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# Epidemic Simulation Framework: Design, Implementation, and Accuracy Analysis

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## Abstract

Large-scale decisions can significantly impact the health, security, and economic well-being of a society, making it essential to provide appropriate tools and data for informed decision-making. However, in situations of uncertainty as witnessed with COVID-19, it is prudent to utilize simulation tools that can project future scenarios and assess their effects on a population. With the computational capabilities available today, population simulations can closely mimic real-world dynamics. By setting parameters and observing their impact, decision-makers can evaluate different scenarios and assess their consequences on the population.

In this study, we present an Epidemic Simulation Framework to replicate the spread of infectious diseases within a population using the Susceptible-Infectious-Recovered (SIR) model on a 2D plane, supported by a software application tool. This tool serves as a valuable resource for researchers, policymakers, and the general public by allowing them to create and manipulate populations with varying sizes and characteristics, incorporating parameters such as vaccination, quarantine, and infection rates. By utilizing this tool, users can proficiently introduce infectious individuals and closely monitor the subsequent dynamics of disease spread. The tool not only offers real-time data concerning the distribution of individuals across different disease stages but also presents informative graphs and charts that vividly depict the progression of the epidemic.

To evaluate the accuracy of this framework, we gathered authentic data on the dissemination of COVID-19 in Algeria. By comparing this data with the simulation results generated by the tool, we observed a noteworthy correlation between the two. This substantiates a strong correspondence between the simulation outcomes and the actual advancement of the disease.

Key words: Simulation, Epidemic, Disease, SIR model, Interactive

**Dedication**

*To my beloved mother, my dear father,*

*To my little sister and brothers*

*To my friends*

*Nacer*

*To my beloved mother, my dear father,*

*To my amazing sisters*

*To my friends*

*Amel*

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Thank you.

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## List of Abbreviations

SIR - Susceptible-Infectious-Recovered (epidemic model)

SIRV - Susceptible-Infectious-Recovered-Vaccinated (epidemic model)

SARS - Severe Acute Respiratory Syndrome

MERS - Middle East Respiratory Syndrome

COVID-19 - Coronavirus disease 2019

LMIC - Low and Middle-Income Countries

WHO - World Health Organization

R0 - R-naught (Basic Reproduction Number)

PDF - Probability Density Function

CDF - Cumulative Distribution Function

GUI - Graphical User Interface

CSV - Comma-Separated Values

## Introduction

The Covid-19 pandemic has underscored the importance of epidemiology in comprehending and managing infectious diseases [1]. Consequently, researchers have developed simulation tools such as Covidsim to study and control Covid-19 outbreak in 137 low and middle-income countries (LMICs). The tool was developed by Imperial's MRC Centre for Global Infectious Disease Analysis, London [2].

This report presents a framework supported by a simulation tool that employs the SIR (Susceptible, Infectious, Recovered) model to simulate epidemic scenarios, categorizing the population into susceptible, infectious, and recovered individuals. By simulating the spread of epidemics and analyzing their long-term impact, this tool assists public health officials, policymakers, and researchers in understanding disease transmission patterns, evaluating control measures, and devising preventive strategies [3][4][5]. The user-friendly interface of the interactive simulation tool enables individuals with limited knowledge of epidemiology to explore various scenarios, experiment with intervention strategies, and observe real-time outcomes.

This approach not only provides valuable insights for decision-making and research but also raises awareness about the importance of adhering to regulations and intervention methods among diverse users. Ultimately, the tool contributes to the promotion of public health by enhancing the understanding of disease dynamics and supporting well-informed decision-making to effectively mitigate the impact of future outbreaks [6][7][8].

Our primary objectives focused on two main areas of investigation. Firstly, we aimed to understand the dynamics of virus propagation within a population, taking into account factors such as its potency, contagiousness, and population attributes such as density. Secondly, we aimed to examine the impact of various intervention methods, including vaccination and social distancing, on disease transmission.

The Covid-19 pandemic has underscored the significance of epidemic modeling and simulation as essential tools for understanding disease dynamics. Simulation models offer valuable insights into the spread of infectious diseases, enabling the development of effective strategies for outbreak mitigation and informed intervention measures. Furthermore, the integration of an interactive tool not only educates but also engages the public, fostering proactive participation in public health initiatives. In summary, this

project aims to enhance preparedness and response capabilities, ultimately minimizing the impact of future epidemics.

The simulation tool will facilitate the exploration of diverse epidemic scenarios and allow for the analysis of different parameters and intervention strategies to comprehend their impact on epidemic dynamics. The specific objectives of this report are as follows:

- Definition of a Framework that describes the guidelines of the simulation of a specific disease.
- Development of a Simulation Model: The first objective is to develop a simulation model based on the SIR (Susceptible-Infectious-Recovered) model.
- Implementation of an Interactive Tool: Users will have the ability to interact with the tool seamlessly, modify parameters in real-time, and observe the resulting effects on disease spread.
- Evaluation of Intervention Strategies: This objective entails assessing the effectiveness of various interventions, such as vaccination campaigns and quarantine policies, through rigorous experimentation within the simulation.
- Validation with Real-World Data: The final objective is to validate the simulation model by comparing its outputs with real-world data on the spread of infectious diseases.

The report is organized into three main chapters. The first chapter, Literature Review, provides a theoretical background and a comprehensive review of relevant literature in epidemiology. It establishes the project's foundation by discussing key concepts and theories. The second chapter, known as the Methodology, concentrates on the technologies and techniques employed to develop the interactive epidemic simulation tool. It outlines the specific methodologies and approaches used in the development process. Finally, the third chapter, Results, Analysis & Discussions, presents the application tests and analyzes the effects of various parameters. It also compares real-world data with the simulation output, facilitating a comprehensive understanding of the project's findings and insights.

# Chapter 1
# Literature Review

# Chapter 1: Literature Review

## 1.1 Overview

Epidemiology is the study of the distribution and determinants of diseases and health conditions in populations [9][10]. Epidemics can occur when an infectious disease spreads rapidly through a population, causing significant illness and mortality. The impact of epidemics can be devastating, both in terms of public health and the economy [11]. Understanding how epidemics spread and the factors that contribute to their transmission is crucial for public health officials and policymakers to make informed decisions. There are different types of epidemics, including outbreaks, epidemics, and pandemics [12]. Outbreaks are localized epidemics that occur in a specific geographic area or population. Epidemics occur when an infectious disease spreads rapidly through a population, affecting a large number of people. Pandemics are global epidemics that affect multiple countries and continents [12]. This chapter lays the groundwork for the research project by providing a theoretical background and a comprehensive examination of relevant literature in the field of epidemiology. It discusses important concepts and theories, offering a clear understanding of the existing knowledge in this area of study.

## 1.2 Epidemiology Terms

In this section, we will define important terms that are essential for understanding and explaining the results. By providing straightforward explanations of these terms, we aim to ensure that readers have the necessary knowledge to discuss and interpret the findings accurately.

### 1.2.1 Incubation Period

The incubation period of a disease is the time between when a person is infectious and when they start showing symptoms. The incubation period is important because it affects the transmission dynamics of the disease. Diseases with a longer incubation period can spread more easily because infectious individuals may not know they are sick and can unknowingly spread the disease to others [13][14].

### 1.2.2 Virulence

Virulence in epidemiology refers to the severity of disease caused by a pathogen, indicating its ability to harm or cause illness in infected individuals. It encompasses factors such as the pathogen's genetic makeup, virulence factors, and the host's immune

response, influencing the overall impact and potential complications of the infection. Understanding virulence is crucial for assessing the severity of outbreaks and guiding appropriate public health measures [15][16][17].

### 1.2.3 Basic Reproduction Number ($R_0$)

The basic reproduction number ($R_0$), also known as “R naught” or “R zero” serves as a measure of how contagious or easily a disease can spread among individuals. It is a commonly used metric in the fields of epidemiology and public health, and is often discussed in both academic literature and popular media. $R_0$ holds significant importance as a fundamental tool for studying the dynamics of infectious diseases. When referring to a specific disease outbreak, $R_0$ is typically represented by a single numeric value or a range of values, indicating the potential for the outbreak to continue or subside. In general, $R_0$ of an epidemiological model represents the average number of new infections caused by a single infectious individual [18][19] (Figure 1) in a population that is entirely susceptible to the disease.

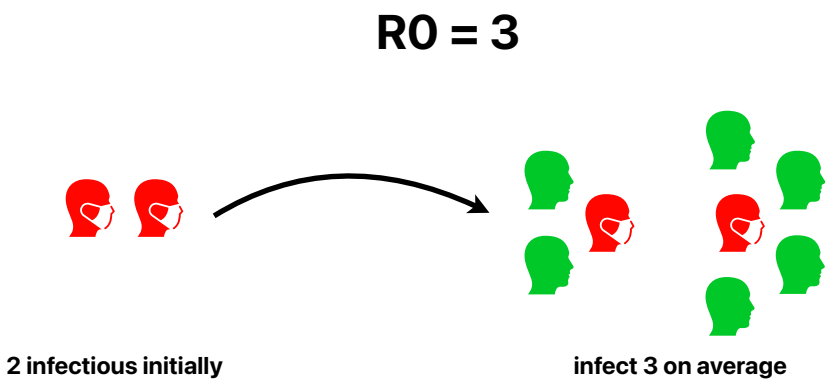


*Figure 1 - Basic Reproduction Number Demonstration*

The basic reproduction number serves as a valuable indicator to predict whether a disease will persist or disappear. According to established references in mathematical epidemiology, when $R_0$ is less than 1, the number of infectious individuals decreases over time, leading to the elimination of the disease. Under certain additional assumptions, the population eventually reaches a state where there are no infectious individuals, known as a disease-free equilibrium. On the other hand, when $R_0$ is greater than 1, the number of infectious cases increases, reaches a peak, and then declines to zero in the case of epidemic models. In the case of endemic models, $R_0$ causes the disease to stabilize at a certain level, known as an endemic equilibrium [20][21].

The measurement and modeling of R0, along with its application, should be approached with caution due to its indirect nature, dependence on model structures and assumptions [20]. In the context of the simulation, the basic reproduction number ($R_0$) is computed using Equation 1.

$$R_0 = \frac{number\ of\ infections\ today}{number\ of\ infections\ two\ days\ ago} \quad (1)$$

## 1.3 Epidemiology

Epidemiology is a scientific discipline that focuses on studying the distribution and determinants of health-related events, particularly diseases, within populations. It encompasses the investigation of patterns, causes, and effects of diseases, as well as the development of strategies for disease control and prevention. Epidemiologists collect and analyze data to understand the frequency and distribution of diseases, identify risk factors, and assess the impact of interventions. By studying the epidemiology of diseases, researchers can gain insights into disease transmission dynamics and guide public health policies and practices [22][23].

## 1.4 Phases of Disease Transmission

### 1.4.1 Epidemic

An epidemic occurs when the occurrence of cases of a particular disease exceeds what is normally expected within a given population, geographic area, or time period [24]. During an epidemic, there is a rapid and substantial increase in the number of cases, resulting in a significant burden on healthcare systems and potentially leading to severe morbidity and mortality. Epidemics can arise from various factors, such as the introduction of a new pathogen, changes in pathogen virulence or transmissibility, and environmental or social factors that promote disease spread. Understanding the dynamics of an epidemic is crucial for implementing timely and effective control measures [24][25][26].

### 1.4.2 Endemic

Endemic refers to the constant presence or usual prevalence of a disease within a specific population or geographic area. Unlike an epidemic, where there is a sudden surge in cases, endemic diseases persistently occur at a relatively steady level, often with periodic fluctuations. Endemic diseases are often influenced by factors such as host susceptibility, pathogen persistence, environmental conditions, and human behavior. Monitoring and

managing endemic diseases require ongoing surveillance, targeted interventions, and public health strategies to minimize the disease burden and maintain control over time [24][27].

### 1.4.3 Eradication

Eradication refers to the complete elimination of a disease from a specific population or the global population. Eradicating a disease involves permanently reducing the incidence of infection to zero through deliberate efforts. Successful eradication efforts have been demonstrated in the case of diseases like smallpox, which was declared eradicated in 1980 [28]. Eradication requires a combination of robust surveillance systems, effective vaccines or treatments, widespread public health interventions, and global coordination. Achieving eradication is a significant milestone and represents the highest level of disease control, offering long-term protection against the disease [5][29].

## 1.5 Compartmental Models

Compartmental models are a common technique used in mathematical modeling, especially when studying infectious diseases. These models divide the population into different groups, like "Susceptible," "Infectious," or "Recovered". Each compartment represents a distinct stage of infection or disease progression [30][31].

