Simulation and Analysis of Infectious Disease Spread with the SEIQR Model

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Abstract

In the realm of infectious disease modeling, understanding the dynamics of transmission and the impact of interventions is of paramount importance. This report presents a comprehensive SEIQR model tailored to infectious diseases that do not confer immunity but consideres it only at Recovered stage. The model incorporates six compartments: Susceptible (S), Exposed (E), Infected (I), Quarantine (Q), Recovered (R), and Susceptible (S), representing the stages individuals traverse throughout the disease progression.

Key hypotheses and assumptions underpinning the model include a homogeneous spatial distribution, adherence to the law of mass action for host mixing, a constant per capita contact rate (Beta), and the potential for temporary recovery and non-permanent immunity. Within this framework, the model describes the journey of individuals through latent, infectious, and recovery phases, as well as the potential for quarantine and natural death.

This report endeavors to provide a comprehensive tool for simulating and analyzing the spread of infectious diseases. By incorporating these components, the model allows for the investigation of various scenarios and interventions to better inform public health decision-making. The findings contribute to our understanding of disease dynamics and the effectiveness of control measures.

The SEIQR model, as outlined in this report, holds promise as a valuable resource for epidemiologists, public health officials, and policymakers seeking to combat infectious diseases with complex transmission dynamics.

1. Introduction

Infectious diseases have been a persistent and formidable challenge throughout human history, shaping populations, societies, and public health practices. The emergence of novel pathogens and the reemergence of known infectious agents have underscored the importance of understanding the dynamics of disease transmission, spread, and control. In this context, mathematical models have proven to be indispensable tools for unraveling the complex interplay of factors that govern the course of epidemics and pandemics.

The SEIQR model, an extension of the classical SIR (Susceptible-Infectious-Recovered) model, is one such mathematical framework that plays a pivotal role in the study of infectious disease dynamics. This model introduces additional compartments, each representing distinct stages in the progression of an infectious disease. In particular, the SEIQR model includes Susceptible (S), Exposed (E), Infected (I), Quarantine (Q), Recovered (R), and Susceptible (S) compartments. It provides a comprehensive representation of disease dynamics, allowing for the incorporation of crucial factors such as latent periods, temporary immunity, and the impact of public health interventions.

This report endeavors to delve into the SEIQR model, with a specific focus on infectious diseases that do not confer permanent immunity upon recovery. While some infectious diseases elicit robust and lasting immunity in those who survive, many others, such as certain emerging infectious diseases, do not. The absence of durable immunity presents unique challenges in disease control and intervention strategies.

The SEIQR model considered in this report is not merely a theoretical construct; rather, it serves as a practical and versatile tool for understanding the spread of infectious diseases within a population. Our aim is to provide a comprehensive examination of the SEIQR model and its application to infectious diseases with temporary immunity. By doing so, we can shed light on the nuanced dynamics of such diseases and explore the efficacy of different intervention strategies.

This report is structured as follows: We will first present a thorough description of the SEIQR model, outlining the compartments, assumptions, and parameters that underlie our study. We will then discuss the data sources and methods employed in the parameter estimation and model calibration. Subsequently, we will present the results of model simulations and analyses, followed by a detailed discussion of our findings and their implications.

Through this comprehensive exploration, we aim to con-

tribute to the field of infectious disease epidemiology and provide insights that can inform public health decision-making, particularly in the context of infectious diseases with temporary immunity. The SEIQR model, with its capacity to capture the intricate dynamics of such diseases, holds the potential to be an invaluable resource for epidemiologists, public health officials, and policymakers in their ongoing efforts to mitigate the impact of infectious diseases.

1.1. SEIQR Model and Disease Dynamics

The SEIQR model represents a pivotal advancement in mathematical epidemiology. While the traditional SIR model classifies individuals into only three compartments—Susceptible, Infectious, and Recovered—the SEIQR model extends this framework to incorporate Exposed and Quarantine compartments, each with distinct implications for disease spread and control. This enhanced granularity enables the SEIQR model to capture features like latent periods, temporary immunity, and the impact of quarantine measures, making it a valuable tool for studying a wide range of infectious diseases.

1.2. Temporary Immunity and Disease Resurgence

In the context of infectious diseases, the duration and nature of acquired immunity following recovery vary widely. Certain diseases, such as measles and mumps, provide robust and long-lasting immunity in those who survive infection. In contrast, others, including seasonal coronaviruses and some emerging infectious diseases, do not confer permanent immunity. Understanding the dynamics of diseases without lasting immunity is of critical importance, as it has implications for the potential for disease resurgence and the effectiveness of vaccination programs.

1.3. SEIQR Model and Intervention Strategies

A key strength of the SEIQR model is its capacity to inform the assessment of intervention strategies. Researchers have utilized this model to evaluate the impact of quarantine measures, vaccination programs, and social distancing interventions. As the SEIQR model reflects the transient nature of immunity, it is especially suited for assessing the long-term implications of interventions in diseases without permanent immunity.

1.4. Applications of the SEIQR Model

The SEIQR model has been applied to a plethora of infectious diseases, including but not limited to influenza, HIV/AIDS, and COVID-19. In the context of diseases without permanent immunity, it allows for the exploration of scenarios in which individuals may become susceptible again after a period of temporary recovery. This feature is particularly relevant for understanding the dynamics of emerging infectious diseases and seasonal outbreaks.

2. Population Dynamics and Departure from the Constant Population Constraint

In the realm of epidemiological modeling, one of the fundamental considerations is the size and dynamics of the population under study. The ”constant population constraint” is a simplifying assumption that posits a stable population size throughout the modeling period, with no births, deaths, immigration, or emigration affecting the population. This constraint is often applied in theoretical models and short-term simulations to streamline the analysis of disease dynamics.

