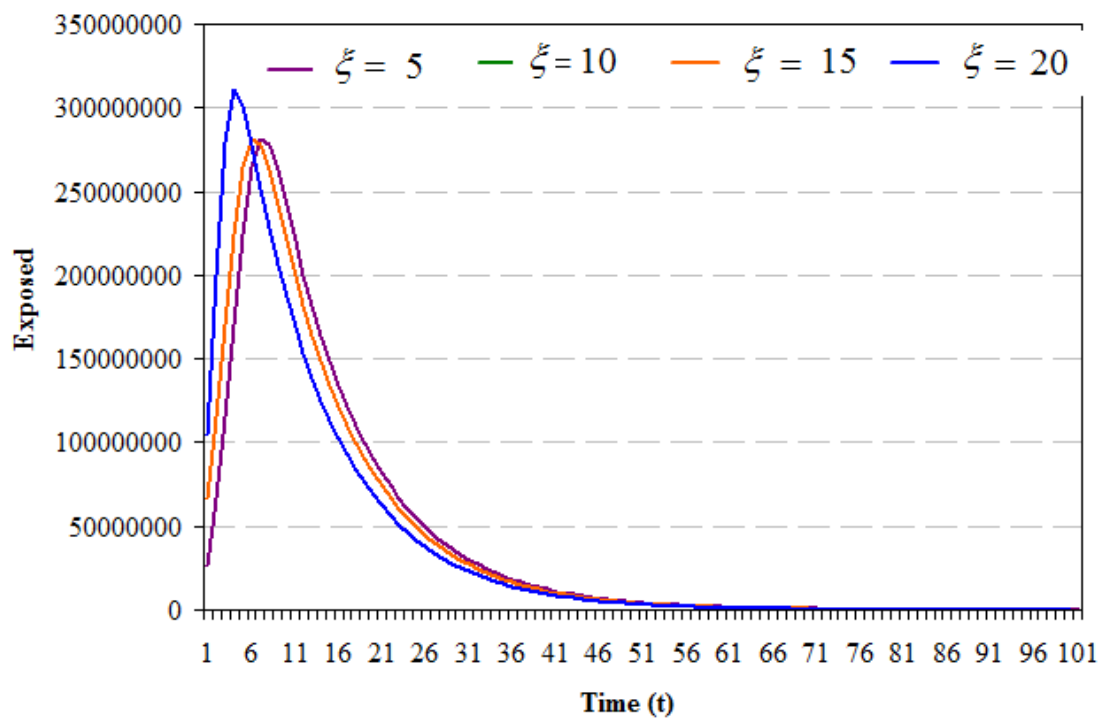


Figure 4.40: Behaviour of Exposed (E) class for different average number of contacts per day per case (ξ) values

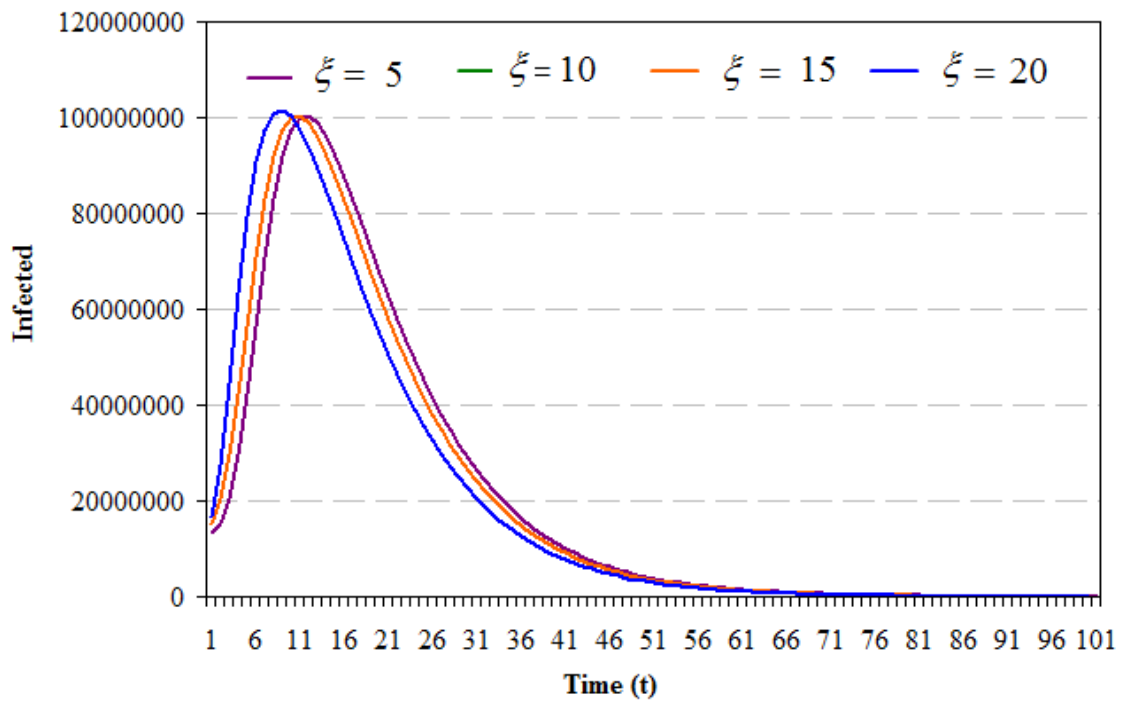


Figure 4.41: Behavior of Infected (I) class for different average number of contacts per day per case (ξ) values

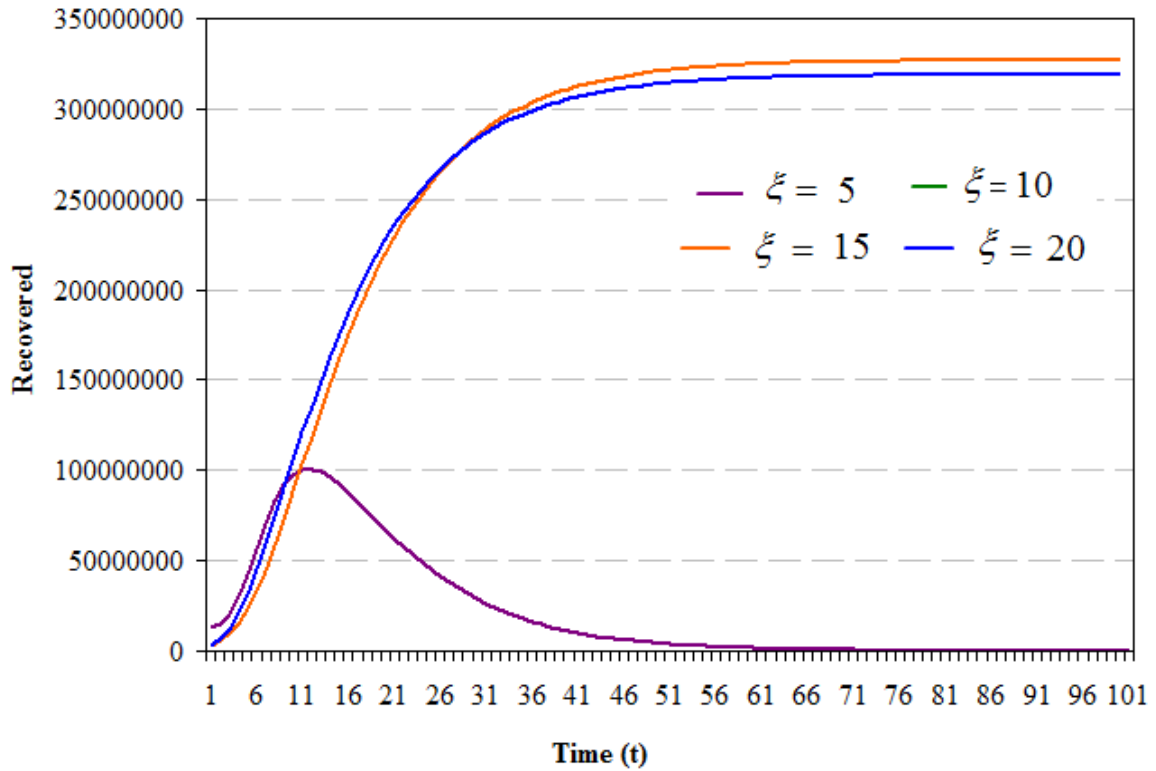


Figure 4.42: Behavior of Recovered (R) class for different average number of contacts per day per case (ξ) values

4.6.7 Sensitivity Analysis of natural death rate (μ)

In Figure 4.43, the variation of the population of susceptible individuals over time has been investigated for the values of $\mu = 0.25$, $\mu = 0.5$, $\mu = 0.75$ and $\mu = 1$. Here, the most appropriate μ The value for the actual data is calculated as $\mu = 0.25$ by the parameter estimation method. According to this value, it is observed that the number of susceptible individuals decreased over time compared to other values of μ in the simulation. Similarly, in Figures 4.44 to 4.47, for different $\mu = 0.25$, $\mu = 0.5$, $\mu = 0.75$, and $\mu = 1$ values μ which is the transmission coefficient of the disease, the time-dependent variation of the population in vaccination, exposed, infected, and recovered individuals has been examined, respectively. As can be seen in Figure 4.44, when the value of μ increases the effect of vaccination, resulting in a decrease in the population.

Similarly, the variation of exposed and infected individuals in the population over time is investigated for different μ values in Figures 4.45 to 4.46. According to the Figures, it is observed that μ has no significant effect on the exposed and infected population. In Figure 4.47, when the value of μ is decreased, then the recovered individuals also decrease, and the importance of μ is increased. The model's sensitivity to variations in the natural death rate (μ) is explored in Figures 4.43 to 4.47. Changes in μ impact the susceptible, vaccinated, exposed, infected, and recovered populations over time. This analysis highlights the interconnectedness of demographic factors and disease dynamics, emphasizing the need for accurate estimates of natural death rates for robust modelling.