### 1.5.1 SIR Model

The SIR model is a type of compartmental model that is widely used due to its simplicity and versatility. Many derivative models are built upon this basic form, which comprises three compartments: S, I, and R. The S compartment represents the number of susceptible individuals, i.e., those who have not yet been infectious with the disease but can become infectious upon contact with an infectious individual. The I compartment represents the number of infectious individuals, i.e., those who have been infected with the disease and can transmit it to susceptible individuals. The R compartment represents the number of recovered or deceased individuals, who have either recovered from the disease and entered the recovered compartment or died. It is assumed that the number of deaths is negligible with respect to the total population. This compartment may also be referred to as "removed" or "resistant". The SIR model is widely used in the study of infectious diseases that are transmitted from human to human, like measles, mumps, and rubella. A spatial SIR model simulation can be used to model the spread of disease across a population. The S, I, and R variables represent the number of people in each compartment

at a specific time, and their values can vary over time due to changes in the number of susceptible, infectious, and recovered individuals. The model is dynamic, which means that the numbers in each compartment can fluctuate over time [32][33][34].

### 1.5.2 SIRV Model

The Susceptible-Infectious-Recovered-Vaccinated (SIRV) model is an expanded variant of the well-established Susceptible-Infectious-Recovered (SIR) model, designed to incorporate the impact of vaccination on the susceptible population. The SIRV model is a widely-used tool for modeling infectious disease dynamics and evaluating the potential effects of vaccination programs on disease transmission. By considering the effects of vaccination in conjunction with the traditional SIR compartments, the SIRV model allows for a more comprehensive understanding of the dynamics of infectious diseases and the potential impact of vaccination interventions [32][35][36].

## 1.6 Probability

Probability, in general, refers to the measure of the likelihood or chance of an event or outcome occurring. It is a mathematical concept used to quantify uncertainty and provide information about the chances of different outcomes in a given situation. Probability is expressed as a value between 0 and 1, where 0 represents impossibility (an event will not occur) and 1 represents certainty (an event will definitely occur).

In the context of epidemiology, probability plays a crucial role in understanding the relationship between exposures and the risk of health effects. Probability calculations involve considering various factors, including the prevalence and incidence of diseases, exposure levels, demographics, and other relevant variables. By analyzing these factors and applying probability theory, researchers can estimate the probability of disease occurrence within a population or specific groups, evaluate the impact of different risk factors, and develop strategies for disease prevention and control.

Probability in epidemiology allows researchers to quantify the likelihood of disease outcomes, understand the magnitude of associations between exposures and health effects, and assess the effectiveness of interventions. It helps in identifying individuals or populations at higher risk, informing public health policies and guidelines, and evaluating the impact of preventive measures on disease burden [37][38].

### 1.6.1 Uniform Distribution

Uniform distribution, also known as rectangular distribution, refers to a probability distribution in which all outcomes within a given range have equal probability. In other words, each value within the range has the same likelihood of occurring [39].

In a uniform distribution, the probability density function (PDF) is constant over the entire range of possible values, resulting in a rectangular shape when plotted on a graph. The PDF assigns equal probabilities to all values within the range and is typically represented as shown in Equation 2

$$f(x) = \begin{cases} \frac{1}{(b - a)} & for \quad a \leq x \leq b \\ 0 \quad for & x < a \ or \ x > b \end{cases} \tag{2}$$

where $a$ and $b$ represent the lower and upper limits of the range, respectively[40].

The cumulative distribution function (CDF) of a uniform distribution is a linear function, increasing steadily from 0 to 1 over the range from a to b. When the value is below the starting point 'a', the probability is 0, meaning it cannot occur. On the other hand, when the value is beyond the ending point 'b', the probability is 1, indicating it is certain to happen as summarized in equation (3 [40]

$$f(x) = \begin{cases} 0 \ for \ x < a \\ \frac{x - a}{b - a} \ for \ a \leq x \leq b \\ 1 \ for \ x > b \end{cases} \tag{3}$$

The uniform distribution is often used in situations where each outcome has an equal chance of occurring, such as in random number generation, simulations, certain sampling techniques and in epidemiology [41]. It provides a simple and symmetric probability model in which all values are equally likely.

## 1.7 Mathematical Disease Modeling

The utilization of mathematical models in examining the transmission of infectious diseases has been a subject of investigation for many years. Among the various models developed, the SIR (Susceptible-Infectious-Recovered) model introduced by Kermack and McKendrick in 1927 as demonstrated in Equations 4, 5 and 6

$$\frac{dS}{dt} = -\beta SI \tag{4}$$

$$\frac{dI}{dt} = \beta SI - \gamma I \quad (5)$$

$$\frac{dR}{dt} = \gamma I \quad (6)$$

Where $\beta$ is the transmission coefficient and $\gamma$ is the recovery rate. Adding the three equations together implies that the total population $N = S + I + R$ is constant [42][43].

The SIR model was initially designed to depict the spread of diseases like measles, smallpox, and influenza [42]. Over time, it has been widely employed to simulate the transmission dynamics of different infectious diseases, including HIV, Ebola, and Covid-19 [44][45][46].

Due to its simplicity, the SIR model has certain limitations. For instance, it assumes a homogeneous mixing of the population, which may not accurately represent the true social and spatial structure of a population [47]. Additionally, the model assumes uniform susceptibility and infectivity among individuals, which may not hold true in reality. Consequently, more complex models have been developed to address these limitations and account for population heterogeneity, such as the SEIR (Susceptible-Exposed-Infectious-Recovered) model [48].

Despite these limitations, the SIR model has proven to be a valuable tool for studying the transmission of infectious diseases and informing public health policies. For example, the model was instrumental in simulating the spread of SARS in Hong Kong, aiding the government in implementing effective control measures [49]. Similarly, the model was utilized to simulate the spread of H1N1 influenza in Mexico, assisting in the development of vaccination strategies [50].

Numerous studies have employed the SIR model to investigate the impact of various control measures on disease transmission. For instance, Kucharski et al. [51] utilized the SIR model to assess the impact of school closures and social distancing measures on the spread of COVID-19 in the United Kingdom. Their findings demonstrated that a combination of school closures and social distancing measures significantly reduced the number of infections.

Rosella et al. explored the influence of viral load on disease transmission. The authors propose a novel epidemic model that considers the viral load of individuals as a determining factor. Through microscopic and macroscopic analysis, the authors highlight the significance of viral load in understanding epidemic dynamics [52].

Another study evaluates the usefulness of early-stage Susceptible-Infected-Recovered (SIR) modeling in public health, using COVID-19 as an example. The researchers develop a modified SIR model using Markov chain simulations to estimate the number of beds needed in Wuhan during the early stages of the epidemic. By comparing eight scenarios to real-world data, they find that the model performs better when updated data is used. The study concludes that early-stage SIR modeling can provide valuable information for public health systems and accurately predict epidemic trends [53].

Authored by Ian Cooper, Argha Mondal, and Chris G. Antonopoulos, another article explores the effectiveness of the Susceptible-Infectious-Recovered (SIR) model for studying the spread of COVID-19 in different communities. The SIR model allows for an increase in the number of susceptible individuals during surge periods and provides insights and predictions beyond recorded data alone. By analyzing diverse populations and significant parameters, the authors demonstrate the importance of modeling the spread of COVID-19 using the SIR model. Mathematical models, such as SIR, play a crucial role in estimating disease transmission and guiding effective intervention strategies [54].

Additionally, an article discusses a comparative study of mathematical models for epidemic diseases and their application to strategic management. The authors focus on the SIR (Susceptible-Infectious-Recovered) model and its parameters in Saudi Arabia during a 275-day period. They estimate the parameters from recorded data and use them to predict values for subsequent periods. The study highlights the effectiveness of lockdown and social distancing measures in controlling the spread of the disease. The maximum number of daily active infected cases is determined, and the authors emphasize the importance of mathematical models in developing strategies to combat epidemics [55].

In summary, the SIR model has played a crucial role in understanding and managing the spread of infectious diseases. While it has certain limitations, its simplicity and effectiveness have made it a valuable tool in informing public health policies. Recent advancements, such as incorporating spatial heterogeneity, integrating machine learning techniques, and considering dynamic network structures, have further improved the accuracy and predictive capabilities of the SIR model, enabling more effective epidemic control strategies.

## 1.8 Conclusion

In conclusion, epidemiology plays a vital role in understanding and addressing the spread of infectious diseases. The utilization of mathematical models, particularly the SIR model, has been extensive in simulating disease dynamics and guiding public health interventions. Despite SIR model's limitations, recent research have improved its accuracy, enabling more effective control strategies. Our study will employ the SIR model, hence in the subsequent chapter, we will present our work, which expands upon it to develop a disease spread simulation tool.

# Chapter 2
# Methodology

# Chapter 2: Methodology

## 2.1 Overview

The methodology chapter focuses on describing the development process of an epidemic simulation framework capable of simulating disease spread in a two-dimensional (2D) plane using the SIR (Susceptible-Infectious-Recovered) model under three different scenarios: Basic, Community, and Central Place. The simulation tool incorporates various adjustable parameters, such as population size, infection radius, initial number of infectious individuals, and quarantine policies, enabling users to experiment with different values through a user-friendly graphical interface. This flexibility allows for a wide range of simulations with diverse outcomes. The chapter elaborates on the methodology's steps, including the functions of the physics engine governing individuals' movement within the simulation space, the design and implementation of the core SIR model, the integration of each parameter and its associated functionalities, and the data collection processes for both storage and real-time visualization. Furthermore, the chapter addresses the challenges encountered during the development process and discusses the solutions that were implemented to overcome them. This chapter provides an encompassing framework for the development of an interactive epidemic simulation tool.

## 2.2 Software Tools

### 2.2.1 Python Programming Language

The Python programming language, known for its high-level and general-purpose nature, was employed as the primary tool for developing the project at hand. Its design principles prioritize code legibility through the utilization of significant indentation via the off-side rule. Python can support various programming paradigms, including procedural, object-oriented, and functional programming. Owing to its vast set of libraries and large, active community.

Guido van Rossum initiated the development of Python in the late 1980s, as a successor to the ABC programming language. The first version, Python 0.9.0, was launched in 1991. Subsequently, Python 2.0 was released in 2000, followed by a major revision, Python 3.0, in 2008. However, Python 3.0 was not entirely backward-compatible with prior versions. Despite this transition, Python continues to rank as one of the most widely used programming languages according to various rankings and surveys [56].

### 2.2.2 Pymunk

Pymunk is a 2D physics library for Python, built on top of the Chipmunk 2D physics library. It provides an easy-to-use interface for incorporating 2D rigid body physics into Python-based applications such as games, simulations, and demonstrations.

Pymunk has been in active development for over 15 years and has been utilized in various successful projects, including three Pyweek game competition winners, multiple scientific papers, and a self-driving car simulation. Its effectiveness and versatility make it an essential resource for developers seeking to implement 2D physics simulation in various applications [57].

### 2.2.3 Pygame

Pygame is a Python module that enables the creation of video games and multimedia programs with added functionality using the SDL library. It is highly portable and runs on multiple platforms and operating systems. Pygame is free and open source. Pygame's versatility and ease of use make it a valuable tool for building prototypes and simulations, particularly in the fields of computer graphics, human-computer interaction, and game studies. With optimized C and Assembly code for core functions, Pygame is fast and can easily be used on handheld devices, game consoles, and computers. It is modular, allowing developers to use specific parts of the library as needed. These features make Pygame a suitable tool for building an epidemic simulation tool [58].

## 2.3 Assumptions for SIR Model

It is important to note that the SIR model used in this report make several assumptions about the population:

- The population is fixed, meaning that no one is born or dies during the duration of the model.
- Each disease has an incubation period of zero, meaning that as soon as a person is infected with the disease, they can immediately spread it to others.
- The time of being infectious is equal to the length of the disease, meaning that the recovery time of the disease is fixed for all individuals.
- The population is homogeneous, meaning that each individual is assumed to have the same health conditions, age, social status, and other characteristics.

## 2.4 Approach & Design

The tool built in this project is based on simulating people as particles in a 2D space using physics. Each person will be in one of 3 main states (Susceptible, Infectious or Symptomatic and Recovered) in a basic scenario. Two other states (Asymptomatic, Vaccinated) will be presented further with more complex simulations.

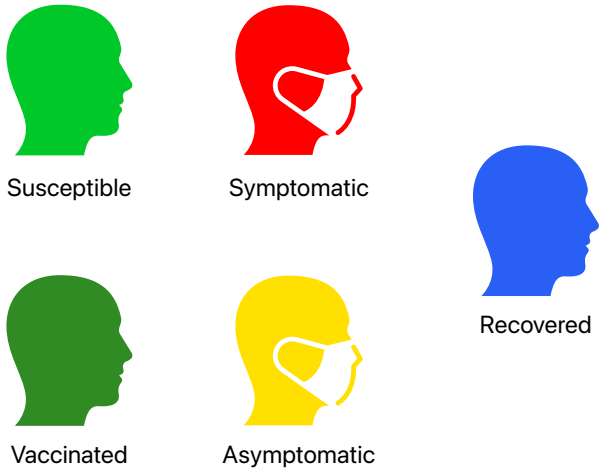


*Figure 2 - The Five States of the Population*

The concept involves simulating a population in a two-dimensional plane, where each individual is represented as a point with specific position and velocity. The primary factor influencing disease transmission is the distance between an infectious individual and a susceptible individual.