However, in many real-world scenarios, populations are far from static, and demographic factors play a pivotal role in shaping infectious disease dynamics. In this research, we acknowledge and embrace the dynamic nature of populations, which may experience changes in size due to births, deaths, immigration, and emigration. The presence of these demographic processes is a significant departure from the constant population constraint.

To capture the complexities of population dynamics, our SEIQR model accommodates these changes through the inclusion of demographic terms in the equations governing transitions between compartments. Specifically, natural mortality (d * S, d * E, d * I, d * Q, d * R) is considered for each compartment to account for the effect of deaths unrelated to the disease and (μ) is considered in Infection and Quarantine compartment which refers to death related to disease. (b) is the recruitment rate considered in Susceptible compartment. These terms reflect the dynamic nature of populations, and their presence allows our model to more accurately represent the interactions between infectious disease transmission and demographic factors.

3. Model Description

The SEIQR model, an extension of the traditional SIR (Susceptible-Infectious-Recovered) model, is a versatile mathematical framework used for studying the dynamics of infectious diseases within a population. It introduces additional compartments to capture the various stages of disease progression and offers a more comprehensive understanding of infectious disease transmission. In this model, individuals are categorized into six compartments: Susceptible (S), Exposed (E), Infected (I), Quarantine (Q), Recovered (R), and Susceptible (S) again. Each compartment represents a distinct stage of disease progression, and transitions between these compartments are governed by a set of differential equations.

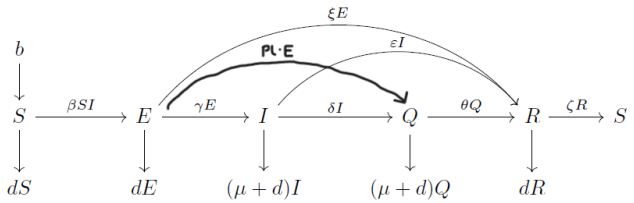

Figure 1. Schematic diagram of SEIQR Model.

3.1. Compartments and Transitions

3.1.1 Susceptible (S)

The S compartment represents individuals who are susceptible to the disease. However, not all susceptible individuals are equally at risk. Some may enter a latent period before becoming exposed, while others may be removed from the population due to natural death (d * S).

3.1.2 Exposed (E)

The E compartment represents individuals who have been exposed to the infectious agent but are not yet infectious themselves. This exposed phase accounts for the incubation period of the disease. Natural death (d * E) can also affect this compartment. Additionally, some exposed individuals may transition to other compartments based on specific factors.

3.1.3 Infected (I)

The I compartment represents individuals who are actively infected with the disease and can transmit it to others. Individuals can move from the exposed compartment to the infected compartment upon reaching an infectious stage. Some individuals may recover or enter quarantine, while others may die due to disease-related factors (mu + d).

3.1.4 Quarantine (Q)

The Q compartment represents individuals who have been identified as infected and are isolated or quarantined to prevent further disease transmission. These individuals can eventually recover or face risks of disease-related death (mu + d). Quarantined individuals may also transition to the recovered compartment (R) or return to the susceptible compartment.

3.1.5 Recovered (R)

The R compartment represents individuals who have recovered from the disease and may have developed temporary immunity. Some individuals in the recovered class may eventually return to the susceptible class due to the transient nature of immunity. Natural death (d * R) is also considered in this compartment.

3.2. Mathematical Model

$$\frac{dS}{dt} = b - \beta SI + \zeta R - dS \tag{1}$$

$$\frac{dE}{dt} = \beta SI - (\gamma + \xi)E - dE - PlE \tag{2}$$

$$\frac{dI}{dt} = \gamma E - (\epsilon + \delta)I - (\mu + d)I \tag{3}$$

$$\frac{dQ}{dt} = \delta I - \theta Q - (\mu + d)Q + PlE \tag{4}$$

$$\frac{dr}{dt} = \epsilon I + \theta Q + \xi E - \zeta R - dR \tag{5}$$

3.3. Model Parameters

The SEIQR model is parameterized by various factors, including but not limited to:

1. **b**: The recruitment rate of susceptible individuals to the population.
2. β: The parameter controlling how often a susceptible-infected contact results in a new exposure.
3. ϵ: The rate of recovery and movement into the recovered phase.
4. γ: The rate at which an exposed individual becomes infective.
5. d: The natural mortality rate (unrelated to the disease).
6. μ: The disease-related death rate constant in compartments I and Q.
7. θ: The rate at which individuals return to the recovered class R from compartments Q.
8. δ: The rate constant for nodes leaving the infective compartments I for quarantine compartment.
9. Pl: The rate of nodes leaving exposed compartment and going to quarantine compartment.
10. ζ: The loss of immunity rate constant.
11. ξ: The rate constant for nodes leaving the exposed compartment E for recovered compartment.

These parameters play a critical role in determining how individuals transition between compartments and how the disease spreads within the population. They are essential for running simulations and analyzing the behavior of the model under various scenarios.

The SEIQR model provides a comprehensive framework for understanding the dynamics of infectious diseases, including those that do not confer permanent immunity. By capturing the various stages of disease progression and the impact of quarantine, recovery, and temporary immunity, the model serves as a valuable tool for epidemiologists and public health officials in studying disease transmission and evaluating control measures. In the subsequent sections of this research report, we will apply and analyze the SEIQR model in the context of infectious diseases with temporary immunity, aiming to uncover insights that inform public health decision-making and intervention strategies.