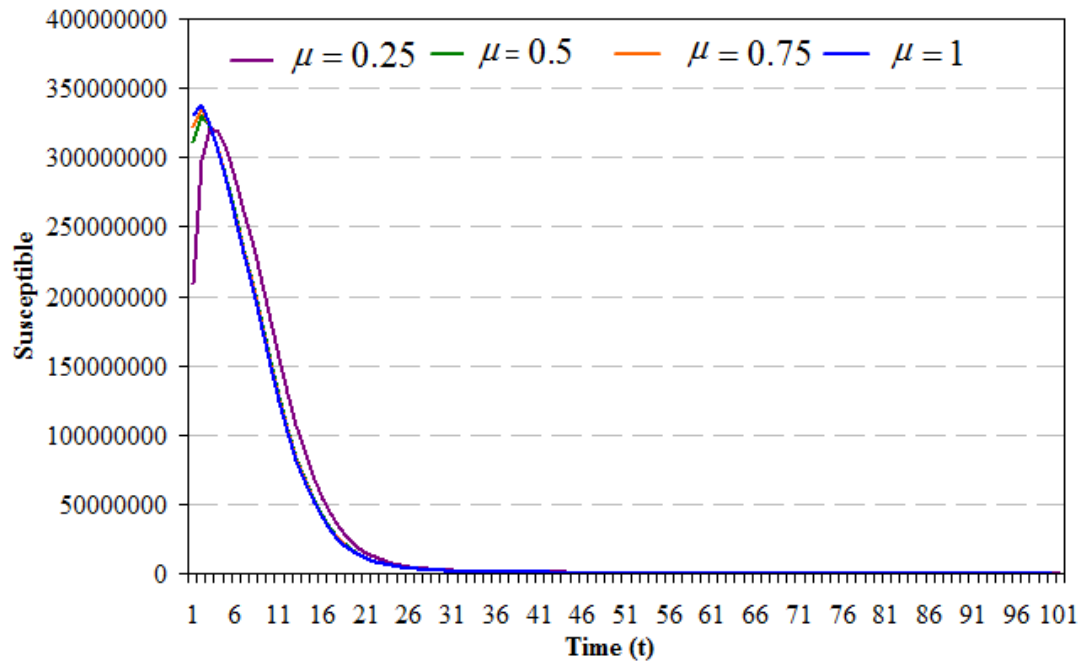


Figure 4.43: Behavior of Susceptible (S) class for different natural death rates (μ) values

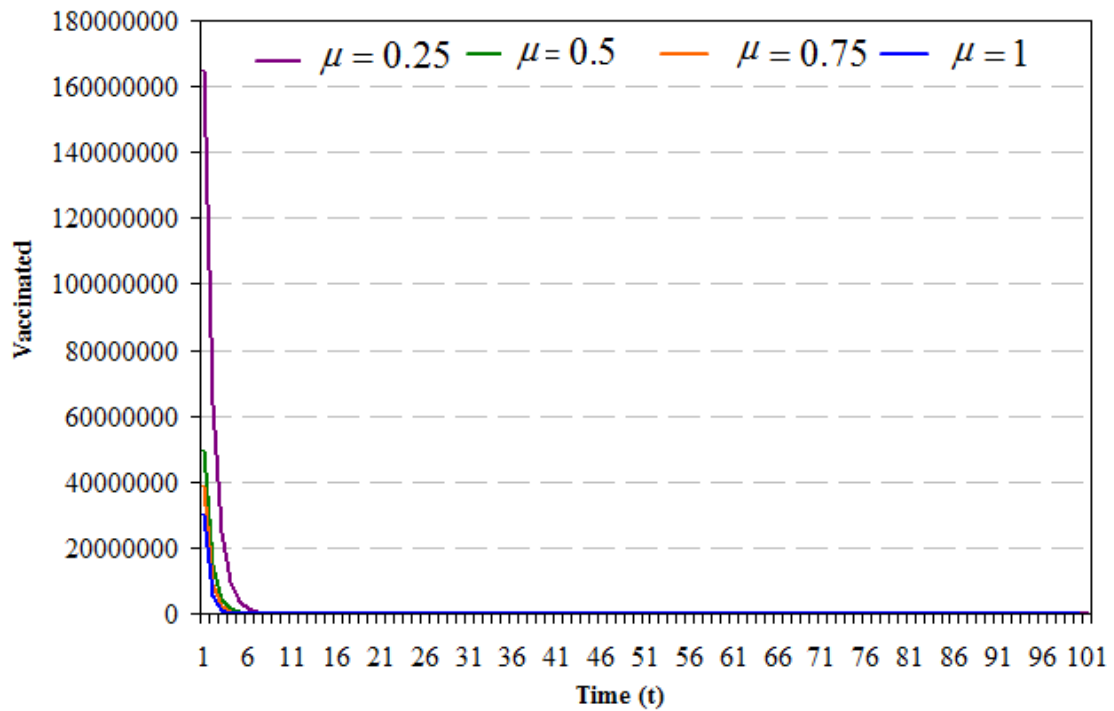


Figure 4.44: Behavior of Vaccinated (V) class for different natural death rates (μ) values

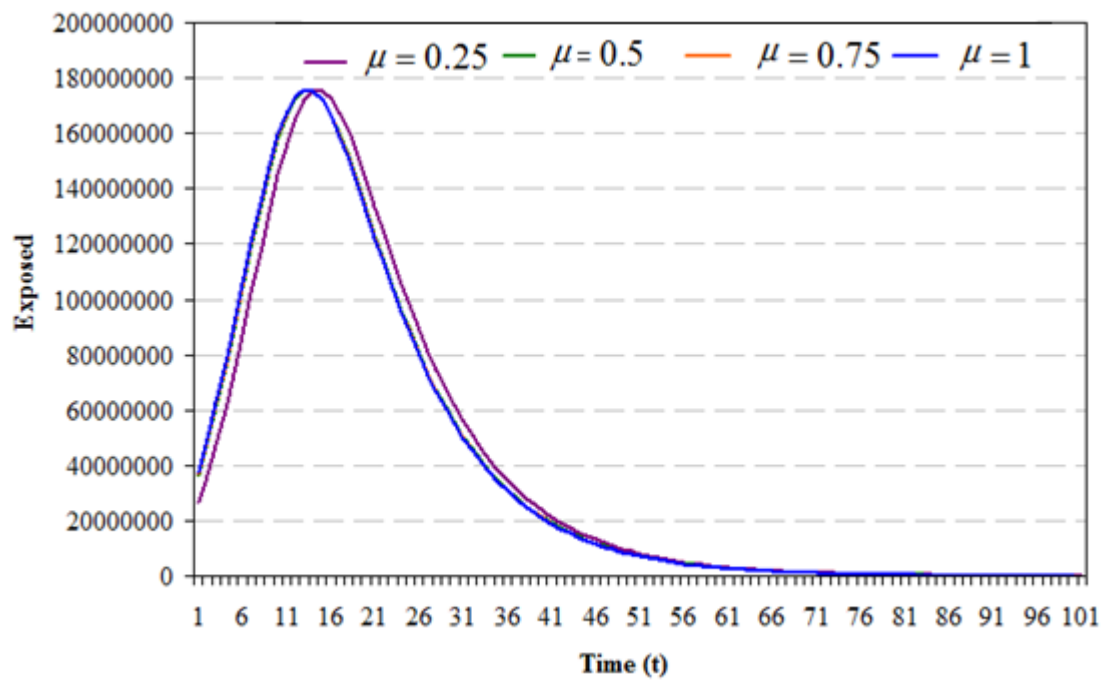


Figure 4.45: Behavior of Exposed (E) class for different natural death rates (μ) values

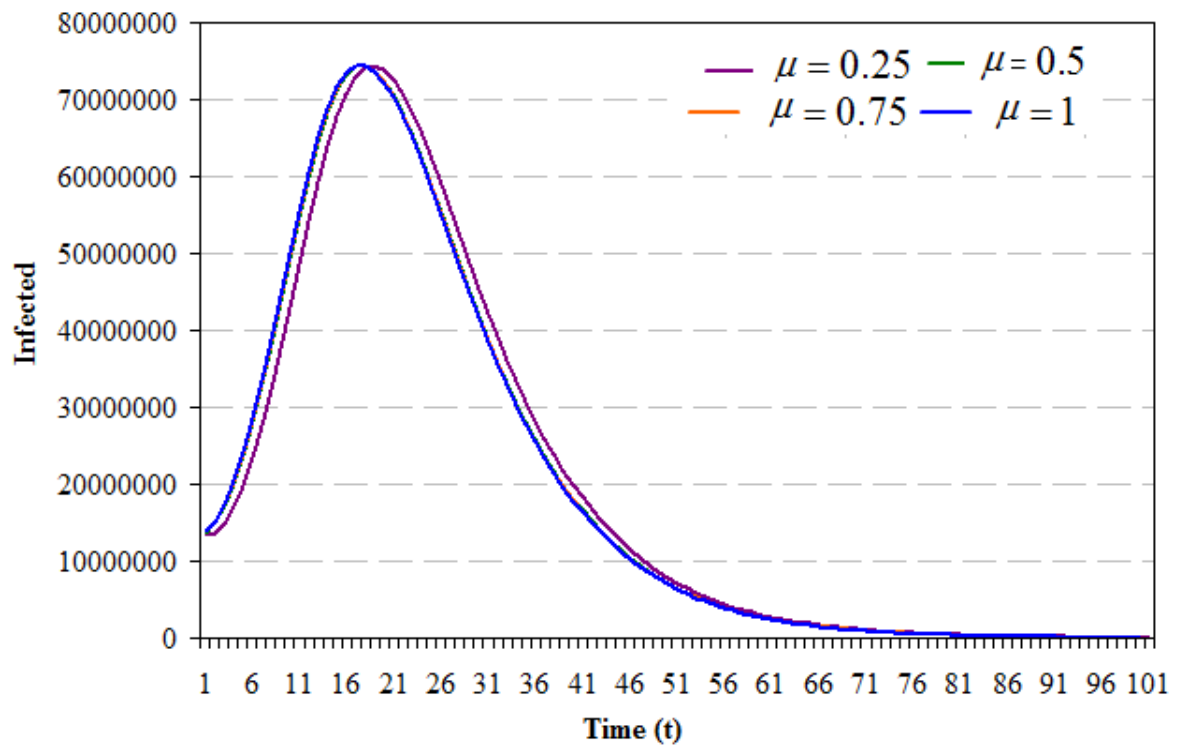


Figure 4.46: Behavior of Infected (I) class for different natural death rates (μ) values

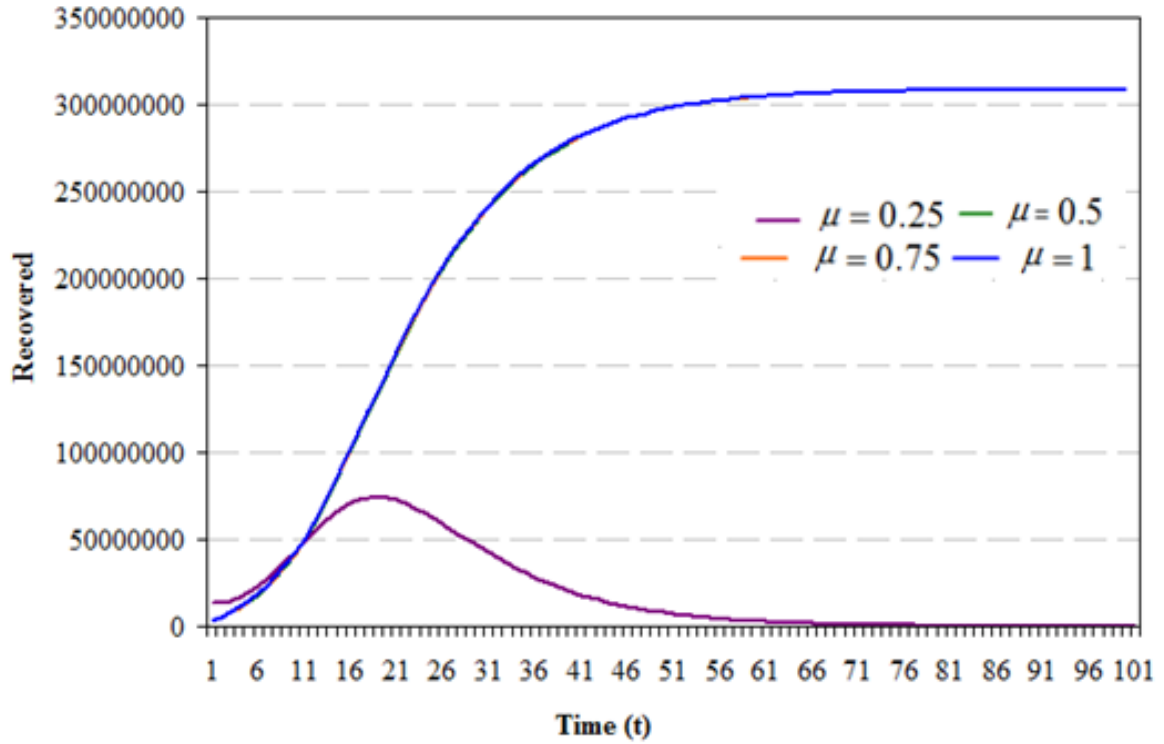


Figure 4.47: Behavior Recovered (R) class for different natural death rates (μ) values

4.6.8 Sensitivity Analysis of Vaccination Rate (τ)

Similarly, to study the relation between the vaccination rate and the Behavior of the S , V , E , I , and R populations, the SVEIR model was run for the different values. $\tau = 0.001$, $\tau = 0.01$, $\tau = 0.1$ and $\tau = 1$ while all other parameters were fixed. The Figures 4.48 to 4.52 exhibit the variations in S , V , E , I , and R under the influence of τ respectively. The Behavior of the trends demonstrates that the S , E , I , V , and R do not pose more variations with respect to τ . It appears that only for a higher value of $\tau = 1$, the trends of S , V , E , I , and R abruptly increase, while for other small values of τ the slight variations in the dependent variables are observed. The analysis also suggests that the time duration for the S and V is too small to be affected by the τ while for other classes, E , I , and R , the time to reach the asymptotic value is significant. This analysis emphasizes the vital role of vaccination rates in shaping the pandemic's trajectory and highlights the need for effective vaccination strategies.