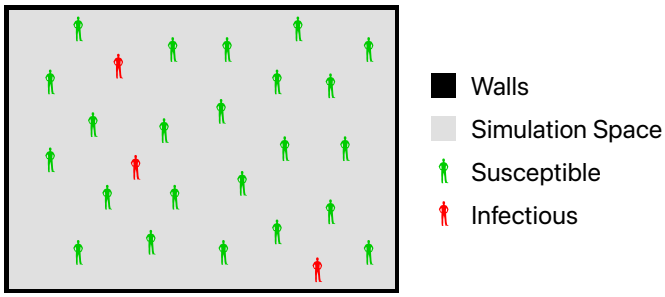


*Figure 3 - Visual Representation of the Simulation Space*

In a simulation that involves 500 individuals, calculating the distance between each person can quickly become a resource-intensive task. This challenge can significantly affect the simulation's performance, hindering its accuracy. To overcome this challenge, we came up with an innovative approach that involved using collisions as an indicator of

disease spread. By making use of the collisions between individuals, we could determine whether an infection should be transmitted or not. We used a larger transparent physical object that is attached to a smaller visible shape (Figure 4). This approach creates the impression that only the distance between two objects could lead to an infection while the real physical objects collided. This novel solution significantly improved the simulation's efficiency and accuracy, providing a more realistic representation of the spread of infectious diseases.

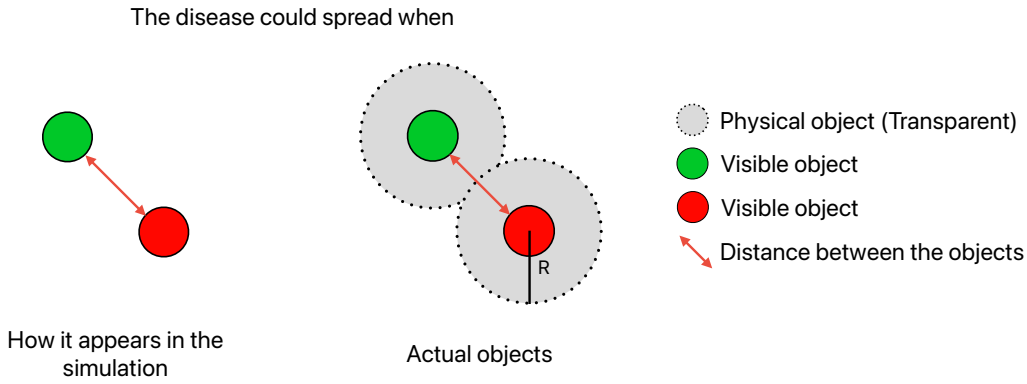


*Figure 4 - Visualization of the True Physical Object*

The foundational component of our simulation involved the creation of a two-dimensional space to serve as the environment for our simulation. This space was populated with individual "people" objects, each assigned a random initial position and velocity. The people objects were modeled to have two key physical attributes: position and velocity; The later were updated over time randomly to make the people's path curved and random avoiding straight directions or sudden direction changes. To facilitate this process, we leveraged Pymunk body class to efficiently manage the objects in the simulation, as well as the computations necessary for updating their positions. Pymunk also has a well optimized collision handling functions that are used to simulate the physical contact or interaction between two individuals. This approach allowed us to create a dynamic and flexible simulation environment, capable of modeling complex interactions and behaviors of the people objects in the two-dimensional space.

Pymunk utilizes the collision type attribute to track each object, enabling the identification of individuals involved in collisions. This information is crucial in determining whether to transmit the disease to a specific person, based on a designated probability of infection. This is done in the callback function generated by the collision. If the callback generates an infection, it will take a specific duration specified interactively

before the person enters to the recovered state. Throughout this duration, if an infected individual comes into contact with other susceptible individuals, there is a possibility of disease transmission occurring. During the simulation, we add any features depending on the scenario. Then, we calculate and record multiple statistics like the practical probability of infection and R0 in order to further analyze the results.

The simulation comprises of three distinct scenarios, namely Basic, Community, and Central Place. In the subsequent sections, we will delve deeper into each scenario and provide a detailed analysis.

## 2.5 Simulation Scenarios

### 2.5.1 Basic

The Basic scenario is the simplest simulation model in which a single compartment represents the entire population. Individuals interact randomly with each other when moving around inside the 2D space. The simulation assumes that each individual has an equal chance of being infected and the virus transmission rate is uniform throughout the population. This scenario provides a baseline for the other scenarios and helps in understanding the basic dynamics of virus transmission in a closed population.

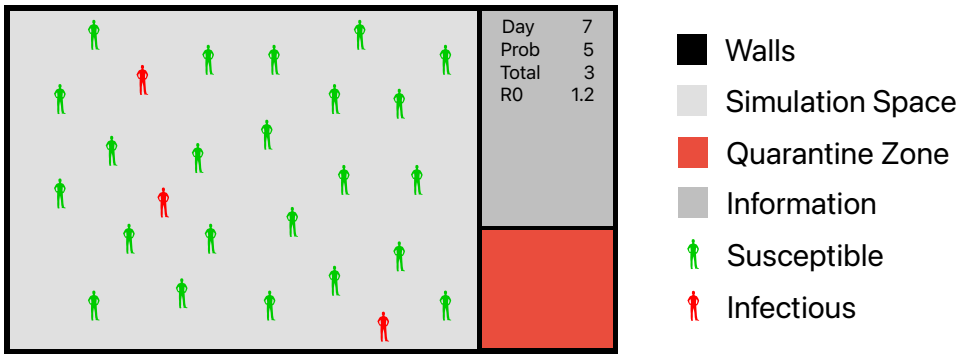


*Figure 5 - Spatial Arrangement of Elements in the Basic Scenario Simulation*

### 2.5.2 Community

In this scenario, the population is divided into nine distinct communities, each with a random population size distributed in a 3x3 grid. Individuals can travel between communities, and the simulation considers more factors such as whether the traveling between communities is allowed or not and more importantly the traveling rate between communities which indicates how many individuals travel from a community to another per week. This scenario is more complex than the Basic scenario and provides insights

into the role of community structure in virus transmission and can inform whether closing the borders between these different communities is a reliable intervention method.

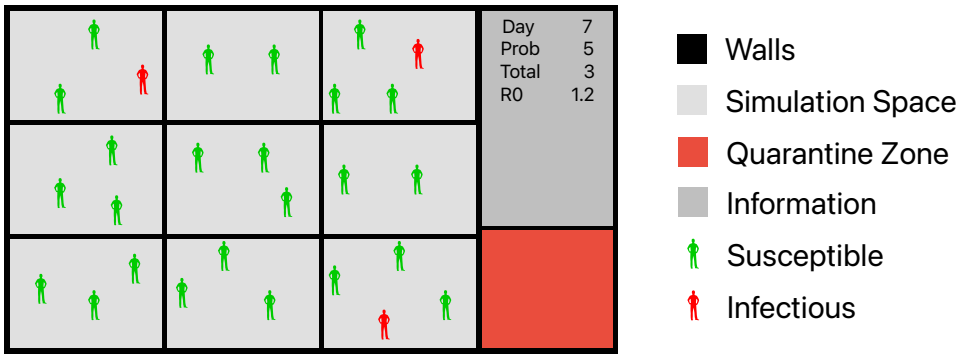


*Figure 6 - Spatial Arrangement of Elements in the Community's Scenario Simulation*

### 2.5.3 Central Place

In a real world, there are places in a community with higher density of population like universities or markets and are potential hotspots for virus transmission. Which is why we developed this scenario that represents places within a community that have high population density. The simulation forces the center to have higher population density by picking random individuals to travel to it. This scenario provides insights into the impact of central places on the spread of the virus within a community. The output of this simulation is more representative to the real world and can help in developing targeted interventions to control the spread of the virus in high-density areas.

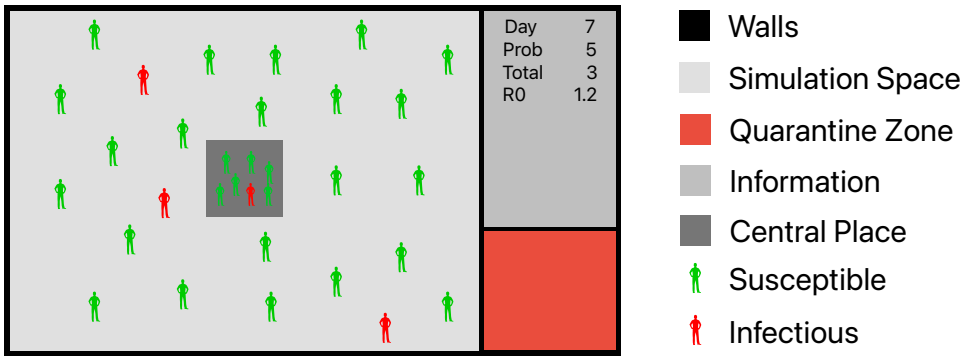


*Figure 7 - Spatial Arrangement of Elements in the Central Place Scenario Simulation*

## 2.6 Simulation Parameters

To facilitate experimentation with the different scenarios previously outlined, a Graphical User Interface (GUI) was developed. This GUI provides users with the capability to

dynamically adjust simulation parameters and observe their impact on the spread of the virus in real-time.

The parameters are categorized into the following four groups:

- Population Parameters
- Disease Parameters
- Control Measures Parameters
- Settings Parameters

### 2.6.1 Population Parameters

#### Population Size

This parameter represents the total number of individuals in the simulated population. The size of the population can have a significant impact on the spread of the virus, as larger populations can lead to more extensive outbreaks.

### 2.6.2 Disease Parameters

#### Infection Radius

The infection radius parameter represents the radius of the circle around the person within which infection can occur. It is calculated in Equation 7.

$$Infection\ Radius = 2 \times R \tag{7}$$

$R$: Radius of physical object in Figure 4

This parameter is essential in determining the likelihood of virus transmission between individuals, as individuals outside of the infection radius are not at risk of infection.

#### Initially Infectious

The Initially Infectious parameter represents the number of individuals who are infectious at the beginning of the simulation. This parameter can be used to model different scenarios, such as a single index case or a larger outbreak at the start of the simulation.

#### Infection Duration

Infection Duration represents the duration of time that an individual remains infectious. It is implemented by incrementing a specific counter attributed to each person individually. The duration of infection can vary between different viruses, and longer durations of infection can lead to more extensive outbreaks.

#### Infection Probability

This parameter represents the probability of an infectious individual transmitting the virus to others. Programmatically, assuming that the infection probability is equal to 20%, at each interaction between a susceptible and infectious person, a random number is generated from a uniform distribution between 0 and 1. Subsequently, the generated number is compared with the infection probability of 20% to determine whether an infection will occur. Notably, If the generated number is less than 0.2 meaning that the value falls within the 20% range, an infection occurs. On the other hand, if the generated number is greater than 0.2 which happens approximately 80% of the time, no infection takes place.

The probability of transmission is subject to various factors that can significantly impact the spread of the virus. These factors include the virulence of the disease, the use of protective measures such as hygiene and masks, and other host and environmental factors. Therefore, accurate modeling and estimation of the probability of transmission require careful consideration of these factors to ensure effective control and prevention of infectious diseases.

### 2.6.3 Control Measures Parameters

#### Quarantine

The Quarantine parameter allows users to enable or disable quarantine within the simulation. Quarantine is a common public health intervention used to control the spread of infectious diseases, and the simulation of quarantine can provide insights into its effectiveness. The tool simulates quarantine by isolating infectious people from the rest of the population.

#### Quarantine After

The Quarantine After parameter defines the time interval between the onset of infection and the initiation of quarantine for an individual. This parameter is a critical factor in modeling various quarantine policies, including prompt quarantine of all symptomatic individuals or delayed quarantine due to a lack of public cooperation or awareness. Understanding the effects of quarantine policies on the epidemic's spread requires examining the impact of these policies under different quarantine timing conditions. Therefore, adjusting the quarantine after parameter in the epidemic simulation tool allows

researchers to explore the interplay between timing and quarantine policies in curbing epidemic outbreaks.

### Symptoms Probability

The Symptoms Probability parameter represents the probability of an individual displaying symptoms after being infected. The same logic used to handle Infection probability is used to handle Symptoms probability.

Notably, the Symptoms probability parameter is particularly relevant in modeling the impact of asymptomatic transmission. This is because asymptomatic individuals can transmit the virus without displaying any symptoms and may be missed in quarantine efforts. Therefore, the accurate estimation and modeling of the Symptoms probability parameter are crucial in controlling and preventing the spread of infectious diseases.

### Traveling

The Traveling parameter is used only in Community's scenario where it allows users to enable or disable traveling between communities within the simulation. When Traveling is enabled, a random individual is selected to travel to a different community every time interval specified by the Traveling rate parameter. This simulation of traveling provides valuable insights into the role of mobility in the spread of infectious diseases. Furthermore, it allows for an examination of the effectiveness of travel restrictions as a public health intervention.