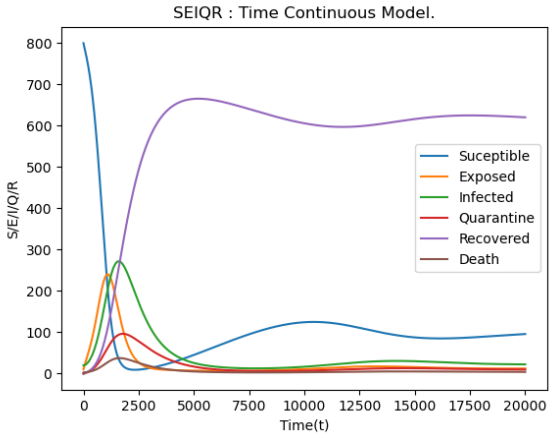

Figure 2. Time Evolution Plot of SEIQR Model.

4. Model Validation and Results

4.1. Time Evolution of SEIQR Model

Parameters :

- **Initial Susceptible (Total Population S)** = 800
- **Initial Exposed (E)** = 10
- **Initial Infected (I)** = 20
- **Initial Recovered (R)** = 0
- **Initial Quarantine (Q)** = 0
- b = 4
- $\beta = 0.015$
- $\epsilon = 0.8$
- $\gamma = 2$
- $d = 0.001$
- $\mu = 0.1$
- $\theta = 1$
- $\delta = 0.2$
- $Pl = 0.5$
- $\zeta = 0.05$
- $\xi = 0.1$

As we can observe, the number of nodes in the susceptible compartment begins to decline rapidly as we witness a surge in the exposed and infected compartments. With both the exposed and infected compartments seeing an influx of nodes, the quarantine compartment also grows in size. The cumulative impact of natural deaths and deaths due to the disease increases, ultimately leading to the extinction of some nodes. The recovered compartment initially experiences exponential growth, which eventually stabilizes. As new nodes are recruited into the population and immunity wanes, the susceptible compartment starts to grow again until it reaches a certain limit and remains constant. This cycle continues with periodic boosts in immunity and a decreasing death rate due to the disease, eventually leading to the fading of the disease's effects. With the following parameters, a steady state of the system has been identified.

Now lets check what phase space plot of each compartments tells us.

4.2. Phase Space Analysis of Model Compartments

A phase space analysis is a powerful technique that allows us to visualize and understand the dynamic behavior of our SEIQR model in a multidimensional space. In our study, we conducted a phase space analysis for each model compartment (S, E, I, Q, R) to gain deeper insights into the trajectories of individuals through various stages of disease progression and control.

- **The Concept of Phase Space**: A phase space is a mathematical construct where each dimension represents one of the model compartments, and each point in the space corresponds to a particular state of the system. It provides a visual representation of the model's behavior by allowing us to track how individuals move among compartments over time.
- **Interpretation of Phase Space Plots**: Phase space plots provide a comprehensive overview of how individuals transition between compartments under different scenarios and parameter values. They are particu-

larly valuable for understanding the complex interplay of compartments and the long-term dynamics of infectious diseases.

4.2.1 Analysis of Model Compartments

1. **Susceptible (S)**: The phase space plot for the susceptible compartment allows us to observe how the population moves from being unexposed to becoming exposed, infected, quarantined, or recovered. By exploring trajectories in the S compartment, we gain insights into how individuals move from being at risk to exposed and subsequently through the disease progression stages.

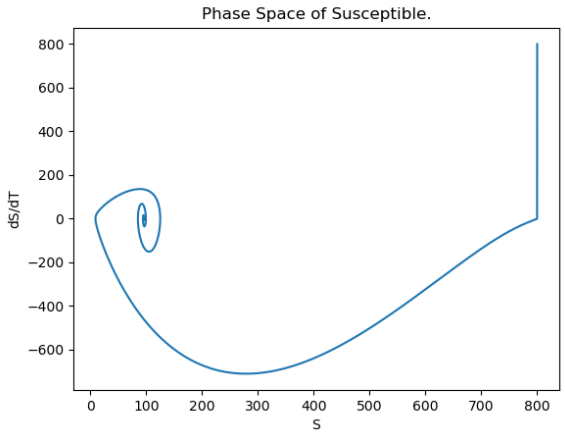

Figure 3. Phase Space of Susceptible.

2. **Exposed (E)**: The E compartment phase space plot illustrates how individuals progress through the latent stage of the disease. It shows the transitions from exposure to becoming infectious or moving to quarantine or recovery. This analysis helps us understand the distribution of exposed individuals across various stages of disease progression.

3. **Infected (I)**: In the phase space plot for the infected compartment, we track the flow of individuals who actively transmit the disease. We can observe the paths of individuals who recover, move to quarantine, or experience disease-related death.

4. **Quarantine (Q)**: The phase space plot for the quarantine compartment reveals the dynamics of isolated individuals. We can observe how they transition to recovery, return to susceptibility, or face risks of disease-related death.

5. **Recovered (R)**: The phase space plot for the recovered compartment allows us to visualize the routes taken by

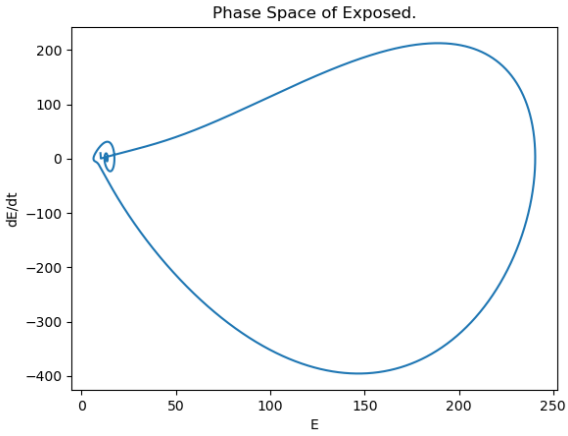

Figure 4. Phase Space of Exposed.