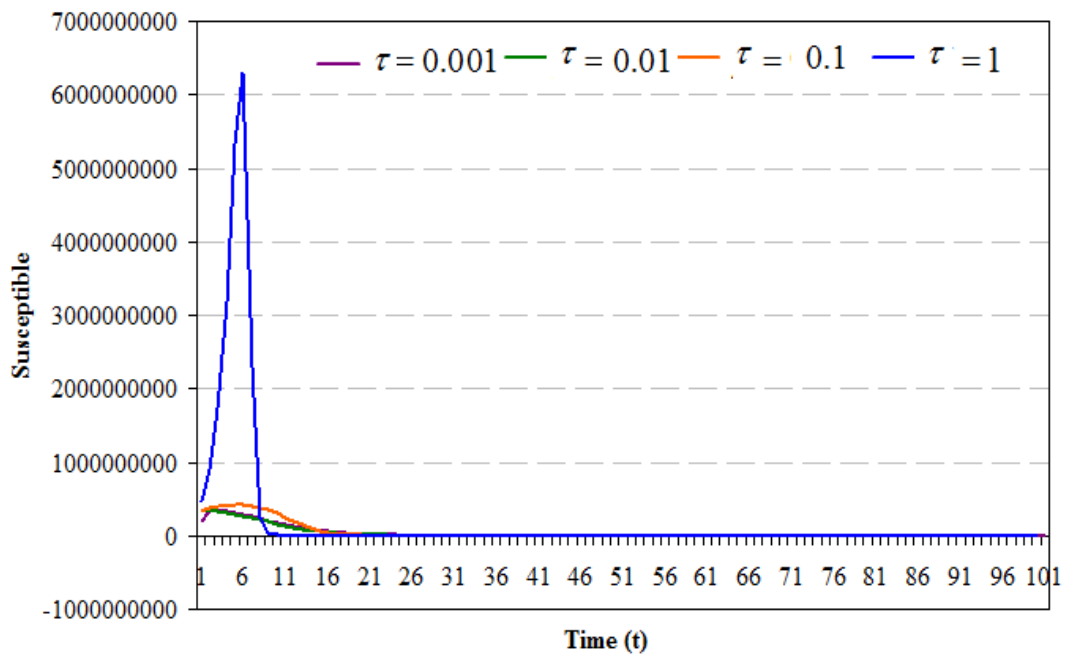


Figure 4.48: Behavior of Susceptible (S) class for different people in vulnerable group starts receiving a vaccination rate (τ) values

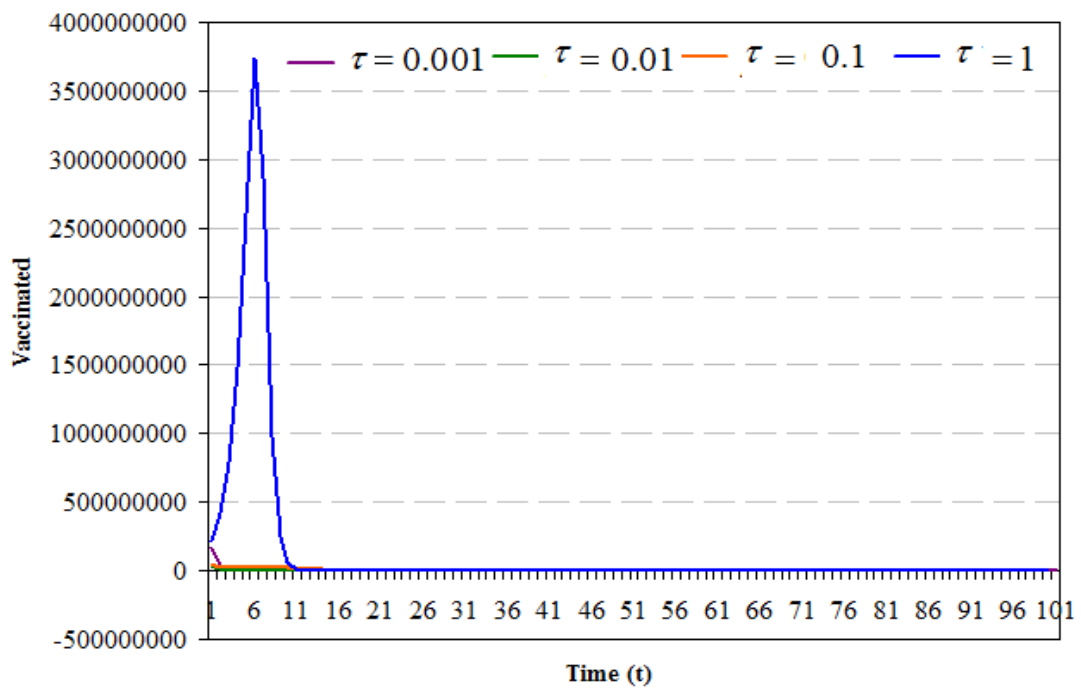


Figure 4.49: Behavior of Vaccinated (V) class for different people in vulnerable group starts receiving a vaccination rate (τ) values

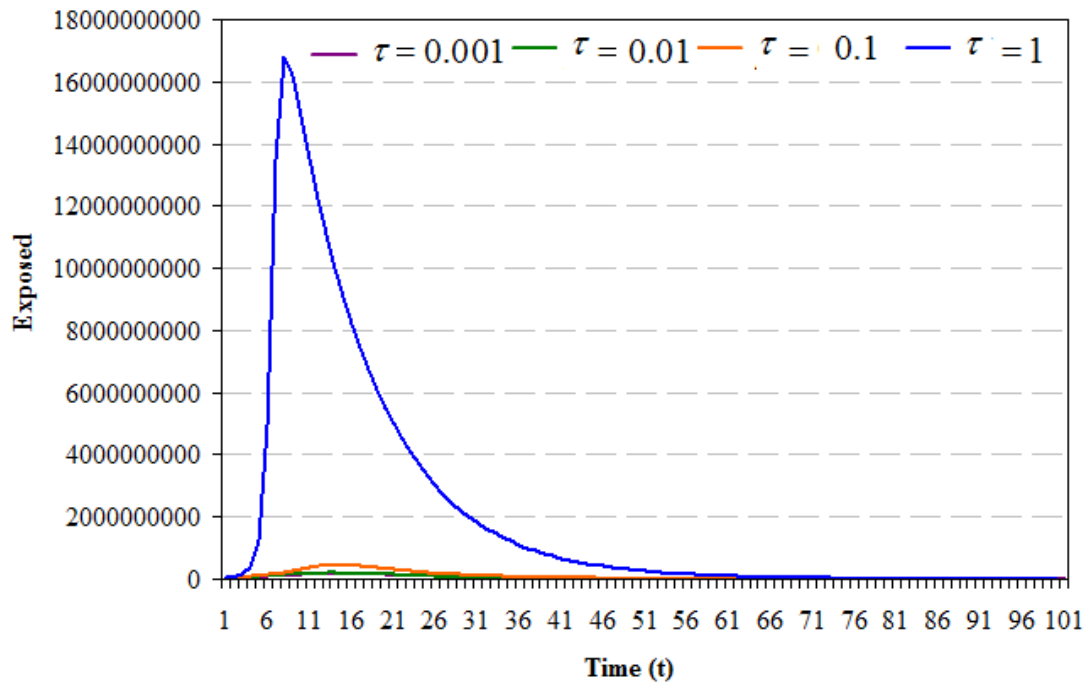


Figure 4.50: Behavior of Exposed (E) class for different people in vulnerable group starts receiving a vaccination rate (τ) values

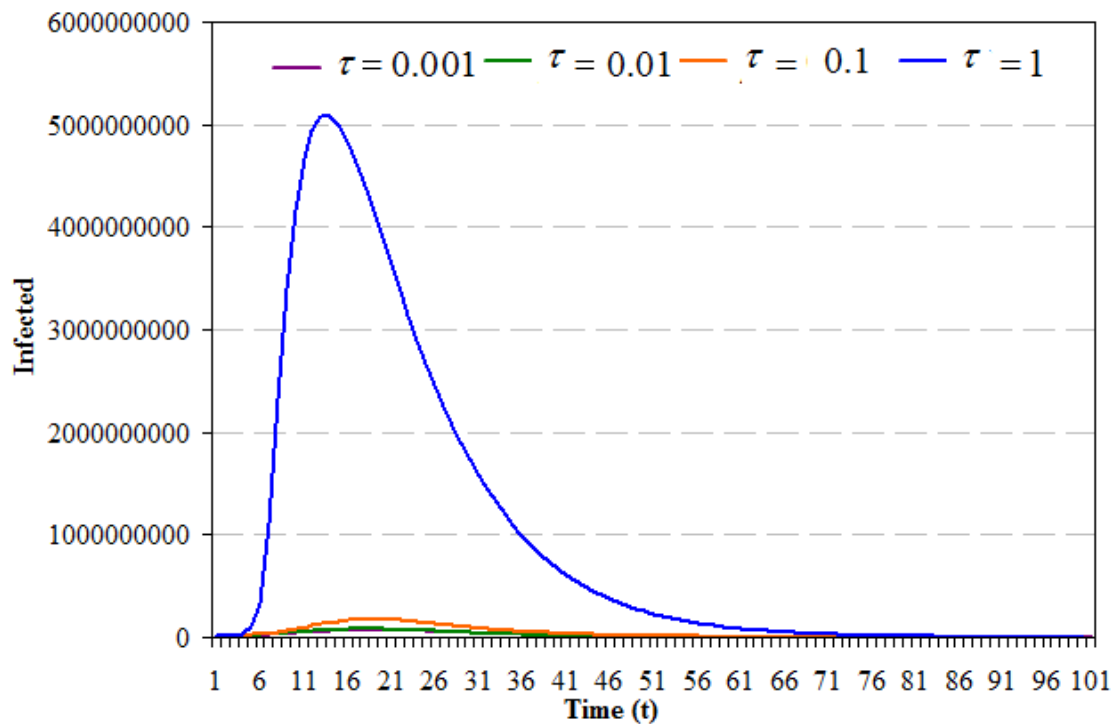


Figure 4.51: Behavior of Infected (I) class for different people in vulnerable group starts receiving a vaccination rate (τ) values