Overall, the Traveling parameter is a useful tool in modeling and analyzing the spread of infectious diseases in complex social networks. By incorporating the mobility factor, the simulation can better capture the real-world dynamics of disease transmission, and facilitate the development of effective control and prevention strategies.

### Traveling Rate

The Traveling Rate parameter represents the frequency at which individuals travel between communities per week. This parameter can be used to model different travel patterns, such as regular commuting or occasional travel for social or cultural events.

### Vaccination

The vaccination parameter allows users to enable or disable the simulation of a vaccination program. The implementation of the Vaccination parameter is based on the concept that the Infection probability of a vaccinated individual is reduced proportionally

to the Vaccine Efficiency parameter. This enables the simulation to reflect the impact of vaccination on disease transmission, and provides valuable insights into the effectiveness of different vaccination strategies.

Vaccination is widely regarded as one of the most effective ways to control the spread of infectious diseases. Therefore, incorporating the Vaccination parameter into the simulation enables the exploration of different vaccination scenarios and their potential impact on disease control.

#### Vaccine Efficiency

The Vaccine Efficiency parameter represents the effectiveness of the vaccine in preventing virus transmission. This parameter can be used to model different types of vaccines, such as those with varying levels of efficacy.

To simulate the impact of a vaccine in reducing the transmission of the virus, the Infection Probability of a vaccinated person is modified using a formula that takes into account the Vaccine Efficiency value. As shown in Equation 8.

$$New\ Infection\ Probability = Old\ Infection\ Probability * (1 - Vaccine\ Efficiency) \quad (8)$$

Since Vaccine Efficiency is a percentage, it takes values between 0 and 1.

### 2.6.4 Settings Parameters

#### Simulation Speed

The simulation speed parameter allows users to control the speed of the simulation.

## 2.7 Data Generation

The interactive epidemic simulation tool offers a convenient way to save the data generated during each simulation. Users can simply click a button in the user interface (GUI) to save the data in a CSV file format (Figure 8). This allows for easy analysis and exploration of the data using popular tools and software. By providing this option, the simulation tool enhances its usability and provides valuable insights into epidemic dynamics and effective intervention strategies.

| | Mode | Population | Infection Radius | Recovery Time | Symptoms Probability % | Theoritical Infection Probability % | Practical Infection Probability % | Quarantine After | Quarantine | Vaccination Effictiviness % | Vaccination | Day | Susceptible | Infected | Removed | Vaccinated | R0 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 0 | Normal | 1000 | 10 | 10 | 100 | 7 | 6.493506 | 5 | False | 90.0 | False | 0 | 985 | 15 | 0 | 0 | 0.000000 |
| 1 | Normal | 1000 | 10 | 10 | 100 | 7 | 7.009346 | 5 | False | 90.0 | False | 1 | 975 | 25 | 0 | 0 | 0.000000 |
| 2 | Normal | 1000 | 10 | 10 | 100 | 7 | 8.633094 | 5 | False | 90.0 | False | 2 | 954 | 46 | 0 | 0 | 3.066667 |
| 3 | Normal | 1000 | 10 | 10 | 100 | 7 | 8.635795 | 5 | False | 90.0 | False | 3 | 921 | 79 | 0 | 0 | 3.160000 |
| 4 | Normal | 1000 | 10 | 10 | 100 | 7 | 7.670455 | 5 | False | 90.0 | False | 4 | 882 | 118 | 0 | 0 | 2.565217 |

*Figure 8 - Example of data generated by a simulation*

## 2.8 Graphical User Interface (GUI)

A practical Graphical User Interface (GUI) was designed specifically for the Interactive Epidemic Simulation Tool. This Graphical User Interface assumes a fundamental role as a conduit between end-users and the simulation tool, serving to facilitate a user-friendly and coherent interaction with the underlying simulation model. Figure 9 demonstrates the GUI.

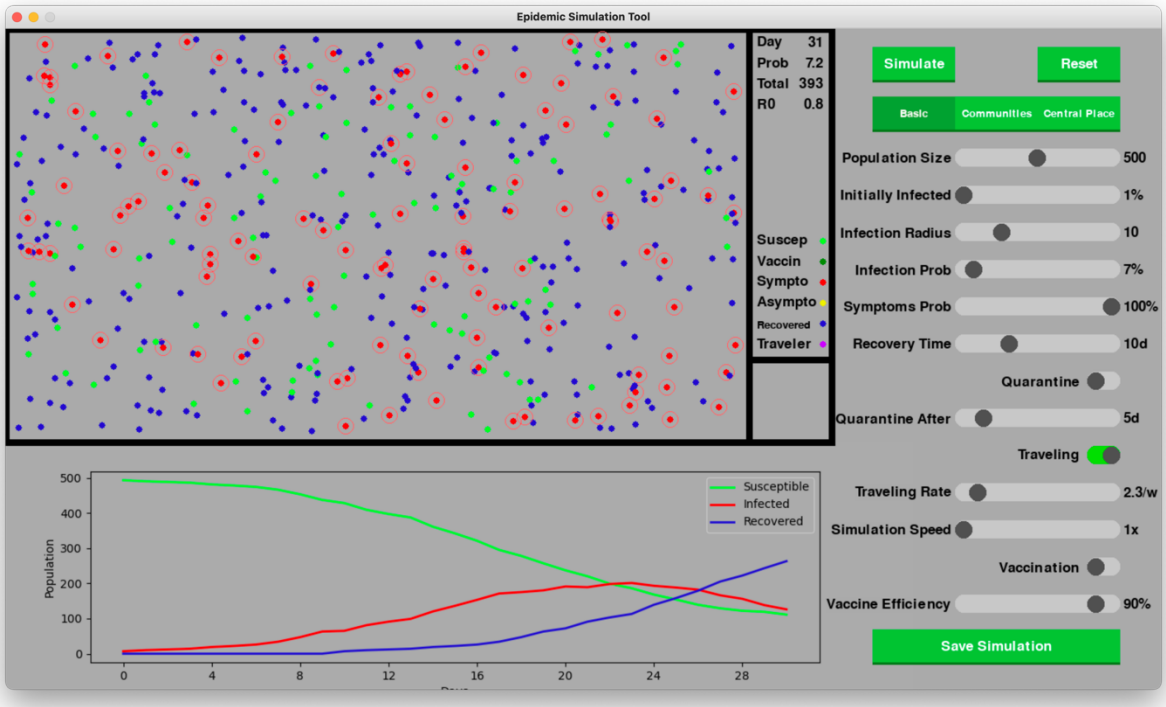


*Figure 9 - Interactive Epidemic Simulation Tool Graphical User Interface*

## 2.9 Epidemic Simulation Framework Flowcharts

In order to visually depict the simulation and its various processes, a series of flowcharts have been developed to outline the key steps and components of the simulation. Figure 10 specifically demonstrates the main program flow of the simulation. This flowchart serves as a visual representation of the sequence of processes that take place within the simulation's main program.

The presented flowchart depicted in Figure 10 illustrates the program's setup and main loop. It commences with the initialization of the graphical user interface (GUI) and establishment of default values for simulation parameters. Upon loading the GUI, the simulation enters a paused state. User interaction with the tool involves modifying parameters and starting the simulation. During the simulation's execution, an initial step

involves updating the velocity of each individual that leads to randomized curved paths. Subsequently, a population-wide iteration is performed to process each person individually. Following the population processing phase, various statistics are computed, such as the total number of infected individuals and the current day… Furthermore, additional functionalities are incorporated based on specific scenarios and parameters, such as community-based travel or increased population density for a central location. Moreover, the implementation of a vaccine campaign may be included. Finally, the physics engine calculates the new positions of each individual, with a frame rate limit set at 30 frames per second to ensure smooth animation. The main loop is then repeated to generate the next frame.

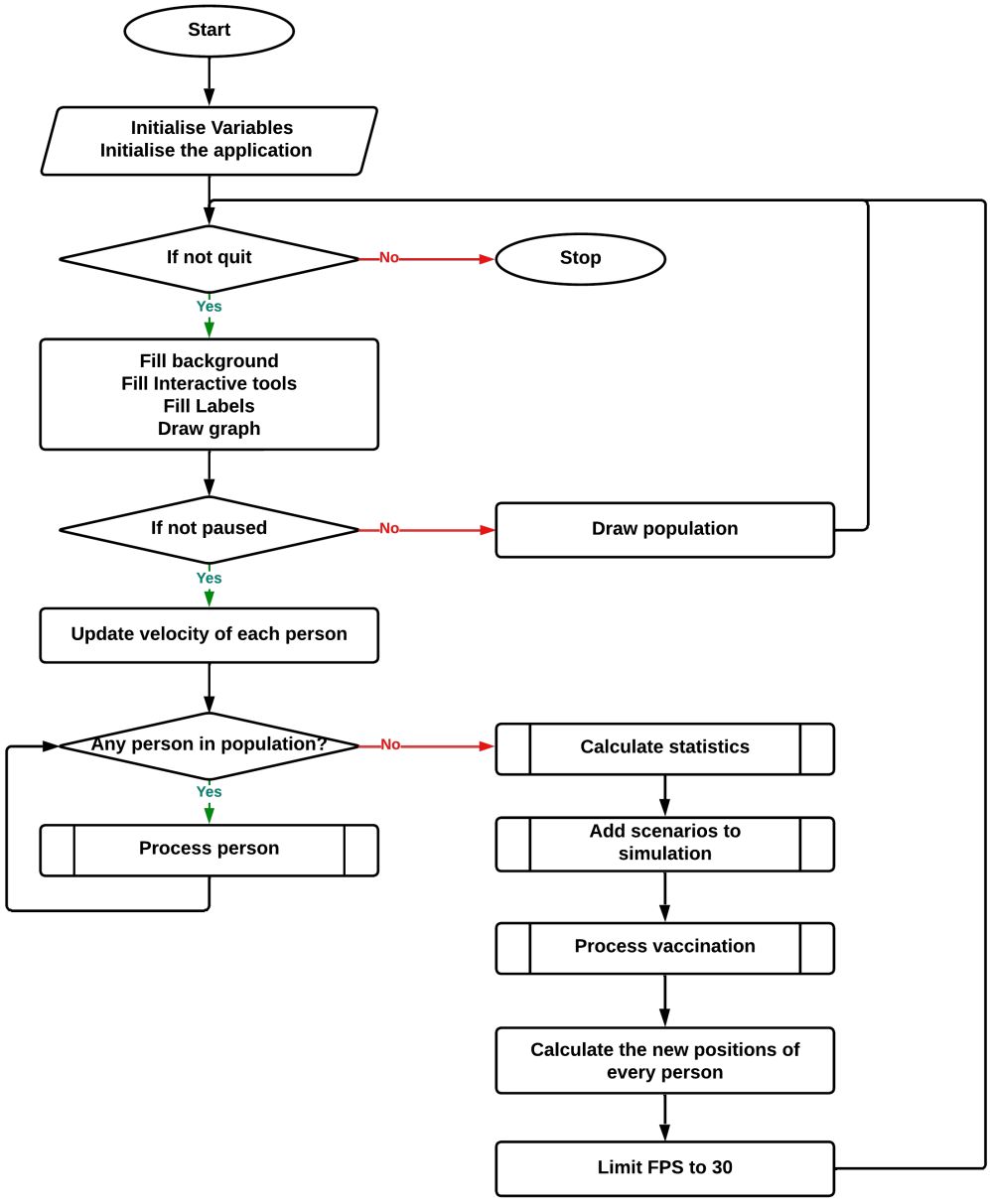


*Figure 10 - Flowchart of Main Program*

The flowchart depicted in Figure 11, illustrates the subroutine known as 'Process Person'. This subroutine is designed to operate on each individual in a given population, and execute appropriate actions based on the individual's current state (Susceptible, Infectious, Recovered and Vaccinated).

If the person is infectious, a counter for the number of infectious individuals and the duration of infection is incremented. If quarantine is enabled and the duration of infection passes the threshold of illness duration before getting detected and quarantined, the individual is moved to quarantine. Finally, the person is drawn as a red or yellow circle whether its state is symptomatic or asymptomatic respectively.

For the three other states namely: susceptible, recovered and vaccinated; Each individual is drawn as a light green, blue or dark green circle respectively.

Every susceptible person in the simulation has a counter for the number of times it has interacted with an infectious individual. The values of each counter are summed in the aim to be used later for calculating the practical probability of infection.