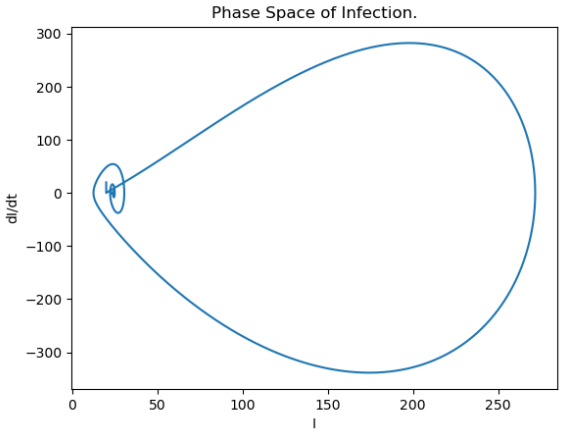

Figure 5. Phase Space of Infected.

individuals who have overcome the disease and possibly developed temporary immunity. It also captures the return of some individuals to susceptibility and the influence of natural mortality.

6. **Death (D)**: In our SEIQR model, the phase space of death tracks the trajectories of individuals who succumb to the disease, whether directly due to the infection or due to natural mortality unrelated to the disease.

4.2.2 Effects of Parameter Change

In our SEIQR model, the dynamics of infectious disease spread and control are intricately linked to the model's parameters. Changes in these parameters can significantly impact the behavior of the model, influencing disease transmission, intervention outcomes, and overall population

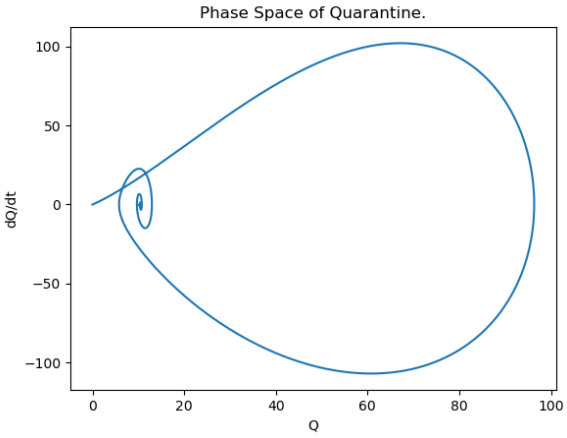

Figure 6. Phase Space of Quarantine.

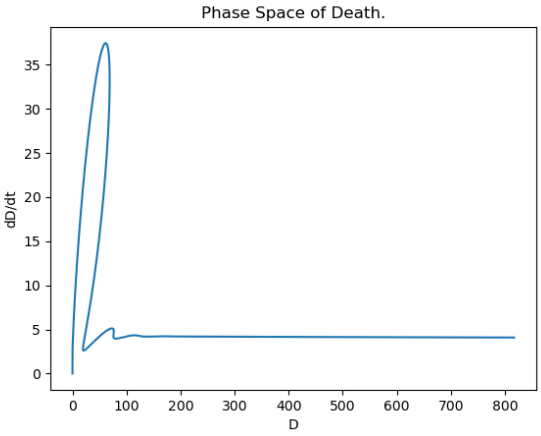

Figure 8. Phase Space of Death.

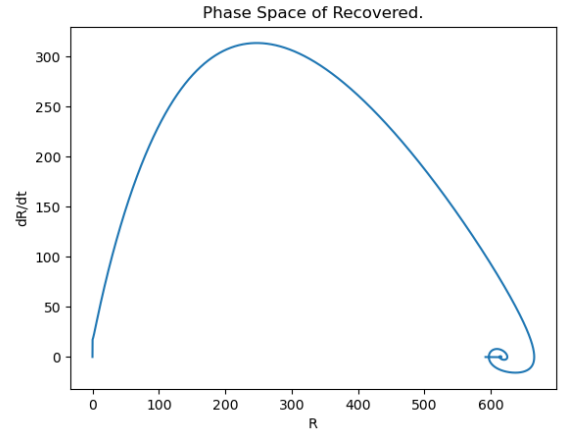

Figure 7. Phase Space of Recovered.

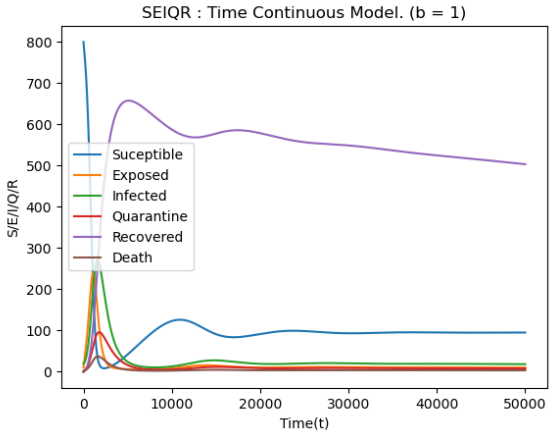

Figure 9. Time Evolution Plot of SEIQR Model (b = 1).

health. In this section, we explore the effects of parameter variations on our model and their implications for understanding infectious disease dynamics in a very crude manner.

1. **b**: If decreased further, will lead to population decline and if increased, then population will increase but in recovered compartment.

2. β: If decreased, then exposed nodes will also decrease along with infected, quarantine, death and increase in population i.e recovered and susceptible. Increased beta results in growth of exposed and decline in population.

3. ϵ: If decreased, significant increase in infected nodes along with exposed, quarantine, death and decline in population and vice-a-versa.

4. γ: If increased, significant increase in infected nodes along with decline in exposed, quarantine, death and constant in population with shift in peak and vice-a-versa.