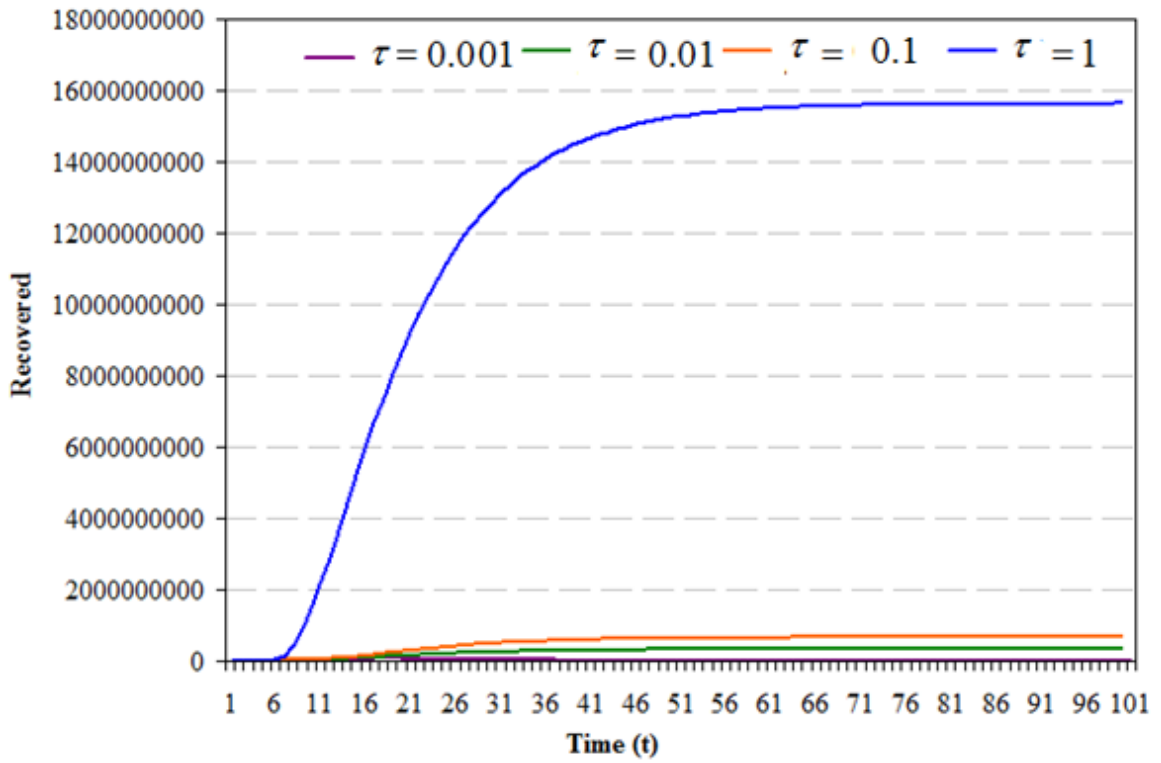


Figure 4.52: Behavior of Recovered (R) class for different people in vulnerable group starts receiving a vaccination rate (τ) values

4.6.9 Sensitivity Analysis of Vaccine Wane Rate (ω)

To analyse the effect of the vaccine wane rate ω on the Behavior of the S , V , E , I , and R populations, the SVEIR model was run for different values, such as $\omega=0.25$, $\omega=0.5$, $\omega=0.75$ and $\omega=1$ while all other parameters were set fixed and are shown in Figures 4.53 to 4.57. In Figure 4.53, the variation of the population of susceptible individuals over time has been investigated for the values of $\omega = 0.25$, $\omega = 0.5$, $\omega = 0.75$, and $\omega = 1$. Here, the most appropriate ω value for the actual data is calculated as $\omega = 0.25$ by the parameter estimation method. According to this value, it is observed that the number of susceptible individuals increased over time compared to other values of ω in the simulation. Similarly, in Figure 4.54, the time-dependent variation of the population in vaccinated individuals has been examined, respectively. The estimated number of vaccinated individuals for the $\omega = 1$ value

obtained by the parameter estimation method is less than the estimated vaccinated individuals for the $\omega = 0.25$, $\omega = 0.5$, $\omega = 0.75$, values. Additionally, for the value $\omega = 1$, the number of vaccinated individuals appears to be more stable than the others. It is observed that the number of vaccinated individuals is also significantly less for the value of $\omega = 1$ compared to other matters of ω during the simulation period. According to Figures 4.55 and 4.56, it is observed that ω has no significant effect on the exposed and infected population. This is interpreted as a result of the vaccine's wane rate not being applied to exposed and infected individuals. In Figure 4.57, the value of $\omega=1$ shows that the recovered individuals are increasing as compared to the other decreasing values of ω . Figures show the variations in S , V , E , I , and R under the influence of ω respectively. It is revealed that the S and V do not pose significant variations for ω , whereas the E and I trends increase to ω and then decrease after reaching the peak point; their period to reach an asymptote is more significant than S and V . The recovered class R is exposed under ω with an abrupt change at $\omega=1$.

Sensitivity to the vaccine wane rate (ω) is explored in Figures 4.53 to 4.57. The analysis reveals how variations in ω influence the susceptible, vaccinated, exposed, infected, and recovered populations over time. Understanding the dynamics of vaccine waning is crucial for long-term planning and the development of sustainable vaccination strategies.

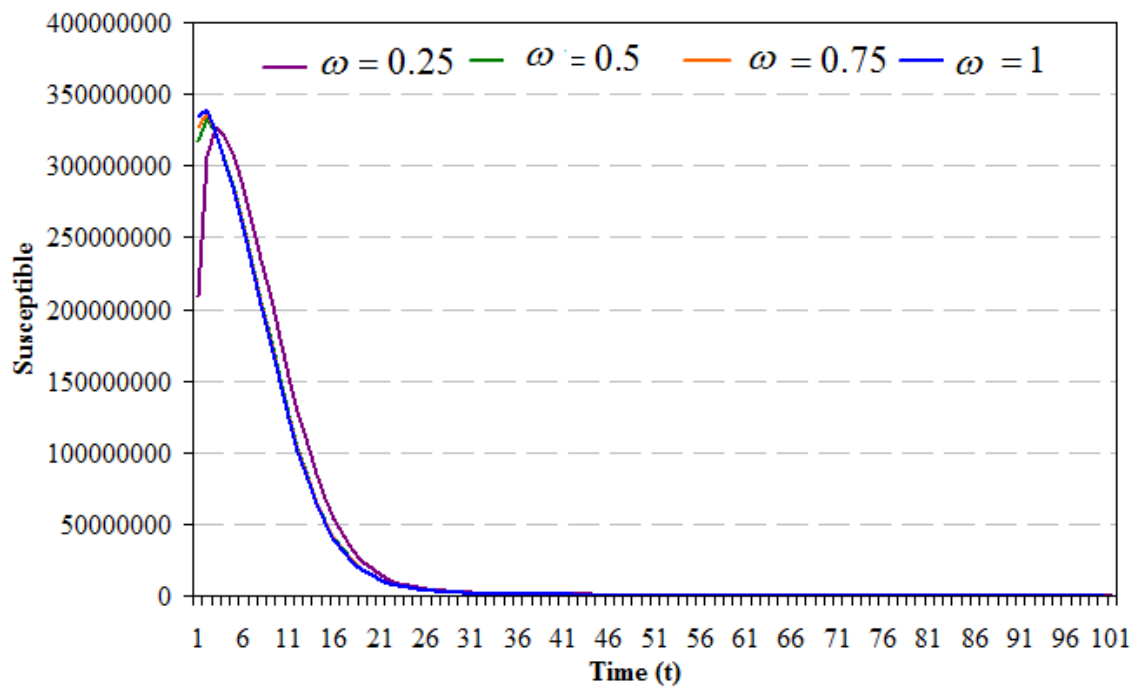


Figure 4.53: Behavior of Susceptible (S) class for different vaccine wane rate (ω) values

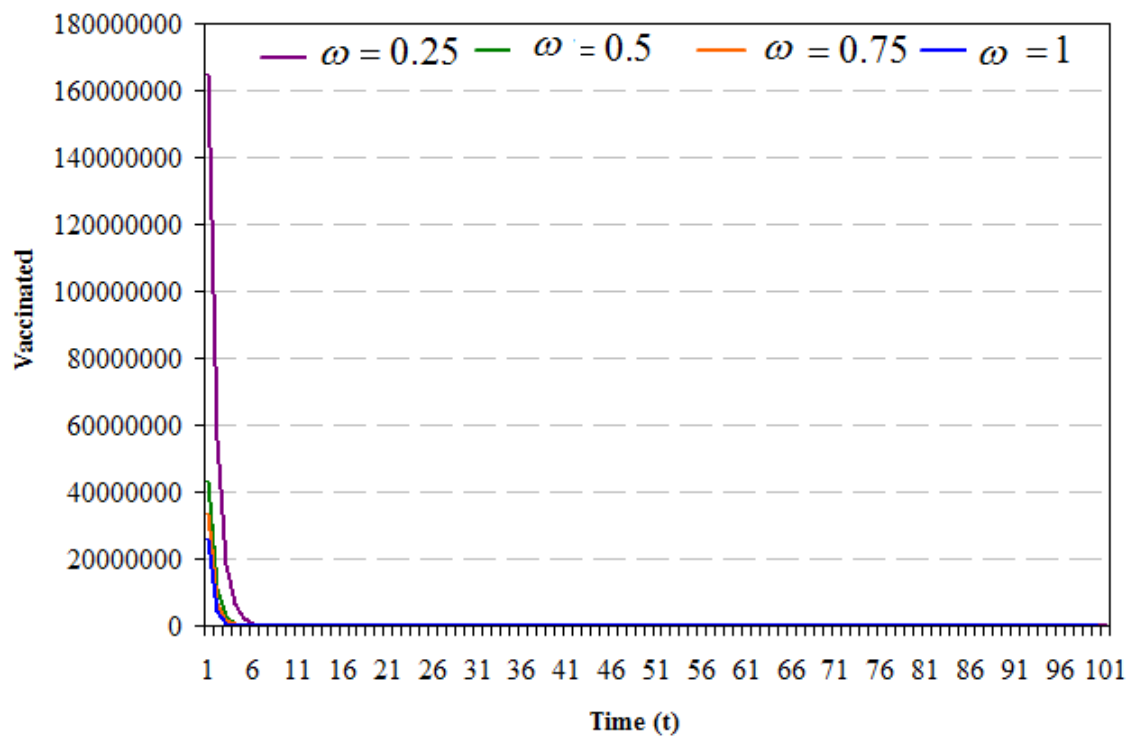


Figure 4.54: Behavior of Vaccinated (V) class for different vaccine wane rate (ω) values