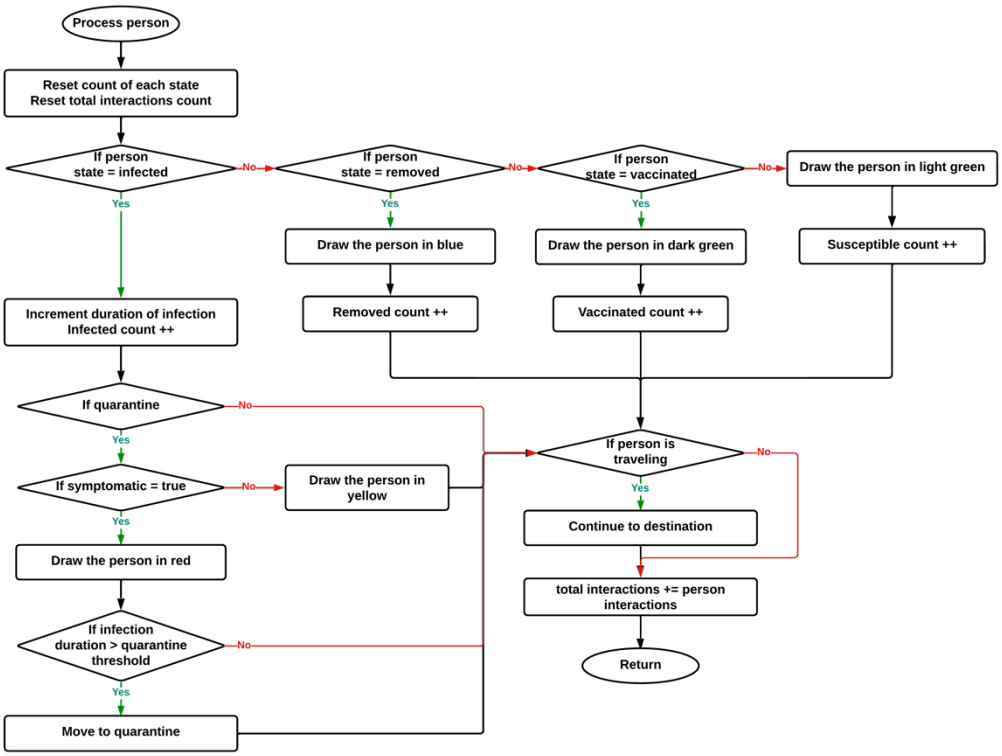


*Figure 11 - Process Person Flowchart*

The flowchart in Figure 12 titled 'Calculate Statistics' is designed to compute and store various statistics related to the simulation. These statistics include the total number of susceptible, infectious or recovered individuals, the practical probability of infection, and

the basic reproduction number (R0) value. The calculations are made every day to avoid unnecessary operations that will cause the system to be slow. This subroutine processes data generated during the simulation to compute these values to help analyze the results.

In the initial step, the precise number of individuals who are infectious is determined for each time frame in order to provide accurate data and ensure real-time updates. Subsequently, the remaining calculations are conducted on a daily basis within the simulation, commencing with the recording of the total number of cases using the formula in Equation 9. After that, the practical probability of infection is computed according to the formula denoted as Equation 10. Following this, the value of $R_0$ is determined in accordance with Equation 1. It is important to note that precautions are taken to prevent division by zero in the last two calculations. Finally, the day counter is incremented, and all the accumulated data is appended to an array. In the event that the count of infected individuals reaches zero, the simulation is paused automatically indicating the eradication of the disease.

$$total\ cases = infectious\ count + recovered\ count \tag{9}$$

$$practical\ probability\ of\ infection = \frac{total\ cases}{total\ interactions} \tag{10}$$

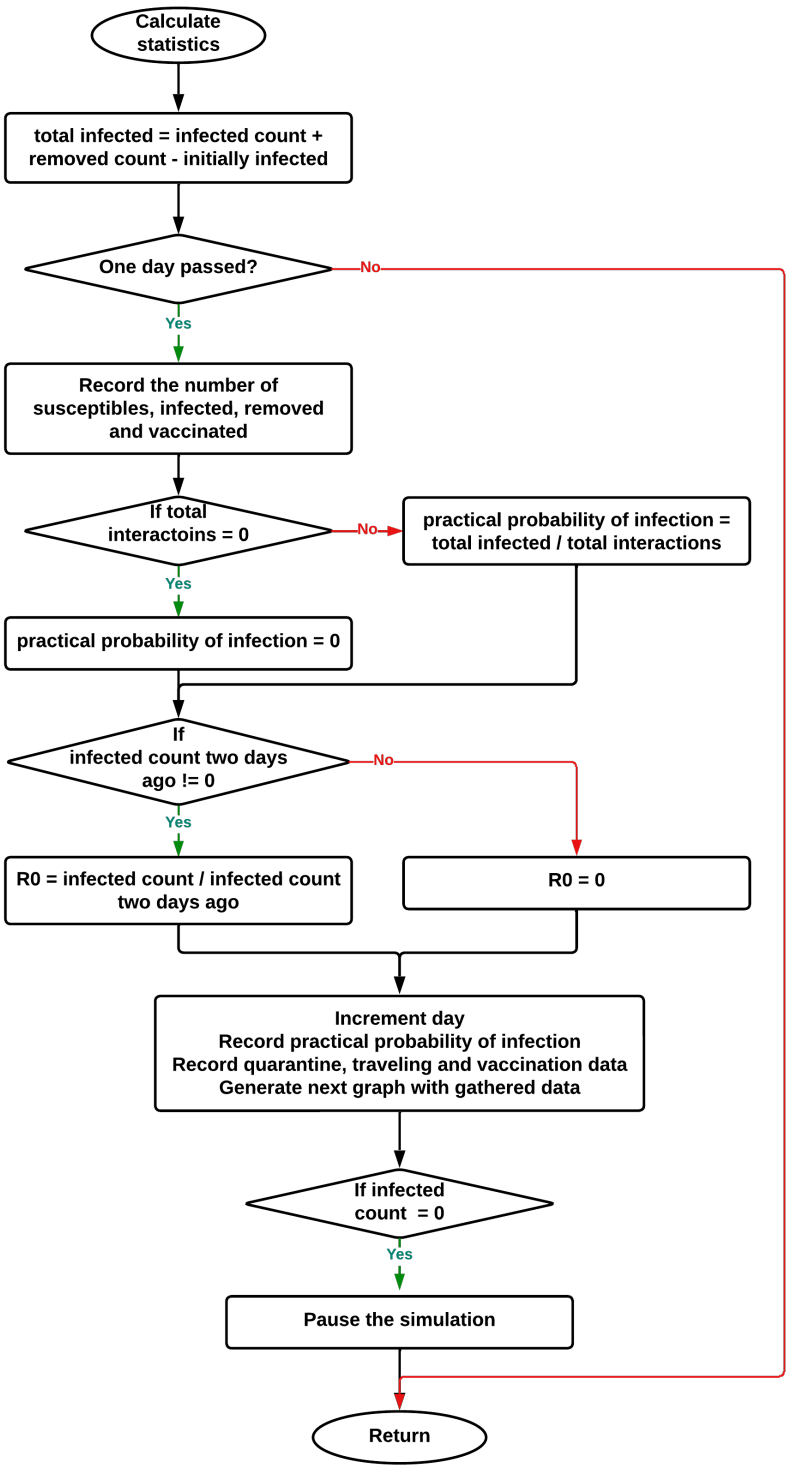


*Figure 12 - Calculate Statistics Flowchart*

The 'Add Scenarios to Simulation' flowchart is designed to implement different actions based on the scenario being simulated, specifically the Community or Central Place scenarios. The flowchart in Figure 13 describes the steps involved in adding scenarios to the simulation and incorporating the appropriate actions.

For the community scenario, if traveling between communities is enabled, a random person is picked every specific duration defined by the frequency of traveling and moved to a different community.

For the central place scenario, the same thing is applied with the destination being the center of the simulation space in order to have a higher population density mimicking markets and other crowded spaces.

As the selection of individuals is determined randomly, a constraint is established to prevent the code from interrupting the displacement of individuals who are already in the process of traveling.

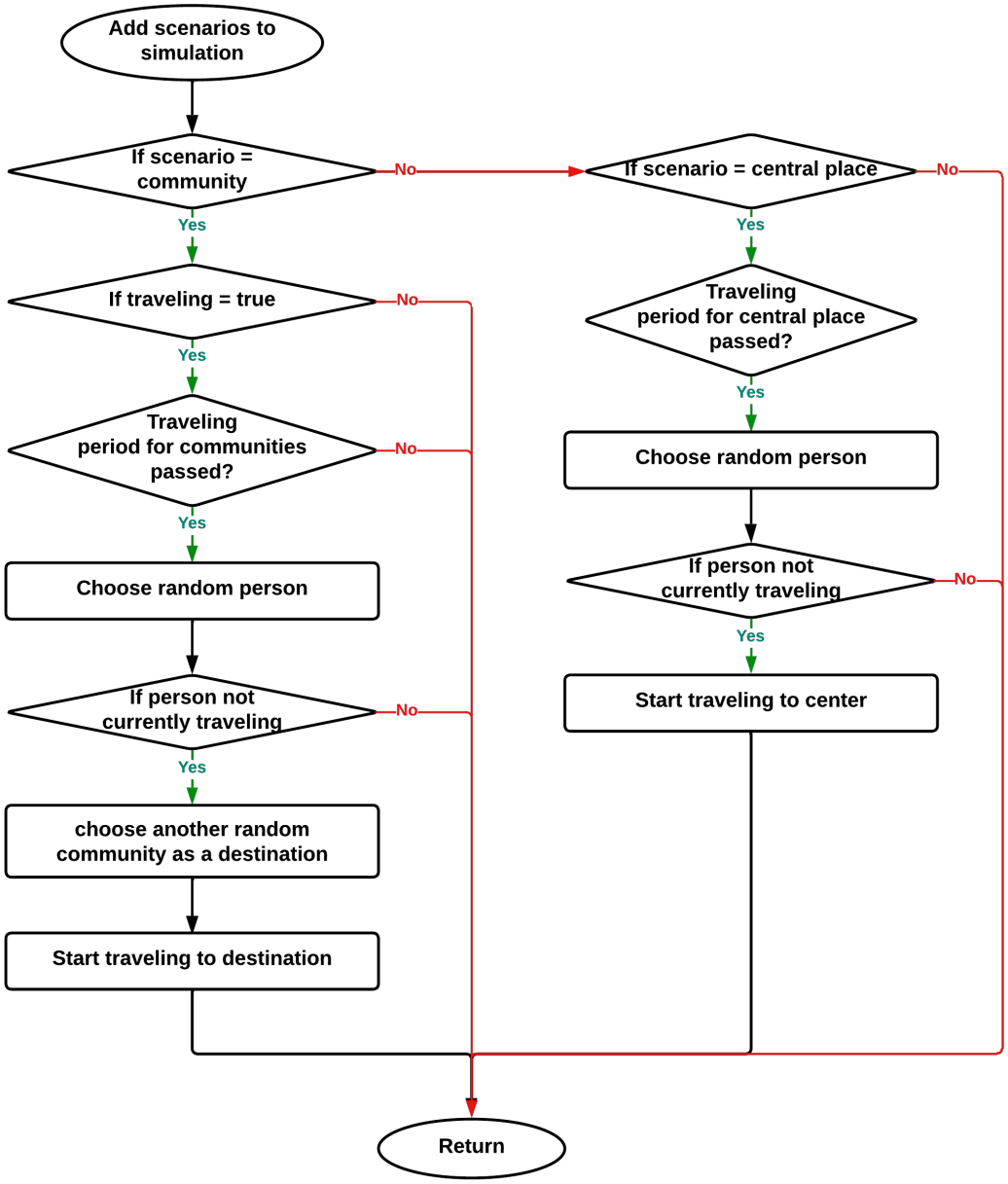


*Figure 13 - Add Scenarios to Simulation Flowchart*

The last flowchart demonstrated in Figure 14 is responsible for processing the vaccination. By vaccinating a random susceptible person at every frame, the new probability of infection will be reduced according to formula in Equation (8).

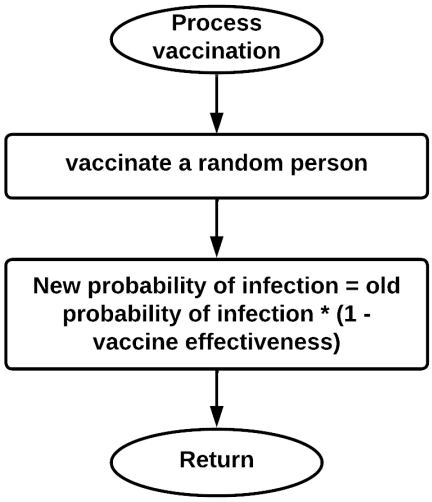


*Figure 14 - Process Vaccination Flowchart*

## 2.10 Conclusion

In summary, this chapter presents a methodology for designing and implementing an interactive epidemic simulation framework. The tool, developed using Python with Pymunk and Pygame libraries, includes three scenarios to explore different population structures and virus transmission. It utilizes collision detection to calculate distances between individuals and offers adjustable parameters that affect the outcomes of the simulation through a GUI. The tool enables data storing and visualization, facilitating the study of epidemic dynamics and intervention strategies. This methodology provides a comprehensive framework for developing an interactive tool to understand and control infectious disease outbreaks. Which leads to the next chapter where the impact of each parameter is demonstrated and discussed. Furthermore, the framework is validated by simulating the early stages of Covid-19 in Algeria.