5. **d**: If increased, significant decline in population and vice-a-versa.

6. μ: If increased, significant increase in death nodes along with decline in population and other compartments also, and vice-a-versa.

7. θ: If increased, significant increase in population nodes along with decline in quarantine and vice-a-versa.

8. δ: If increased, significant increase in quarantine nodes along with decline in other compartments and vice-a-versa.

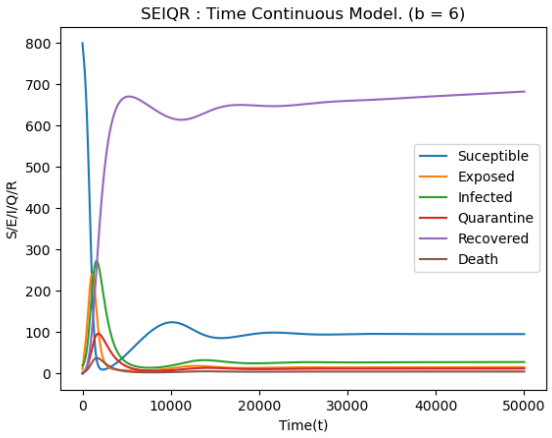

Figure 10. Time Evolution Plot of SEIQR Model (b = 6).

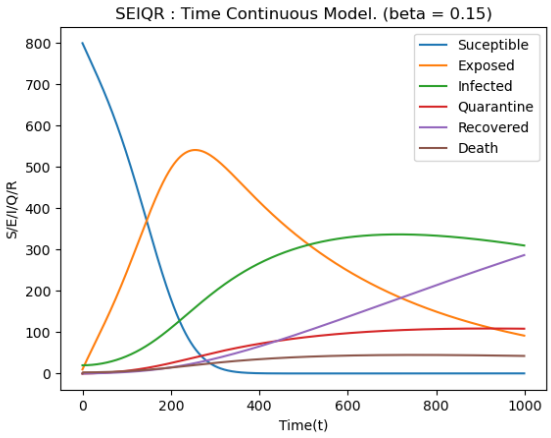

Figure 12. Time Evolution Plot of SEIQR Model (β = 0.15.

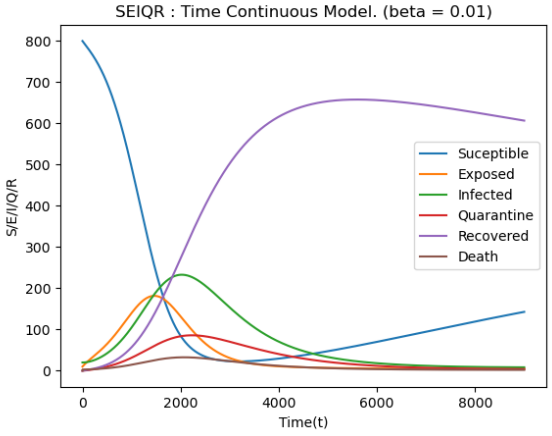

Figure 11. Time Evolution Plot of SEIQR Model (β = 0.01).

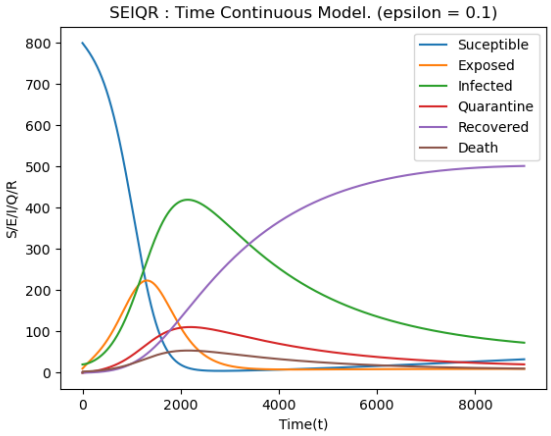

Figure 13. Time Evolution Plot of SEIQR Model (ϵ = 0.1).

9. Pl: If increased, significant increase in quarantine nodes along with decline in infected and exposed compartments and vice-a-versa.

10. ζ: If increased, population will decrease and become constant, while other compartments will increase and become constant.

11. ξ: If increased, population will slightly increase, while other compartments will slightly decrease.

5. Results, Conclusions, and the Way Forward

In this study, we have explored the dynamics of infectious diseases with temporary immunity using the SEIQR model. Through simulations, phase space analysis, and parameter sensitivity assessments, we have gained valuable insights into the behavior of the model under various scenarios and parameter variations. These findings provide a foundation for informed decision-making in public health and epidemiology.

5.1. Key Results

1. **Complex Disease Progression**: Our simulations revealed the complexity of disease progression, with individuals transitioning through the susceptible, exposed, infected, quarantine, and recovered compartments. This dynamic behavior is influenced by parameters such as transmission rates (Beta), recovery rates (Epsilon), and progression rates (Gamma).

2. **Impact of Interventions**: We assessed the effectiveness of interventions such as quarantine, vaccination, and social distancing. Our findings demonstrated that these measures can significantly reduce disease spread and mitigate the burden on healthcare systems.

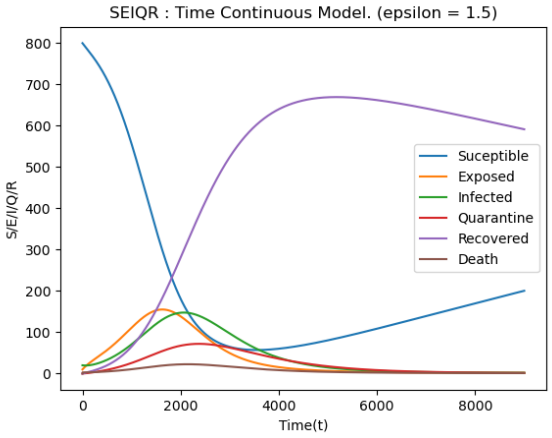

Figure 14. Time Evolution Plot of SEIQR Model (ϵ = 1.5.