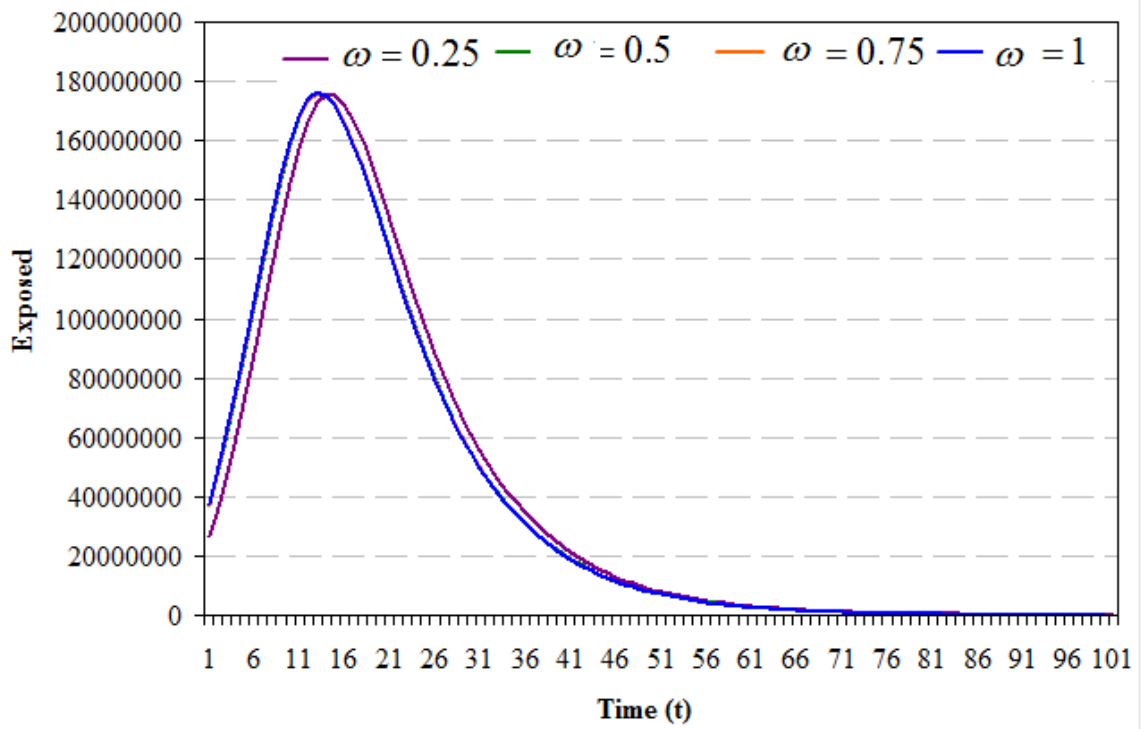


Figure 4.55: Behavior of Exposed (E) class for different vaccine wane rate (ω) values

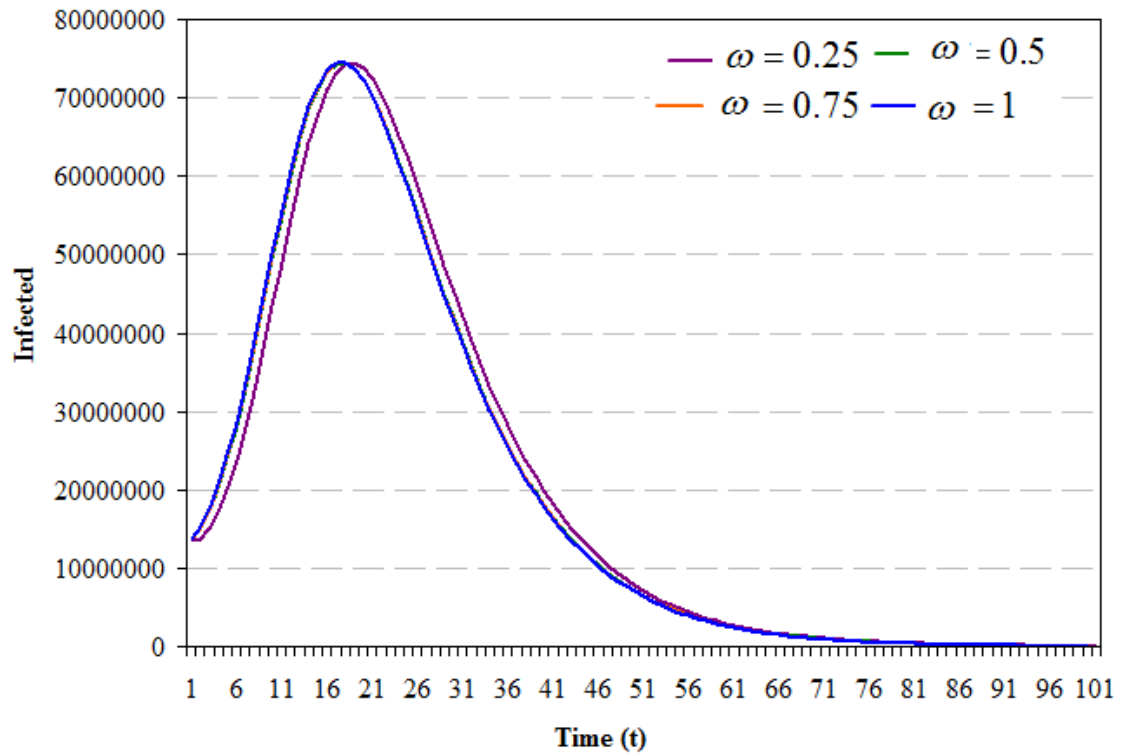


Figure 4.56: Behavior of Infected (I) class for different vaccine wane rate (ω) values

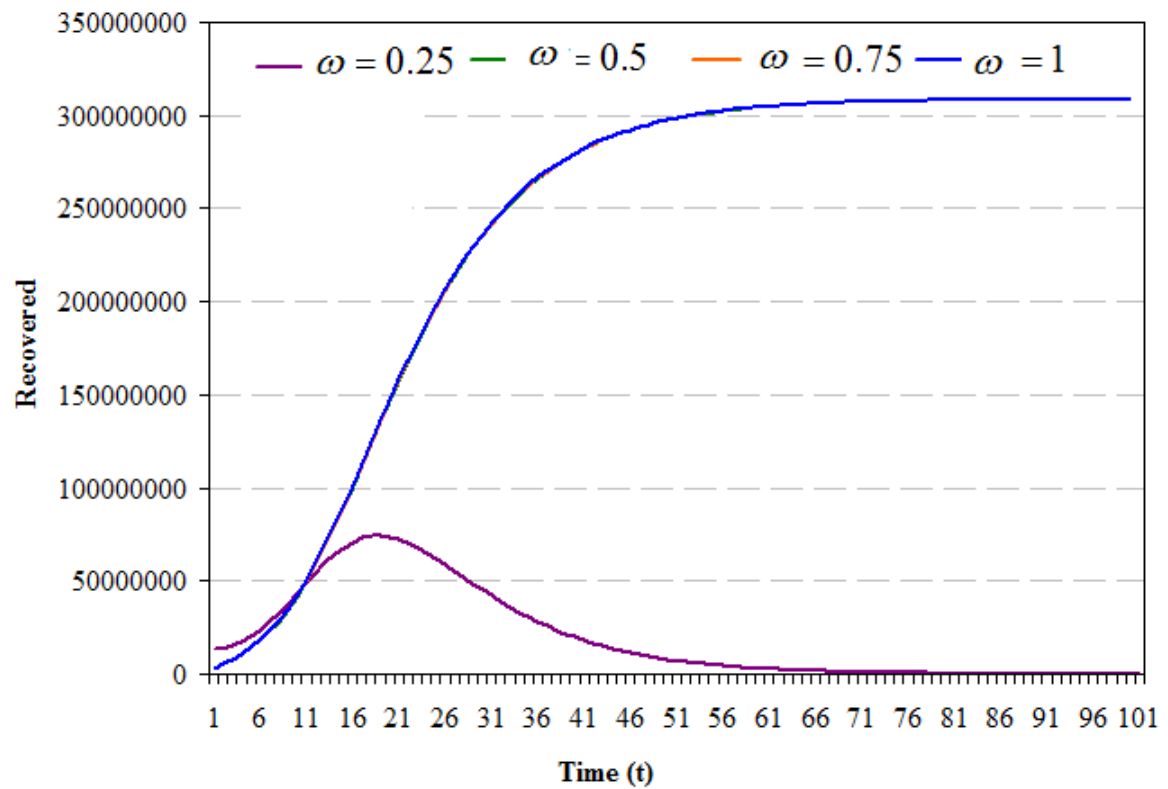


Figure 4.57: Behavior of Recovered (R) class for different vaccine wane rates (ω) values

4.6.10 Sensitivity Analysis of different rate moves to susceptible compartment (λ)

In Figure 4.58, the time variation of susceptible individuals for different values of λ such as $\lambda = 0.25$, $\lambda = 0.5$, $\lambda = 0.75$ and $\lambda = 1$ values of λ is examined. Here, $\lambda = 0.25$ is the value obtained after applying the parameter estimation method. The variation of susceptible individuals in the population over time is investigated for different λ values in Figure 4.58. According to Figure 4.58, it is observed that λ has no significant effect on the susceptible population. In Figure 4.59, it is seen that as the value of λ increases, the number of vaccinated individuals in the population decreases. In Figures 4.60 and 4.61, for different values of λ , the recovered class, the population time in exposed and infected individuals' related variation is studied. here is observed that λ has no significant effect on the exposed. According to Figure 4.62, it is observed that as the λ value increases, the number of recovered individuals

also increases. In other words, a decrease in λ values will cause a reduction in the number of recovered individuals. Figures 4.58 to 4.62 have illustrated the sensitivity of the model to changes with respect to the recovered class (λ). Slight variations in λ lead to significant alterations in the susceptible, vaccinated, exposed, infected, and recovered populations. This analysis emphasizes the role of quarantine strategies in mitigating the impact of COVID-19.

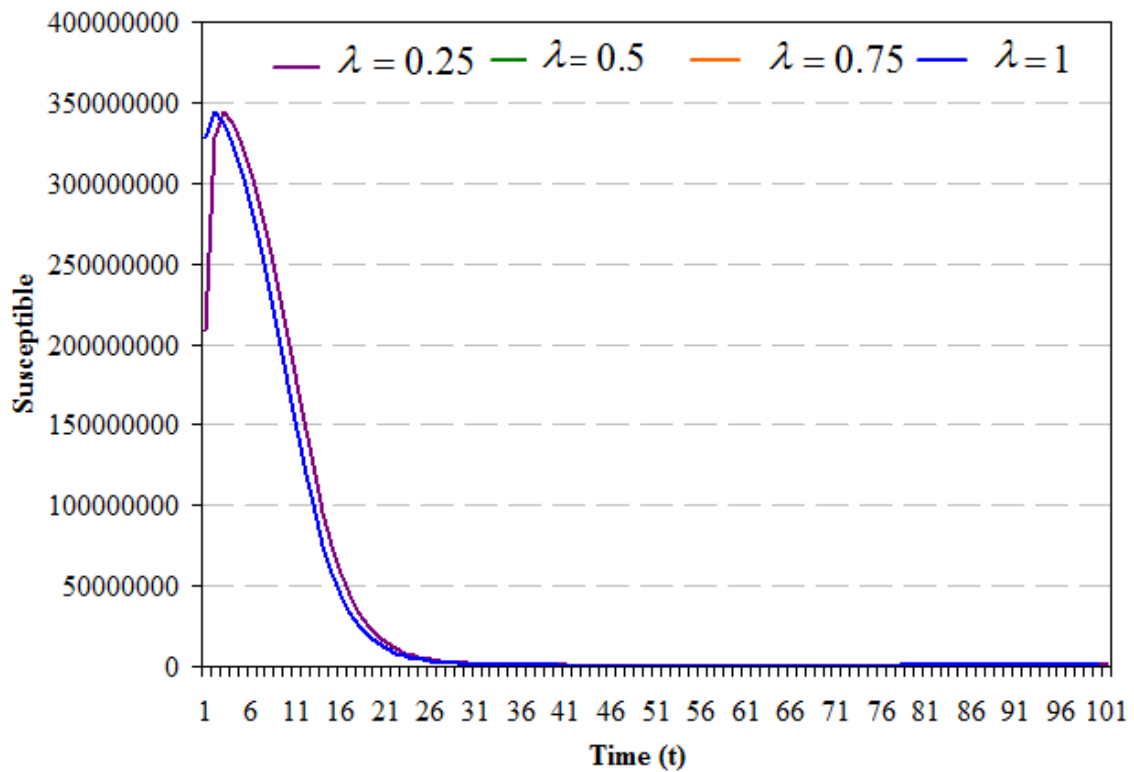


Figure 4.58: Behavior of Susceptible (S) class for different rates at which individuals move into the susceptible compartment (λ) values