# Chapter 3
# Results, Analysis & Discussions

# Chapter 3: Results, Analysis & Discussions

## 3.1 Overview

This chapter provides an in-depth evaluation of the epidemic simulation framework and its effectiveness in modeling the spread of infectious diseases under different scenarios and parameter values. To demonstrate the impact of every parameter, two simulations are implemented with the same setup and different values for the parameter at focus. The generated data is then visualized, analyzed and discussed accordingly. The Real-World Application section validates the epidemic simulation framework by interpreting the results of a simulation compared to the early stages of Covid-19 in Algeria and discussing their implications for public health policy and future research. The chapter concludes by summarizing the main findings and discussing the usefulness of the simulation tool for modeling the spread of infectious diseases.

## 3.2 Results and Analysis

### 3.2.1 Population Parameters

#### Population Size

When comparing the outcomes of epidemic simulations with varying population sizes, it is crucial to take into account the influence of population density on disease transmission. A higher population size typically indicates a denser community with more interactions between people, which can lead to increased disease transmission. This can be verified by the results of simulations 1 and 2 with the corresponding parameters in Table 1.

*Table 1 - Parameters for Simulations with Different Population Size*

| | Simulation 1 | Simulation 2 |
|---|---|---|
| Population Size | 300 | 1000 |
| Infection Radius | 10 pixels | 10 pixels |
| Initially Infectious | 1% | 1% |
| Infection Duration | 10 days | 10 days |
| Infection Probability | 7% | 7% |

Figure 15 show the results of Simulations 1 and 2 respectively:

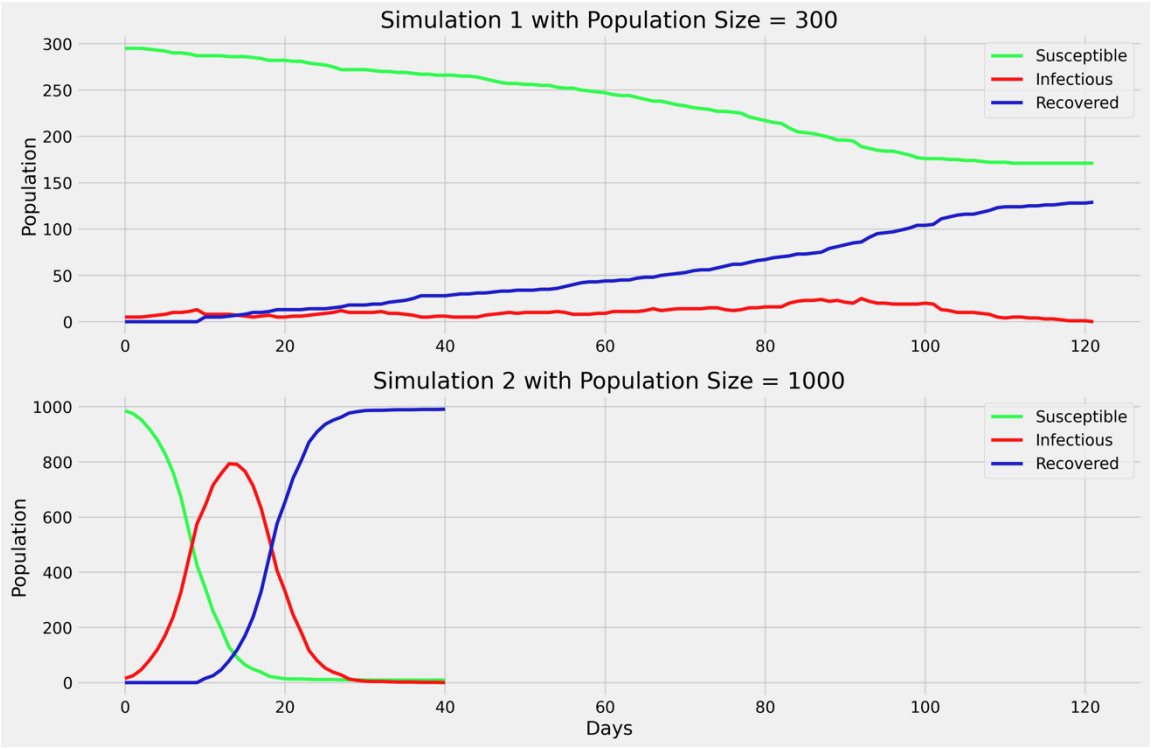


*Figure 15 - Data Visualization for Simulations with Different Population Size*

The results of the two epidemic simulations indicate that population size has a significant impact on disease transmission. In simulation 1, with a population size of 300, the spread of the disease is flat and stable (Figure 15), and the total number of infections is low. The disease is eradicated within 120 days, with a total of 177 infections. This suggests that a smaller population size may limit the spread of the disease, as there are fewer opportunities for infectious individuals to come into contact with non-infectious individuals.

In contrast, simulation 2, with a population size of 1000, shows a steep increase in infections (Figure 15), with 80% of the population being infectious simultaneously by day 15. Additionally, 99% of the population is infected during the 40 days of the simulation. These results demonstrate that a larger population size can significantly increase the spread of the disease. The increased population density and interactions between individuals may facilitate the rapid spread of the disease and make it more difficult to control.

### 3.2.2 Infection Parameters

#### Infection Radius

The objective is to investigate the effect of the Infection Radius on the propagation of the disease by conducting two simulations with varying Infection Radius values. Specifically,

the second simulation will utilize triple the Infection Radius which will represent a more socially engaged society with more total interactions between people. The infection radius could also be attributed to the disease characteristics and whether it could be spread by air or by direct contact like touching. The simulation parameters are outlined in Table 2.

*Table 2 - Parameters for Simulations with Different Infection Radius*

| | Simulation 3 | Simulation 4 |
|---|---|---|
| Population Size | 200 | 200 |
| Infection Radius | 8 pixels | 24 pixels |
| Initially Infectious | 1% | 1% |
| Infection Duration | 10 days | 10 days |
| Infection Probability | 14% | 14% |

The simulations yielded the results demonstrated in Figure 16:

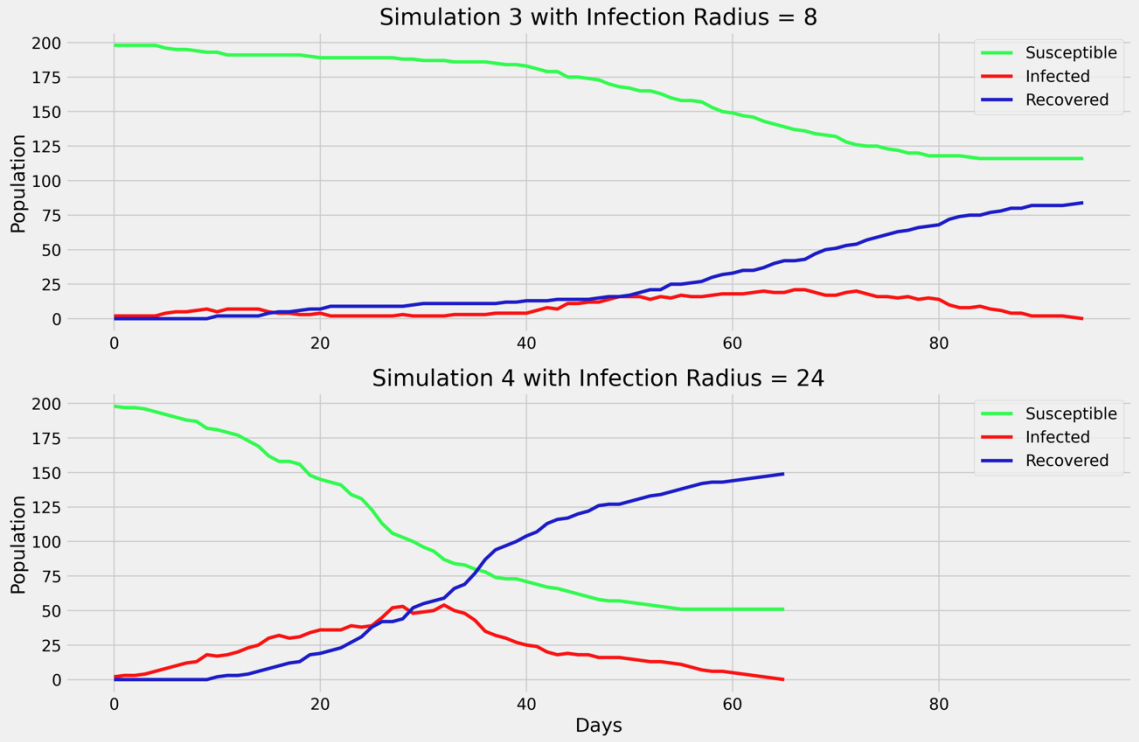


*Figure 16 - Data Visualization for Simulations with Different Infection Radius*

In the first simulation, with an infection radius of 8 pixels, the disease transmission progresses steadily and peaks at 24 simultaneous infections by day 67. This indicates that the disease spreads over a relatively short distance and may be more easily controlled through interventions that limit contact between infectious and non-infectious individuals.

In contrast, in the second simulation, with an infection radius of 24 pixels, the disease spreads at a faster rate, with 25% of the population experiencing simultaneous infections

by day 29. This suggests that the disease can spread over longer distances and may be more difficult to control through traditional interventions.

Interestingly, the differences in infection radius and the rate of disease transmission, both simulations ultimately result in a different number of infections. Simulation 3 experienced just over 75 cases. However, Simulation 4 with the infection radius of 24 noticed a relatively higher number of cases with a total of 150. It is also noteworthy to highlight that the time frame for infection is slightly different, with the first simulation taking 93 days and the second simulation taking 65 days.

### Infection Duration

The duration of infection can be attributed to two potential factors. On one hand, the infection may be classified as acute, which means that the virus typically causes symptoms that develop quickly and last for a relatively short period of time. On the other hand, early intervention and treatment may enable individuals to recover from the infection promptly, leading to a reduced duration of illness. In order to visualize the impact of infection duration, we conducted two simulations with the parameters outlined in Table 3.

*Table 3 - Parameters for Simulations with Different Infection Duration*

| | Simulation 5 | Simulation 6 |
|---|---|---|
| Population Size | 500 | 500 |
| Infection Radius | 10 pixels | 10 pixels |
| Initially Infectious | 1% | 1% |
| Infection Duration | 5 days | 15 days |
| Infection Probability | 7% | 7% |

The data generated is as follows in Figure 17:

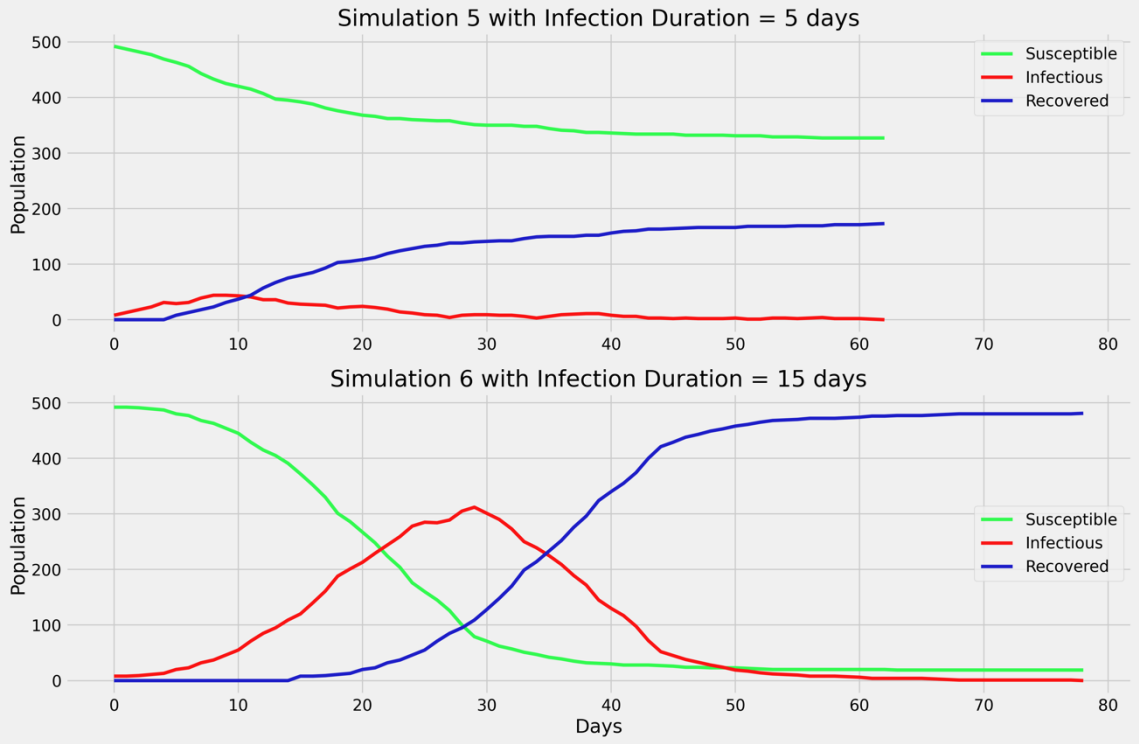


*Figure 17 - Data Visualization for Simulations with Different Infection Duration*

Figure 17 consists of two line-plots that investigate the impact of Infection Duration on disease transmission. The first plot, located on the top, presents the results of a simulation with an infection duration of 5 days. The plot displays a steady and limited transmission rate due to the short duration of illness, leading to the transfer of individuals from the infectious category to the recovered one. This shift reduces the likelihood of further interactions that could result in infection, and ultimately, less than 200 infections were recorded in the 63-day simulation period.