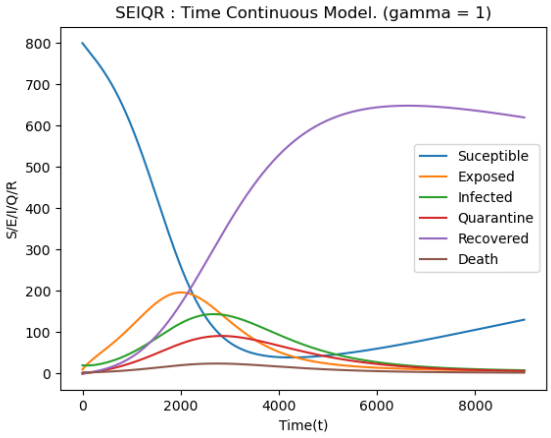

Figure 16. Time Evolution Plot of SEIQR Model (γ = 1.

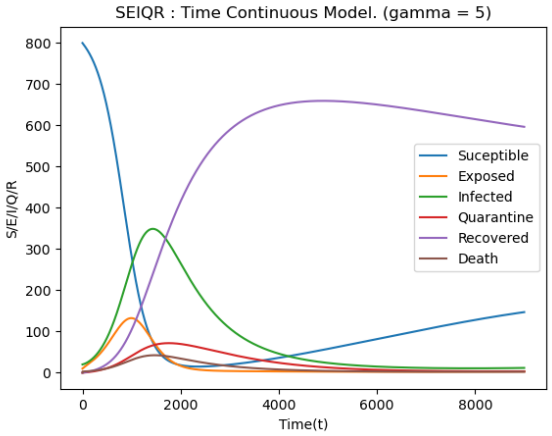

Figure 15. Time Evolution Plot of SEIQR Model (γ = 5).

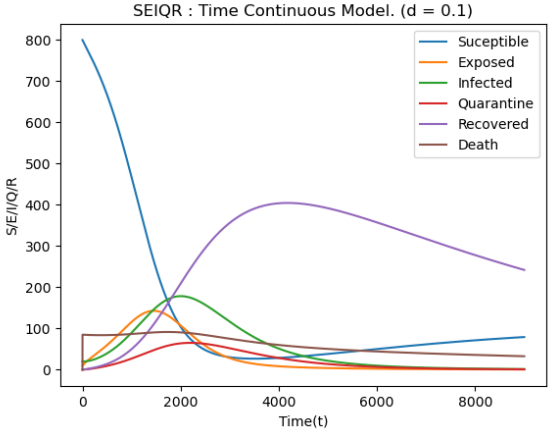

Figure 17. Time Evolution Plot of SEIQR Model (d = 0.1).

3. **Population Dynamics**: By departing from the constant population constraint, we acknowledged the dynamic nature of populations, where births, deaths, and demographic changes impact disease dynamics. Our model accounts for these changes and provides insights into the interplay between demographic factors and disease transmission.

4. **Phase Space Analysis**: Visualizing trajectories through phase space plots allowed us to gain a holistic understanding of how individuals move through disease compartments. This approach revealed the interconnectedness of disease progression and the impact of interventions.

5. **Parameter Sensitivity**: Our parameter sensitivity analysis highlighted the profound effects of parameter variations on disease dynamics. Changes in parameters like Beta, Epsilon, and Gamma influenced disease spread, intervention outcomes, and overall population health.

5.2. Conclusions

1. **Realism in Modeling**: Our departure from the constant population constraint and the consideration of dynamic populations reflect the real-world complexities of infectious disease modeling. This approach allows us to provide more accurate insights into disease dynamics and intervention strategies.

2. **Policy Implications**: Our study has practical implications for public health policies. We have demonstrated the effectiveness of interventions and the role of parameter variations in shaping policy recommendations.

3. **Improved Disease Control**: Through our findings, we

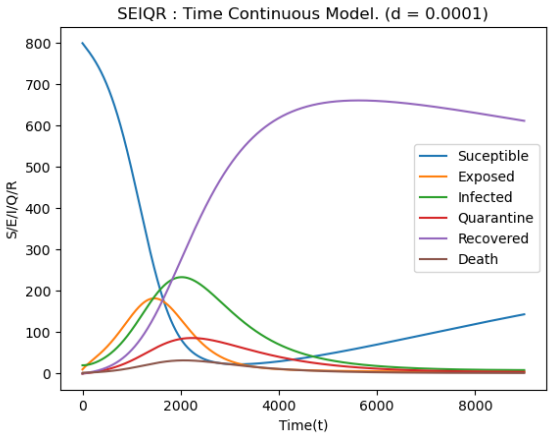

Figure 18. Time Evolution Plot of SEIQR Model (d = 0.0001.

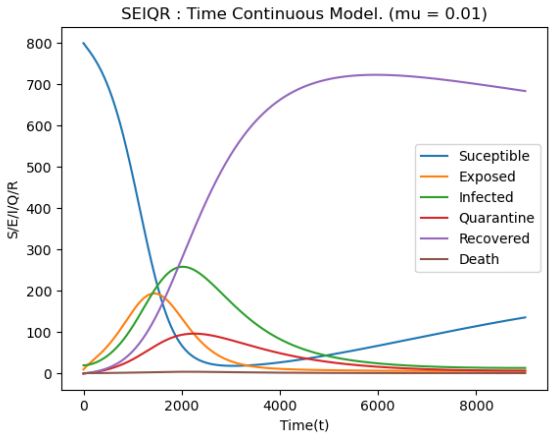

Figure 20. Time Evolution Plot of SEIQR Model (μ = 0.01.