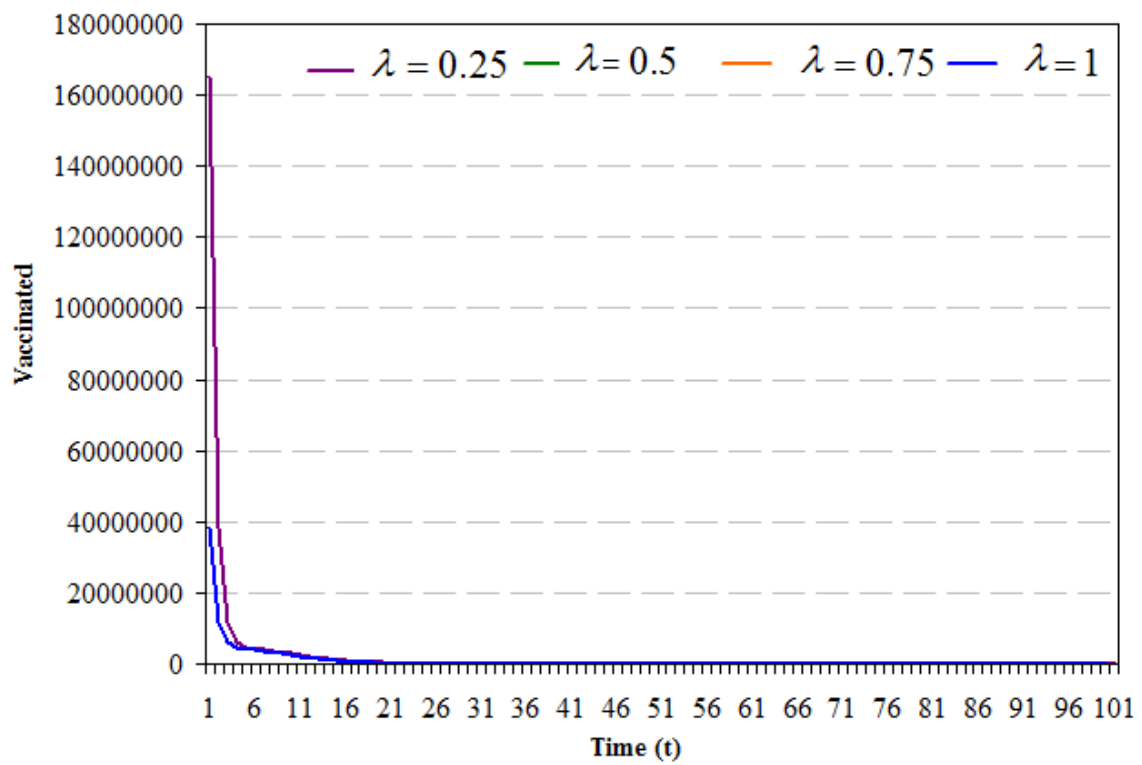


Figure 4.59: Behavior of Vaccinated (V) class for different rates at which individuals move into the susceptible compartment (λ) values

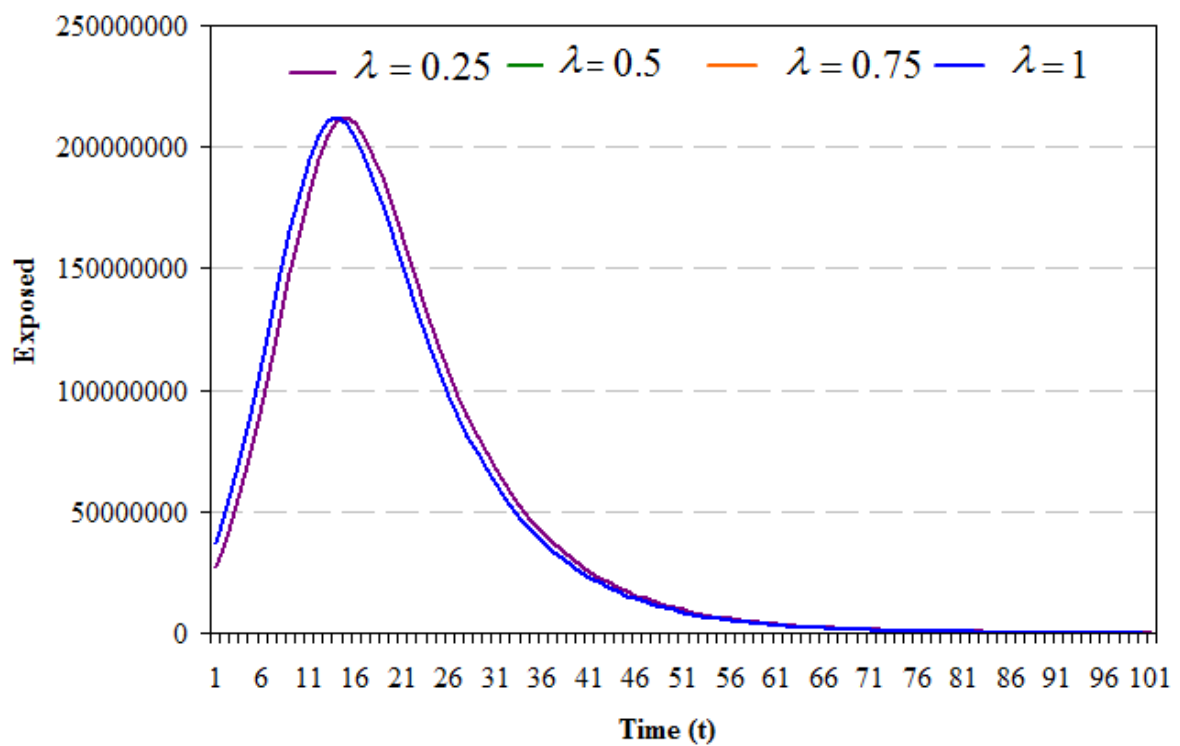


Figure 4.60: Behavior of Exposed (E) class for different rates at which individuals move into the susceptible compartment (λ) values

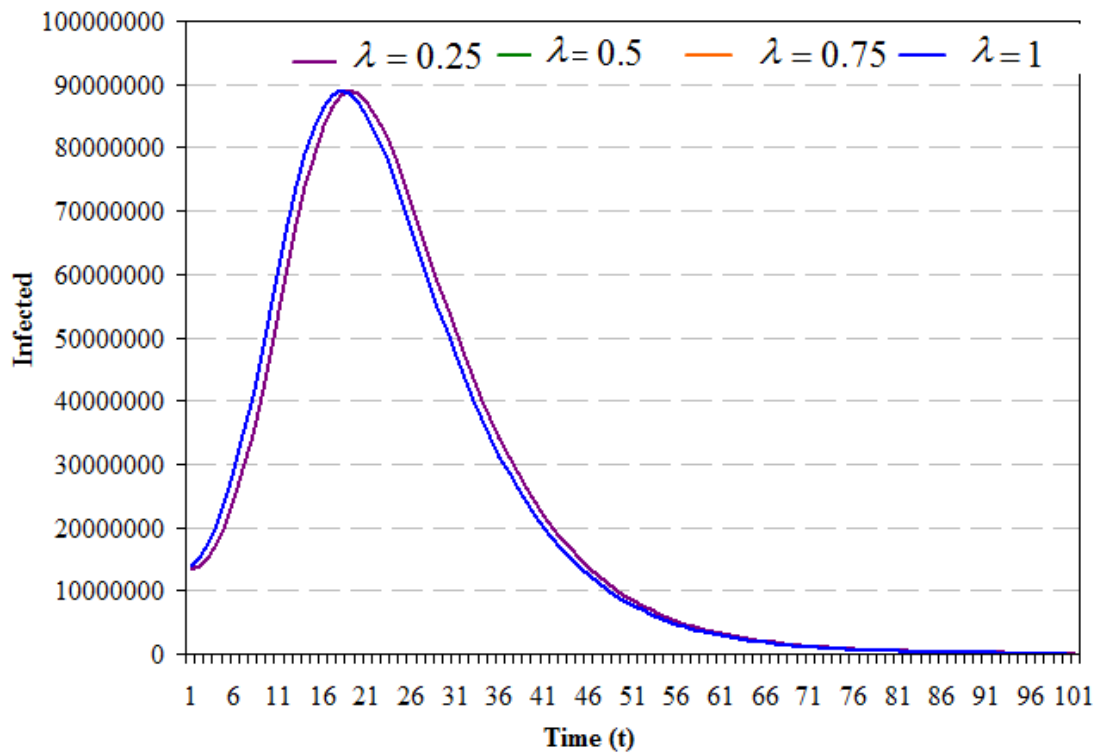


Figure 4.61: Behavior of Infected (I) class for different rates at which individuals move into the susceptible compartment (λ) values

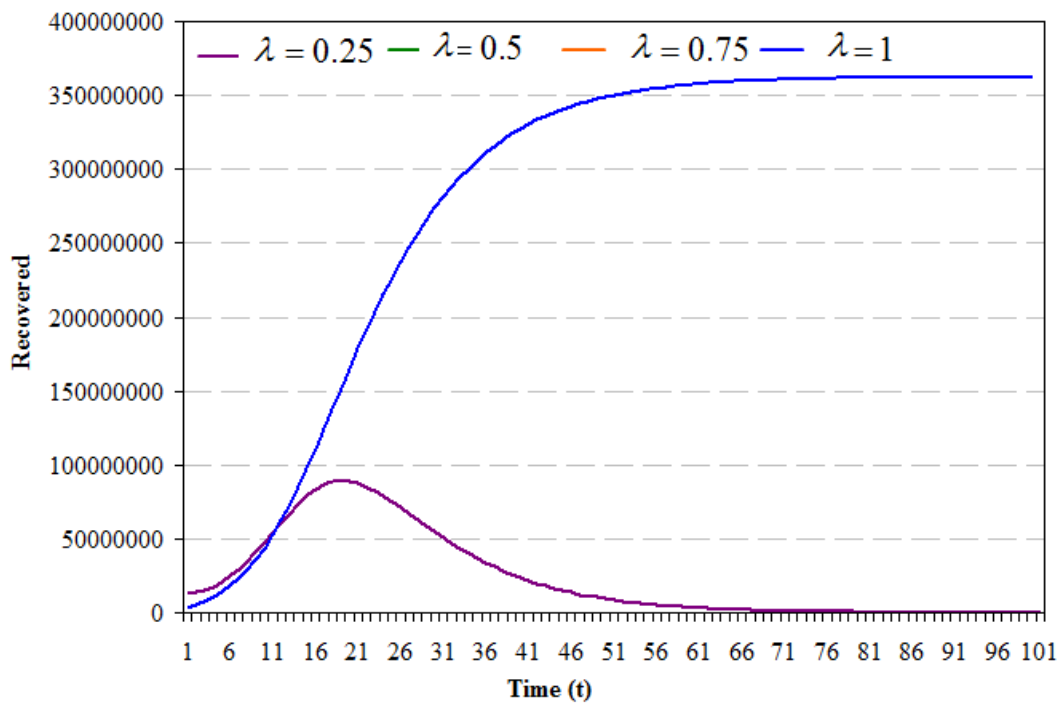


Figure 4.62: Behavior of Recovered (R) class for different rates at which individuals move into the susceptible compartment (λ) values

In summary, the sensitivity analysis emphasizes the complex and interrelated nature of the parameters in the improved SVEIR model. While all parameters are important, the research shows that changes in the transmission rate (β) and recovery rate (γ) significantly impact the model's outcomes. These insights provide valuable guidance for policymakers and researchers seeking to understand and manage the COVID-19 pandemic in Pakistan.