In contrast, the second plot in Figure 17 presents the results of a simulation with an infection duration of 15 days. The plot indicates a rapid increase in infection cases, with a peak of 300 simultaneous infections recorded by day 30. The epidemic persists for a more extended period, approximately 80 days, and reaches a staggering 97% of the population.

The presented results illustrate the significant impact of infection duration on disease transmission rates. A more extended infection duration leads to a higher transmission rate, resulting in a more extensive spread of the disease. These findings emphasize the need for timely intervention measures to reduce the duration of the infection and, consequently, the transmission rate. Such measures include early diagnosis, prompt treatment, and preventive strategies such as quarantine.

### Infection Probability

In order to evaluate the impact of the primary parameter in the simulation, namely 'Infection Probability,' two simulations were conducted with distinct sets of parameters. Lowering the probability of infection may be attributed to a multitude of factors, such as adherence to improved hygiene practices, enhanced respiratory etiquette as better cough protection, and decreased frequency of facial contact. The parameters utilized in the simulations are outlined in Table 4.

*Table 4 - Parameters for Simulations with Different Infection Probability*

| | Simulation 7 | Simulation 8 |
|---|---|---|
| Population Size | 500 | 500 |
| Infection Radius | 10 pixels | 10 pixels |
| Initially Infectious | 1% | 1% |
| Infection Duration | 10 days | 10 days |
| Infection Probability | 5% | 10% |

Figure 18 displays the results for simulations 7 and 8 respectively:

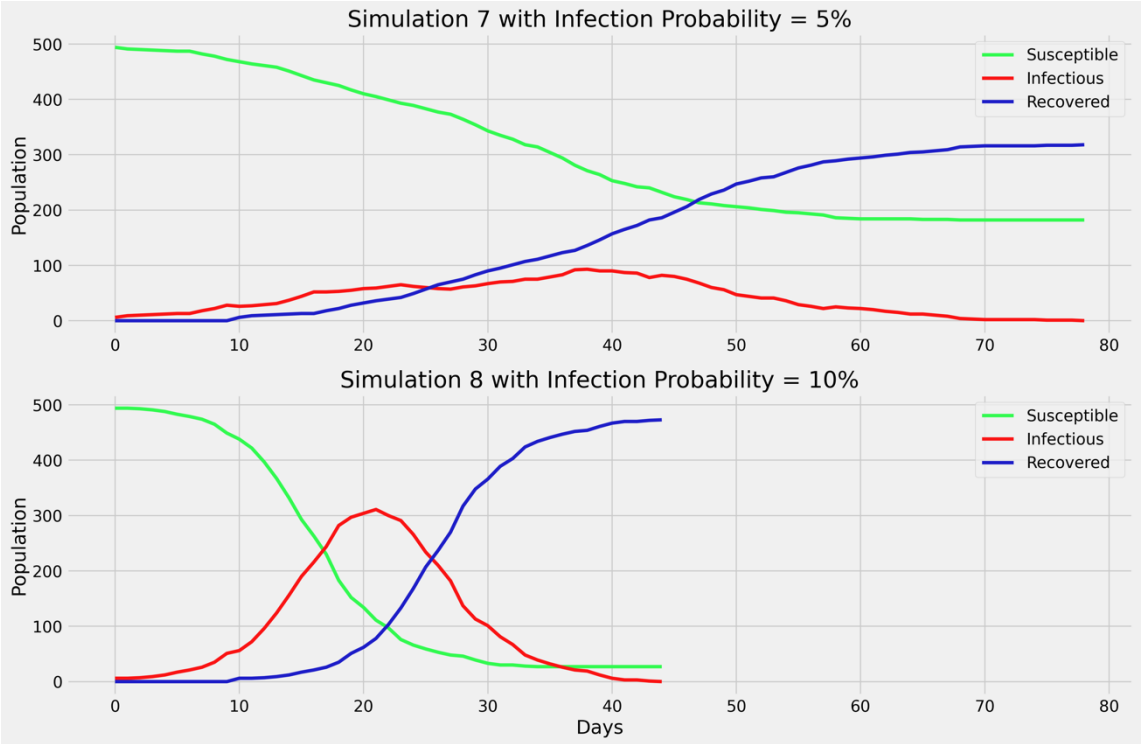


*Figure 18 - Data Visualization for Simulations with Different Infection Probability*

The presented graphs in Figure 18 illustrate the influence of Infection Probability on disease transmission. The first graph, representing a simulation with an infection probability of 5%, displays a slow increase in the number of simultaneous infections over

the initial 40 days. The disease reaches a maximum of nearly 100 simultaneous infections before gradually declining and eventually eradicating in 80 days, resulting in approximately 60% of the population being infectious. Conversely, the second graph shows a simulation with an infection probability of 10%, demonstrating a significantly higher transmission rate, with almost 95% of the population being infectious in less than 45 days. The disease spread at an accelerated rate, with 300 simultaneous infections recorded on day 20.

The presentation of R0, or the basic reproduction number, is a valuable opportunity to expound upon the relationship between this parameter and the transmission rate of infectious diseases. Figure 19 provides a graphical representation of R0 as a function of time, enabling a more comprehensive understanding of how this value influences the spread of diseases.

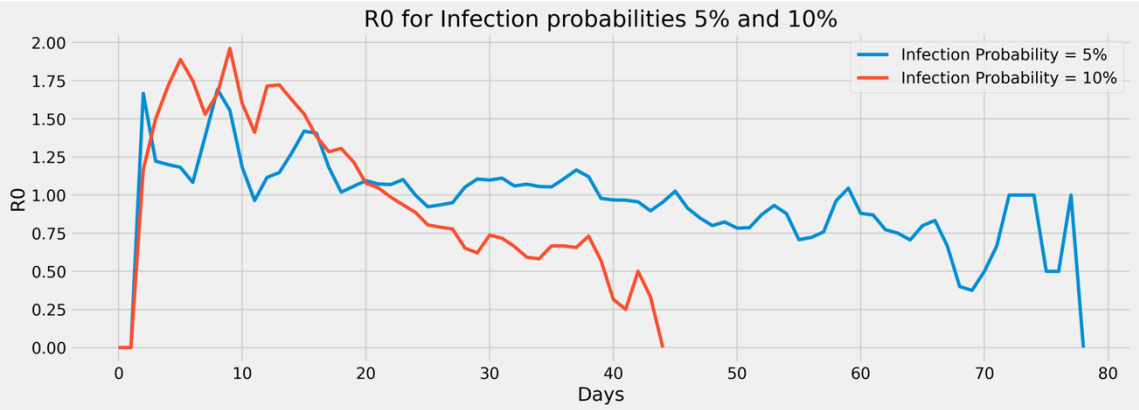


*Figure 19 - R0 for simulations with Different Infection Probability*

The basic reproduction number ($R_0$) serves as a fundamental parameter in assessing the potential for the transmission of infectious diseases. Specifically, $R_0$ is defined as the expected number of individuals who will become infectious by a single infectious individual, within a population where all individuals are susceptible to the disease. Notably, an $R_0$ value greater than 1 suggests that the disease has a high potential for rapid spread throughout a population; this is demonstrated in Figure 19 when $R_0$ value was greater than 1.5 when the virus transmission rate was growing exponentially in simulation 8. While an $R_0$ value of 1 indicates that the number of cases will remain constant. Conversely, an R0 value below 1 suggests that the disease is in the eradication phase. Thus, a clear understanding of this parameter is paramount in developing effective strategies for mitigating disease transmission.

The results of these simulations highlight the critical role of infection probability in disease transmission. Increased infection probability leads to a faster and more extensive spread of the disease, resulting in a higher number of infectious individuals within a shorter duration. Consequently, it underscores the need for public health interventions aimed at reducing infection probability, such as social distancing measures and the use of personal protective equipment.

### 3.2.3 Control Measures Parameters

#### Quarantine

Quarantine, a widely recognized and essential method of intervention in infectious disease control, involves the isolation and restriction of movement for individuals who have been exposed to an infectious disease. Its importance lies in its ability to disrupt the transmission chain by separating potentially infectious individuals from the general population. By effectively limiting contact during the disease's incubation period, quarantine mitigates the risk of further spread within the community. Furthermore, it allows for early identification, close monitoring, and timely intervention for potentially infectious individuals, ensuring prompt medical care and reducing strain on healthcare systems. Notably, quarantine also serves to safeguard vulnerable populations, such as the elderly or immunocompromised, who are at heightened risk of severe illness. Additionally, its implementation communicates the gravity of the situation, instilling public awareness and fostering a sense of collective responsibility in adhering to preventive measures.

To assess the impact of quarantine, we conducted two simulations building upon the scenario presented in Figure 15, specifically Simulation 2. In the following simulations, we implemented a quarantine measure once the number of infections reached a predetermined threshold of 100. By introducing quarantine at this point, we aimed at observing its effect on the subsequent progression of the epidemic. The parameters for simulations 9 and 10 are shown in Table 5.

*Table 5 - Parameters for Simulations with Different Quarantine Policies*

| | Simulation 9 | Simulation 10 |
|---|---|---|
| Population Size | 1000 | 1000 |
| Infection Radius | 10 pixels | 10 pixels |
| Initially Infectious | 1% | 1% |
| Infection Duration | 10 days | 10 days |
| Infection Probability | 7% | 7% |
| Quarantine After | 5 days | 3 days |

The results of the simulations are demonstrated in Figure 20:

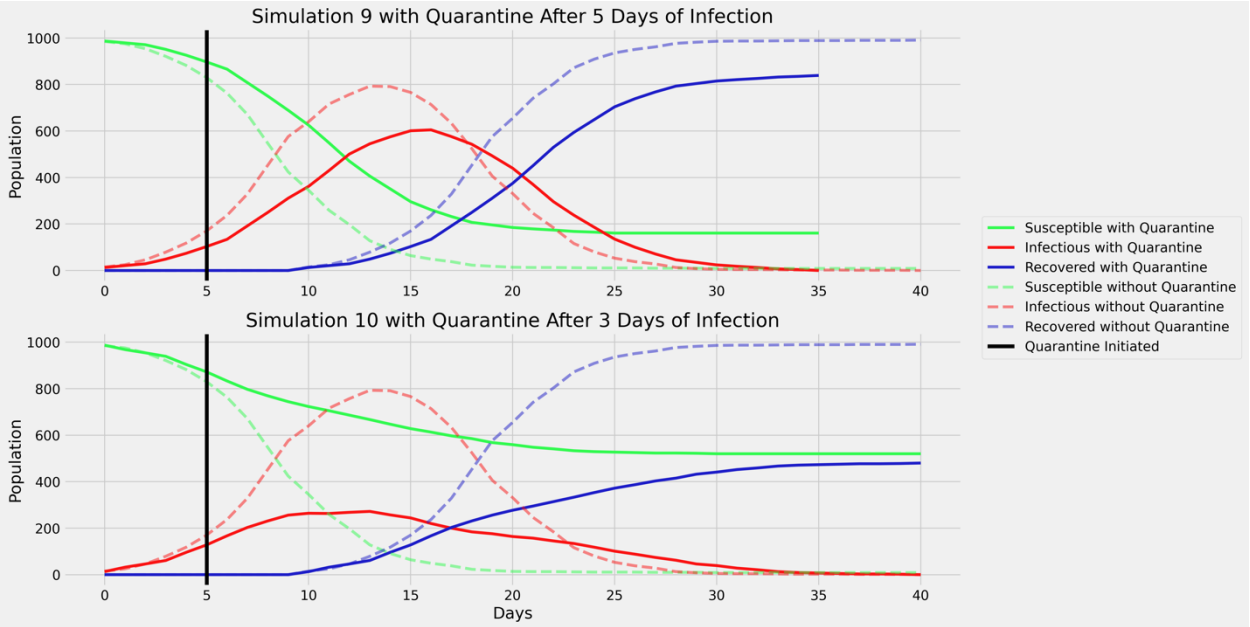


*Figure 20 - Data Visualization for Simulations with Different Quarantine Policies*

Figure 20 illustrates the impact of Quarantine and timely intervention on disease spread within a population. Simulation 9 shows that quarantining infectious individuals after 5 days of illness results in a slightly improved situation compared to Simulation 2 (without quarantine), with slower disease progression and 25% fewer maximum simultaneous infections. However, the overall reduction in total infections is only 20%. In Simulation 10, where individuals are quarantined after 3 days of illness, there is a significant decrease of 70% in the number of simultaneous cases, and only half of the population becomes infectious before the disease is eradicated by day 40. These findings emphasize the crucial role of early detection, swift response, and effective implementation of quarantine measures in mitigating the spread of infectious diseases. Swift and efficient intervention measures are vital to protect public health and limit the impact of outbreaks.