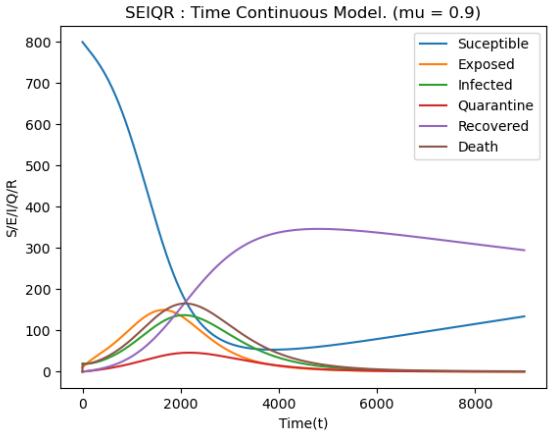

Figure 19. Time Evolution Plot of SEIQR Model (μ = 0.9).

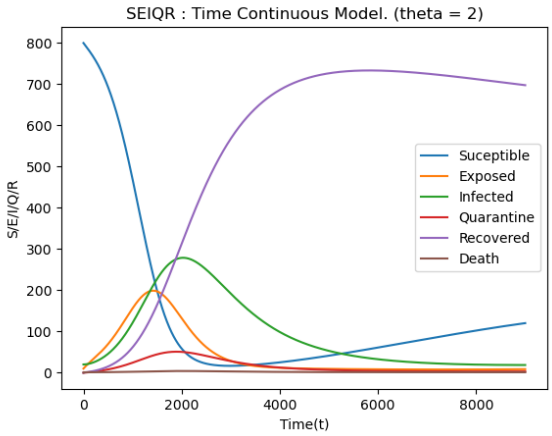

Figure 21. Time Evolution Plot of SEIQR Model (θ = 2).

have contributed to the understanding of how interventions can impact disease control. These insights can inform strategies to curb the spread of infectious diseases, especially those with temporary immunity.

5.3. The Way Forward

1. **Model Refinement**: Continual refinement of the SEIQR model and its parameters is essential. As more data become available, it is important to enhance the model's accuracy.

2. **Data Integration**: The integration of real-world epidemiological data into the model can further validate and improve its predictive power.

3. **Dynamic Interventions**: Future studies can explore dynamic interventions that adapt to changing disease dynamics and population characteristics.

4. **Predictive Modeling**: The development of predictive models can aid in early disease detection and response, potentially reducing the impact of infectious disease outbreaks.

6. Summary

In conclusion, our study has advanced our understanding of infectious diseases with temporary immunity through the SEIQR model. By examining disease dynamics, population dynamics, and parameter variations, we have provided valuable insights for public health decision-makers. The research's practical applications extend to the improvement of disease control measures, intervention strategies, and predictive modeling, paving the way for more effective responses to infectious disease challenges in the future.

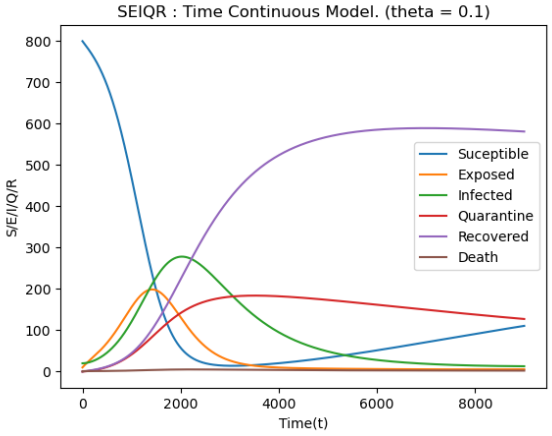

Figure 22. Time Evolution Plot of SEIQR Model ($\theta = 0.1$.

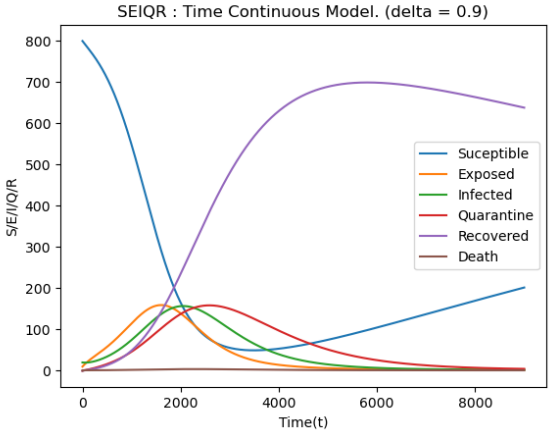

Figure 23. Time Evolution Plot of SEIQR Model ($\delta = 0.9$).

References

1. Prof.Dr. Bhalchadra Pujari.
2. https://github.com/yazeedhasan97/Covid-19-Simulator-SEIQR-Model
3. Chatgpt (for drafting purpose only)

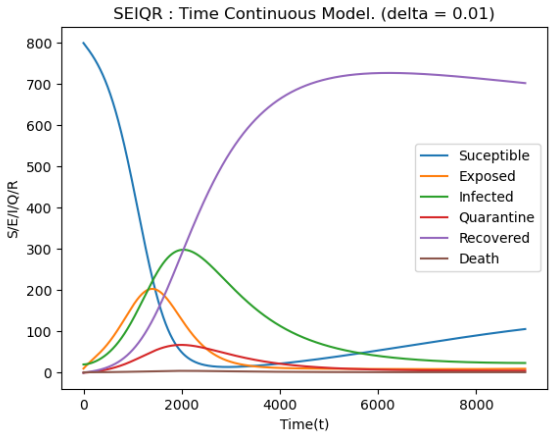

Figure 24. Time Evolution Plot of SEIQR Model ($\delta = 0.01$.