4.7 Simulation of Basic Reproduction Number (R_0) under the influence of sensitive parameters

In the analysis of the relevant reproduction number within the prescribed limits, due consideration is given to the variables. Upon careful examination, it has been ascertained that appropriate measures must be taken to prevent the spread of the disease. This can be achieved by mitigating the factors that contribute to a positive derivative of reproduction numbers and enhancing those that result in a harmful product. More specifically, the sensitivity analysis of the Basic Reproduction Number (R_0) is performed under the simultaneous effect of $\beta, \delta, \gamma, \xi$ and ε values, respectively. In this regard, Figure 4.63 shows the changes in the reproduction number based on the mean daily rate of isolated infectious cases δ and the probability of susceptibility β . It is revealed that with a simultaneous increase in β and δ , the values of the reproductive number decrease. It should be noted that the transition of values of R_0 in the is Figure 4.63 is represented by pseudo color plot where the higher values changes from red color to the lower values with blue color as shown in the color bar. Moreover, Figure 4.64 depicts the changes in the reproduction number according to the infectious period γ versus the average number of contacts per day per case ξ . The Figure shows that with a simultaneous increase in ξ and γ decreases the values of the basic reproductive number. Further, Figure 4.65 depicts the changes in the reproduction number according to the mean daily rate at which infectious cases are isolated δ , versus the infectious

period γ , and it can be observed that an increase in δ leads to a decrease in R_0 . At the same time, the increase in a γ also increases the values of R_0 . Figure 4.66 depicts the changes in the reproduction number according to the death rate due to COVID-19, ε versus the probability of susceptibility becoming infectious per contact β ; it can be observed that the simultaneous increase in the values of β and ε decreases the values of R_0 whereas the magnitude of R_0 is much higher at β and ε . In summary, the R_0 remains more significant than 1 for the combination of β and ε and other parameters; it remains less than 1.

In analysing the reproduction number within the prescribed limits, due consideration is given to the variables. Upon careful examination, it has been ascertained that appropriate measures must be taken to prevent the spread of the disease. In the simulation of sensitivity, one can obtain that the values of R_0 varies under the simultaneous effect of the $\beta, \varepsilon, \xi, \delta, \gamma$ respectively.

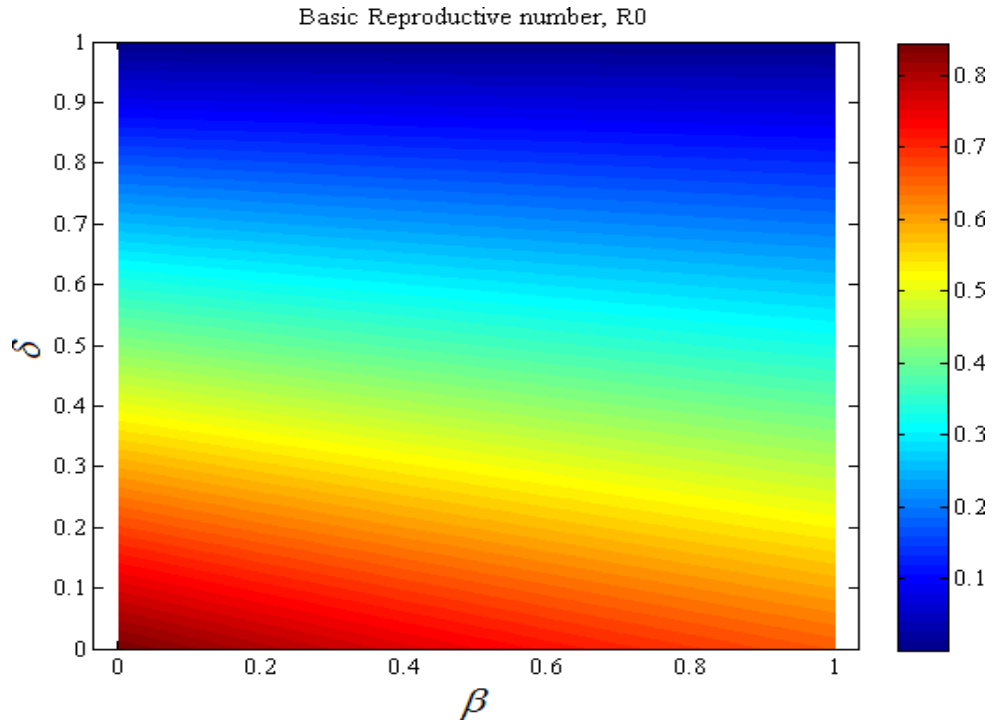


Figure 4.63: Sensitivity analysis of basic reproduction number R_0 under the simultaneous variation in the parameters β and δ

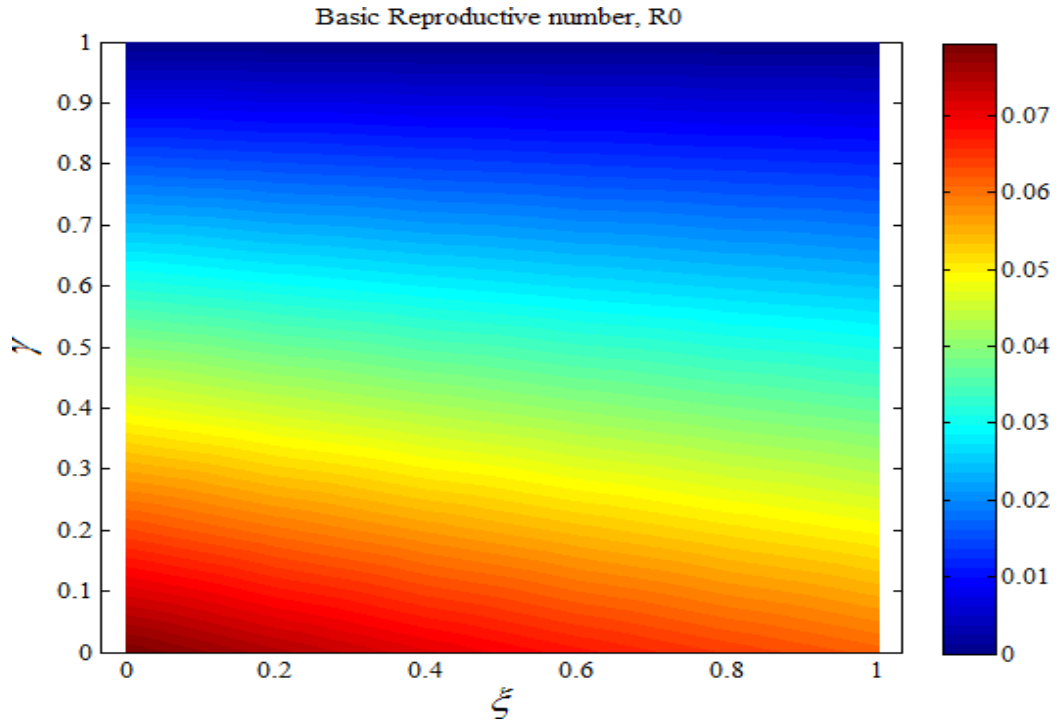


Figure 4.64: Sensitivity analysis of basic reproduction number R_0 under the simultaneous variation in the parameters ξ and γ

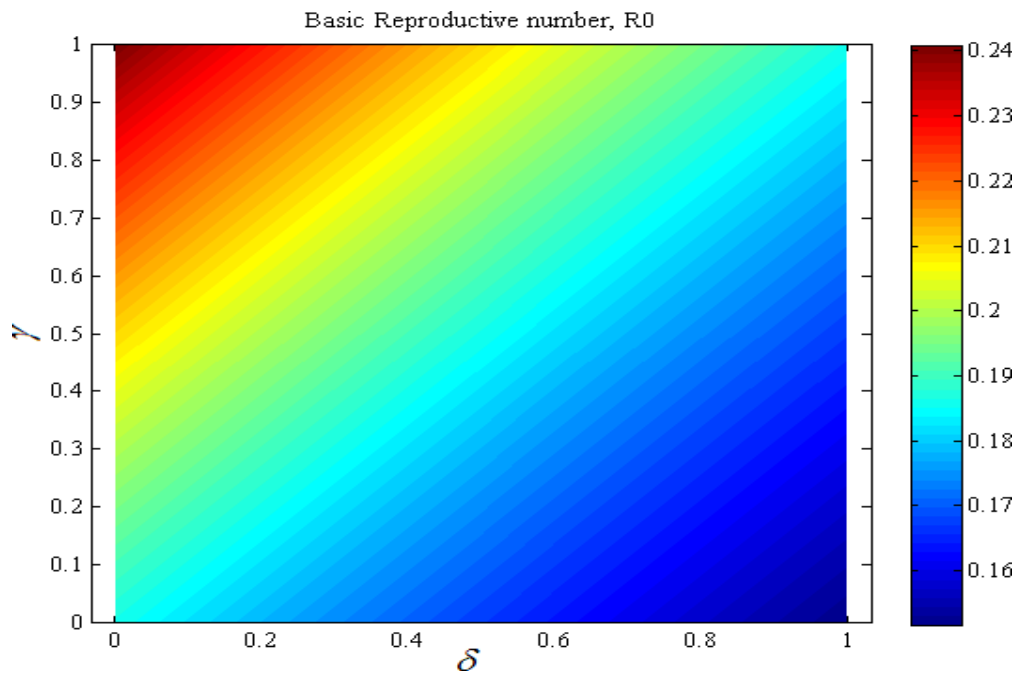


Figure 4.65: Sensitivity analysis of basic reproduction number R_0 under the simultaneous variation in the parameters δ and γ