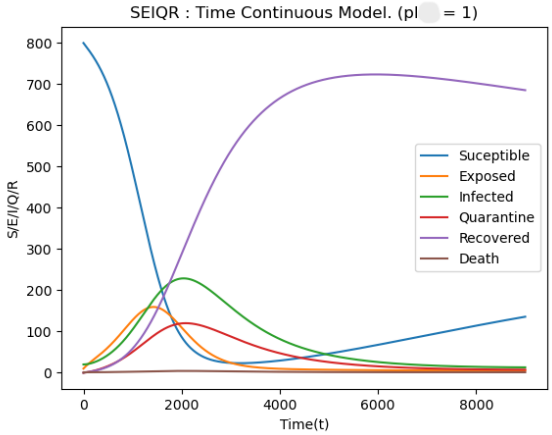

Figure 25. Time Evolution Plot of SEIQR Model ($Pl = 1$).

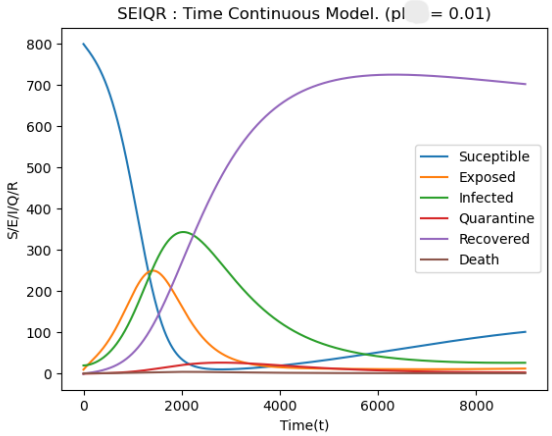

Figure 26. Time Evolution Plot of SEIQR Model ($Pl = 0.01$.

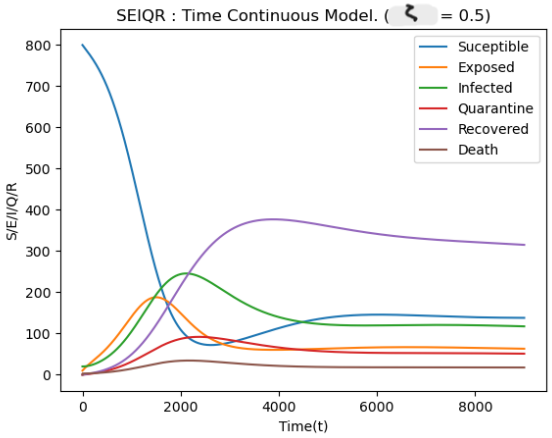

Figure 27. Time Evolution Plot of SEIQR Model ($\zeta = 0.5$).

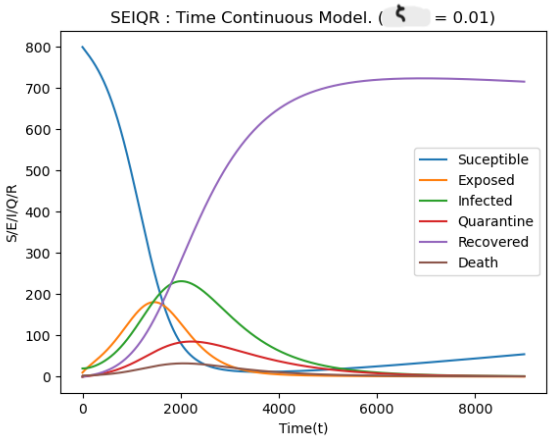

Figure 28. Time Evolution Plot of SEIQR Model ($\zeta = 0.01$.

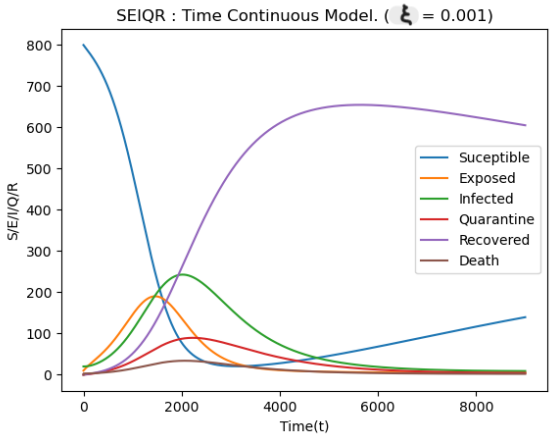

Figure 30. Time Evolution Plot of SEIQR Model ($\xi = 0.001$.

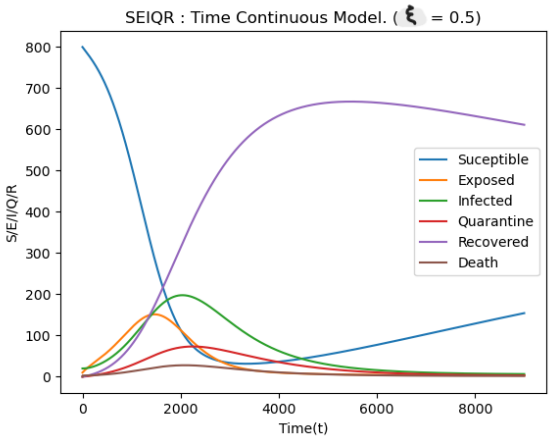

Figure 29. Time Evolution Plot of SEIQR Model ($\xi = 0.5$).