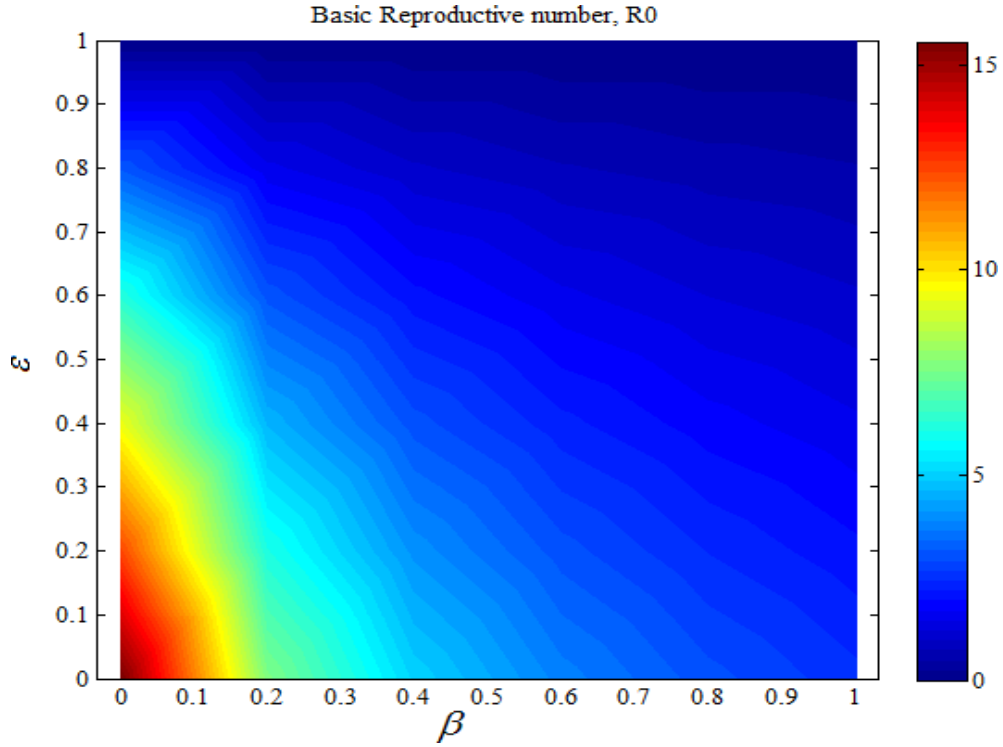


Figure 4.66: Sensitivity analysis of basic reproduction number R_0 under the simultaneous variation in the parameters β and ε

4.8 Summary

This chapter presents extensive results from the proposed SVEIR model for predicting COVID-19 in Pakistan. It thoroughly investigates the dynamics of the pandemic within the context of the country. The numerical solution of the SVEIR model was implemented using data from Pakistan for all five dependent variables, and the Behavior of the predictive trends was discussed. The results of this method were compared with the actual observed data in Pakistan and were found to be in good agreement. Despite the large population, the maximum percentage error remained within an acceptable range, and the results were statistically significant at both the 90% and 95% levels of significance.

Additionally, the model's validation involved a comparison with a benchmark method, which showed that the proposed approach produced lower error rates for the data from Pakistan. To evaluate the variations caused by the parameters in the SVEIR model, a

sensitivity analysis was conducted, analyzing the impact of all involved parameters. Finally, simulations of the basic reproduction number concerning sensitive parameters were presented, which may aid in controlling the spread of COVID-19.

The core of the study lies in the development of a customized SVEIR model, which accounts for vaccination dynamics often overlooked in generic models. Calibration, achieved through parameter estimation using methods such as the least squares curve-fitting, ensures the model aligns closely with real-world data. The findings demonstrate the model's ability to not only replicate historical trends but also provide a predictive lens for future scenarios. The sensitivity analysis critically examines the model's responses to parameter variations, highlighting its robustness and identifying areas of potential uncertainty. The implementation of the model with real-time data bridges theory with practice, showcasing its practical utility in guiding policy decisions. The ensuing discussion critically evaluates the model's strengths and limitations, providing nuanced insights for public health strategies in Pakistan. The conclusion and contribution of the study in light of the results will be explicitly demonstrated in Chapter 5.

CHAPTER 5

CONCLUSION AND RECOMMENDATIONS

5.1 Conclusion

The primary objective of this research study was to develop a mathematical model for Pakistan, incorporating the vaccine factor, to analyze COVID-19 trends in the country. Although numerous studies have been conducted to analyze and predict COVID-19 behavior in Pakistan, their limitations in identifying the disease are significant, especially during the initial outbreak when prompt decisions are crucial. However, the control interventions incorporating the Non-pharmaceutical interventions (NPI) measure for the current scenario in Pakistan, which include vaccination compartments, have not yet been identified. Therefore, there was a need for such a model that covers the mentioned factor.

To achieve the research objective, a systematic process was followed. To propose and formulate a new model, an analogous existing model called STEQIR (Gill et al., 2020) was first evaluated. Subsequently, by incorporating modifications and compartmental analysis, including the control intervention of the vaccine, a new model, namely the SVEIR model, was derived. Some properties relevant to the proposed model and the interpretation of several other parameters involved in the model were also discussed concisely.

The possibility of the analytical solution of the proposed SVEIR model was investigated using Maple software, a symbolic computer algebra system. It was found that the analytical expressions for the SVEIR model appear as an implicit relation for the S variable, and the other four variables are explicit relations for V, E, I, and R, respectively. It

was concluded that, due to the implicit nature of the variable S, the other variables cannot be evaluated uniquely. Therefore, the analytical solution for the SVEIR is quite difficult due to non-linearity in the governing equations.

To find a realistic solution for the proposed model, the values of the parameters involved were calibrated or estimated from the data and literature search. The numerical solution strategy was adopted, utilizing the Runge-Kutta fourth and fifth-order method, which was implemented in R Studio. It was found that the numerical solution can be more practical and provides a stable solution of the SVEIR model. Moreover, the results revealed that the number of Susceptible cases initially increases, reaching a maximum height for a short period. After peaking, the cases decrease gradually, approaching an asymptotic point over time. The number of recovered instances increases, and the vaccinated population decreases. The exposed and infected populations exhibit almost analogous Behavior. The exposed cases increase smoothly to a peak point and then decrease smoothly to reach an asymptotic point. The intensity of the infected population is significantly smaller than that of the exposed population. Following the COVID-19 vaccination, the recovered population exhibits a smooth increase in the number of recovered individuals, reaching an asymptotic point over time. In conclusion, the numerical simulation of all five variables can project the outbreak well over the next few months.

The results of the proposed SVEIR model were compared with the observed data of Pakistan and were found in good agreement. To assess the goodness of the model, the maximum absolute percentage error (MAPE), the root mean square error (RMSE), the sum of squares error (SSE), the coefficient of determination (R^2), and the coefficient of correlation (r) between the actual data and the SVEIR model curves have been calculated. It

was established that, despite the large population of Pakistan, the measured maximum percentage error (MAPE) was within an acceptable range for all five variables, ranging from 9.72 to 15.42, and the results were statistically significant at both 90% and 95% levels of significance. The performance values are strongly acceptable and may provide good forecasts.

The validation of the SVEIR model was also done by comparing the Pakistan scenario with the existing STEQIR (Gill et. al, 2020) model as a benchmarking method, and the comparison revealed that for the Pakistan data, the proposed SVEIR model poses less error as compared to the benchmark method. This shows that the SVEIR model performs better for the Pakistan COVID-19 data as compared to Gill et al (2020).

To assess the variations caused by the working parameters involved in the SVEIR model, the sensitivity analysis was conducted, and the impact of all the parameters involved in the model was analysed. From the study, it was revealed that the transmission rate significantly impacts the long-term Behavior of susceptible, vaccinated, exposed, infected, and recovered populations. Similarly, the transmission infectious coefficient plays a crucial role in determining the peak infection and duration of the contagious period, underlining its sensitivity and importance in modelling the dynamics of COVID-19. The mean daily isolated rate mainly affects the susceptible and exposed populations. The analysis reveals that the death rate ϵ is more sensitive as it produces more variations in almost all population classes. The variations in incubation period have discernible effects on the susceptible, vaccinated, exposed, infected, and recovered populations over time. This emphasizes the importance of accurate estimation of the incubation period rate for precise modelling and prediction of COVID-19 dynamics. The variations in the average number of contacts per day per case show that the small changes lead to significant alterations in the susceptible, vaccinated,

exposed, infected, and recovered populations. Understanding how contact rates influence the spread of the virus is essential for developing targeted interventions and public health measures. The sensitivity of the natural death rate indicates that variations in this rate do not cause significant variations in the SVEIR variable. Variations in the vaccination rate suggest that the time duration for the S and V is too small to be affected by the while for other classes, E, I, and R, the time to reach the asymptotic value is significant. This analysis underscores the critical role of vaccination rates in shaping the course of the pandemic and highlights the importance of adequate vaccination strategies. The vaccine rate performs better for intermediate values of the selected interval. The rate of moving to the susceptible compartment shows that slight variations in λ can lead to significant changes in the susceptible, vaccinated, exposed, infected, and recovered populations.

Finally, the simulation of the basic reproduction number R_0 with sensitive parameters $\beta, \delta, \gamma, \xi$ and ε values, respectively, were obtained that may be helpful to control the spread of COVID-19. From the simulation, it was revealed that the R_0 remains greater than 1 for the probability of susceptibility β , becoming infectious per contact ξ and the death rate for other parameters, it remains less than 1.

The outcome and findings of this study may be essential for policymakers and public health officials in making informed decisions and formulating effective strategies to govern and manage the spread of COVID-19. The understanding gained from this research may guide targeted strategies, promote efficient resource allocation, and contribute to the continuing efforts to mitigate and control the COVID-19 pandemic in Pakistan.

5.2 Contribution

This research has contributed to the field of mathematical modelling by developing a new COVID-19 model specifically tailored to the context of Pakistan. A novel model was

formulated by incorporating a control intervention through the addition of a vaccination compartment and was evaluated using data from Pakistan. This represents a significant contribution to existing knowledge and may be highly valuable in understanding and predicting the Behavior of COVID-19. The results and findings from the proposed model can also offer insights into effective control measures and support policy-making efforts aimed at mitigating the spread of similar infectious diseases that may emerge in the future. Based on this model, public health organizations can better assess the effectiveness of vaccination in reducing and preventing active COVID-19 cases within the population. Consequently, they can plan and implement awareness and vaccination programs more efficiently.

5.3 Recommendations

The present work makes a significant contribution to understanding the behavior of COVID-19 in Pakistan through the proposed SVEIR model. However, several refinements can be made in the future to enhance this study.

The current time-dependent SVEIR model can be extended to a spatio-temporal version by incorporating spatial dimensions corresponding to specific regions. Additionally, the model can be improved by including new variables and parameters that influence the spread of the virus in Pakistan. These may involve considering the impact of virus variants, the effectiveness of different vaccination strategies, the role of non-pharmaceutical interventions, and the influence of seasonal environmental and weather conditions.

Furthermore, the model can be adapted to account for childhood vaccination against COVID-19. For example, children vaccinated at birth could be directly transitioned into the

vaccinated compartment. Incorporating demographic and environmental factors would also enhance the model's precision.

Future research in these areas will contribute to a deeper understanding of COVID-19 dynamics in Pakistan and globally, increasing the accuracy and applicability of mathematical models. These advancements will support evidence-based decision-making, improve public health responses, and aid in the effective management and containment of the COVID-19 pandemic in Pakistan.

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APPENDICES

Appendix A: Journal Publication

1. **Laghari, K.**, Sarbini, I. N., Labadin, J., & Kamboh, S. A. (2025). Sensitivity Analysis of COVID-19 Transmission Dynamics in Pakistan Using Mathematical Modelling. *Applications of Modelling and Simulation*, 9, 12–21. Retrieved from http://arqiipubl.com/ojs/index.php/AMS_Journal/article/view/668.