### Symptoms Probability

To account for the complexities of real-world disease dynamics, where individuals can carry infections without displaying symptoms, we incorporated the parameter of Symptoms Probability into our simulations. To further investigate the influence of varying asymptomatic rates on disease transmission, we conducted Simulation 11 and Simulation 12, both based on the framework of Simulation 10. In Simulation 11, we assumed a symptomatic rate of 80%, implying that 80% of infectious individuals would remain symptomatic. Conversely, Simulation 12 featured a reduced symptomatic rate of 40%, indicating a higher proportion of asymptomatic cases. By analyzing the results of these simulations, we aimed to gain insights into how the presence or absence of symptoms affects the spread and severity of the disease. This investigation underscores the significance of considering symptoms probabilities in epidemic modeling and informing effective intervention strategies.

*Table 6 - Parameters for Simulations with Different Symptoms Probability*

| | Simulation 11 | Simulation 12 |
|---|---|---|
| Population Size | 1000 | 1000 |
| Infection Radius | 10 pixels | 10 pixels |
| Initially Infectious | 1% | 1% |
| Infection Duration | 10 days | 10 days |
| Infection Probability | 7% | 7% |
| Quarantine After | 3 days | 3 days |
| Symptoms Probability | 80% | 40% |

Figure 21 visualizes the results for simulations 11 and 12 respectively

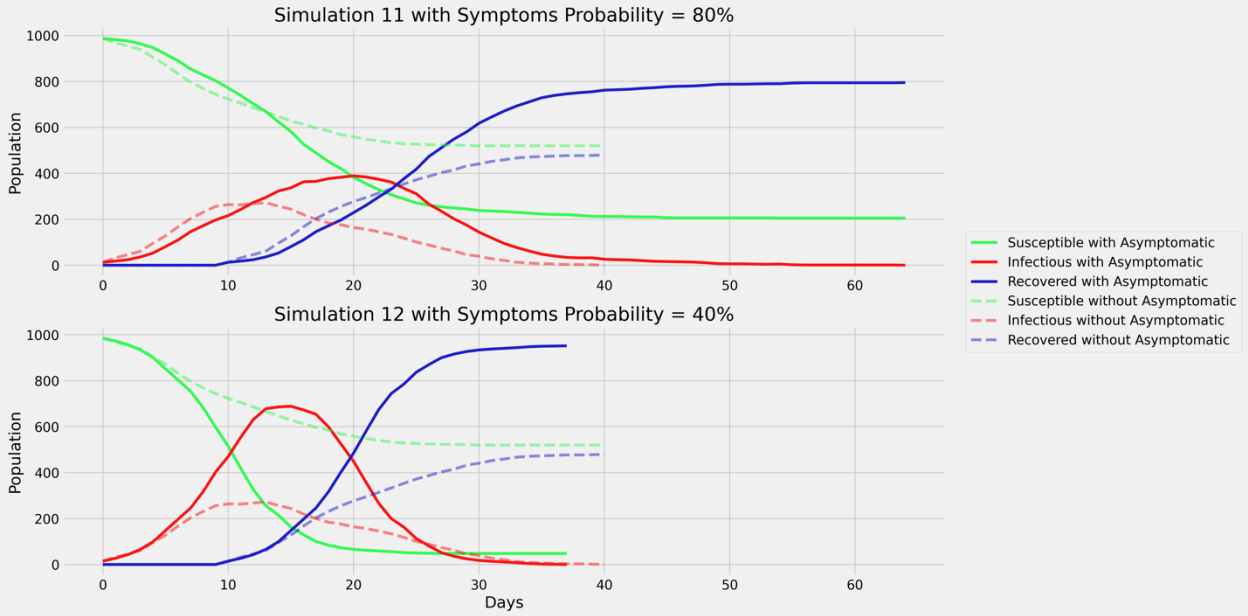


*Figure 21 - Data Visualization for Simulations with Different Symptoms Probability*

Simulation 11 represents an intermediate scenario between quarantining the entire infectious population and taking no action at all, resulting in 400 simultaneous infections by day 20. Approximately 80% of the population is infected within the 63 days of the simulation. This outcome suggests that implementing quarantine measures for a population with a few missed cases has a partial but limited impact on reducing the number of simultaneous infections. In contrast, Simulation 12 closely resembles a scenario where quarantine fails to be effective, with over 95% of the population becoming infectious in less than 40 days. This failure is primarily attributed to a significant proportion (60%) of asymptomatic individuals who continue to spread the disease, evading detection and undermining quarantine efforts. These results underscore the crucial role of symptomatic presentation and successful implementation of quarantine measures in controlling disease transmission. Comprehensive strategies incorporating early detection, timely isolation, and awareness of asymptomatic cases are essential for effective containment of infectious diseases.

These results underscore the crucial role of public awareness and collective collaboration in effectively implementing quarantine measures. The success of quarantine relies heavily on individuals' understanding of the need to isolate themselves when experiencing symptoms. Public education campaigns, clear communication of guidelines, and fostering a sense of responsibility among the population play a pivotal role in ensuring widespread compliance with quarantine protocols. By cultivating a culture of awareness and active participation, communities can enhance the effectiveness of quarantine measures, leading

to a more successful containment of infectious diseases. These findings highlight the significance of asymptomatic cases and emphasize the essential role of individual behavior and societal cooperation in mitigating disease transmission through effective quarantine practices.

### Traveling

In the context of the community's scenario, the traveling parameter plays a significant role in shaping the dynamics of disease spread. To illuminate the influence of traveling rate on the transmission of the disease, we conducted a series of simulations specifically tailored to this scenario. These simulations, denoted as Simulation 13 and Simulation 14, were designed to explore the effect of varying traveling rates on the epidemic's progression. Simulation 13 focused on a higher traveling rate, reflecting a scenario where individuals frequently move between communities. Conversely, Simulation 14 examined a lower traveling rate, representing a scenario where mobility between communities is limited. By comparing the outcomes of these simulations, we aimed to discern the impact of traveling rate on the spread of the disease and assess its role in facilitating or inhibiting transmission between different communities.

Table 7 summarizes the corresponding parameters of the two simulations.

*Table 7 - Parameters for Simulations with Different Traveling Rate*

| | Simulation 13 | Simulation 14 |
|---|---|---|
| Population Size | 500 | 500 |
| Infection Radius | 16 pixels | 16 pixels |
| Initially Infectious | 1% | 1% |
| Infection Duration | 10 days | 10 days |
| Infection Probability | 7% | 7% |
| Traveling Rate | 14 per week | 4 per week |

The data generated in the two simulations are visualized in Figure 22.

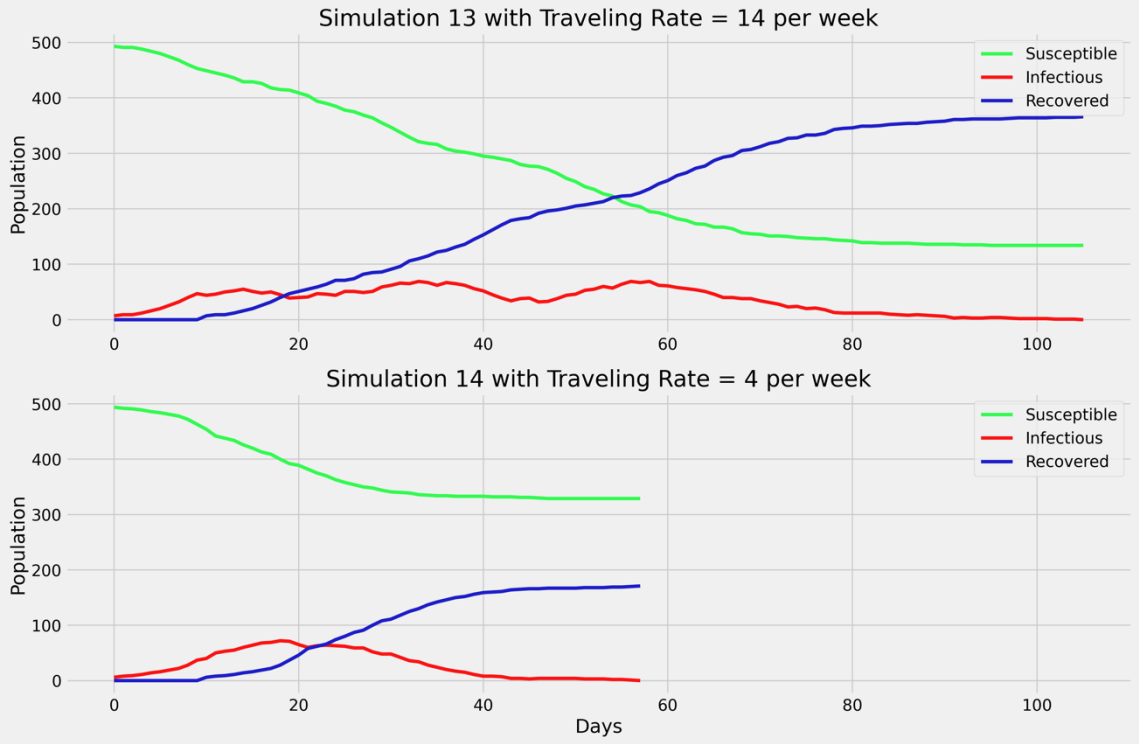


*Figure 22 - Data Visualization for Simulations with Different Traveling Rate*

The analysis of Simulation 13 and Simulation 14 reveals contrasting outcomes regarding the spread of the disease in different communities, influenced by the traveling rate between them. In Simulation 13, the number of infections fluctuates over time, remaining below 100 cases without surpassing this threshold. This behavior can be attributed to the higher traveling rate, which facilitates the transmission of the disease between communities. Consequently, seven communities become compromised, resulting in a total of 366 infections by day 105.

In contrast, Simulation 14 presents a different pattern of disease spread. Initially, there is an increase in infections within the first two communities. However, due to the lower traveling rate between communities, the disease fails to spread beyond these initial areas. As a result, the infection is effectively contained, and the disease is eradicated by day 57 with a total of 171 infections. The distinct outcomes observed in these simulations can be explained by the role of traveling rate in disease transmission. In Simulation 13, the higher traveling rate allows for increased interaction and contact between communities, facilitating the spread of the disease across multiple areas. This results in a higher overall number of infections and the involvement of a larger number of communities in the outbreak. In Simulation 14, the lower traveling rate acts as a limiting factor for disease transmission. The reduced movement between communities restricts the spread of the

infection beyond the initial areas, ultimately leading to containment and eradication within a shorter timeframe.

These findings emphasize the significance of considering the interplay between traveling rate and disease spread in assessing the effectiveness of containment strategies. Implementing measures to regulate or restrict travel between communities can be an effective strategy to mitigate disease transmission, as observed in Simulation 14. This highlights the importance of comprehensive approaches that account for various factors, such as population movement patterns, in designing interventions and control measures to effectively manage and contain infectious diseases.

### Vaccination

In order to examine the effects of vaccination within the SIRV model, an additional category, "Vaccinated," was introduced to the classic Susceptible-Infectious-Recovered framework. Simulations 15 and 16 were based on simulation 6 to showcase the impact of vaccination on disease dynamics. Vaccination in these simulations was initiated once the number of infections surpassed a predetermined threshold of 100. Simulation 15 simulated a scenario with low vaccination efficiency, reflecting a situation where vaccine is ineffective for the different people in the population. In contrast, Simulation 16 represented a scenario with higher vaccination efficiency, aiming to evaluate the potential of vaccination in reducing disease spread and mitigating its impact. Through these simulations, we investigated the influence of vaccination on the overall trajectory of the epidemic, including its ability to reduce infections and limit the severity of the outbreak.

Table 8 demonstrates the different parameters used in the two simulations.

*Table 8 - Parameters for Simulations with Different Vaccine Efficiency*

| | Simulation 15 | Simulation 16 |
|---|---|---|
| Population Size | 500 | 500 |
| Infection Radius | 10 pixels | 10 pixels |
| Initially Infectious | 1% | 1% |
| Infection Duration | 15 days | 15 days |
| Infection Probability | 7% | 7% |
| Vaccine Efficiency | 40% | 90% |

The obtained data is visualized in Figure 23 and Figure 24

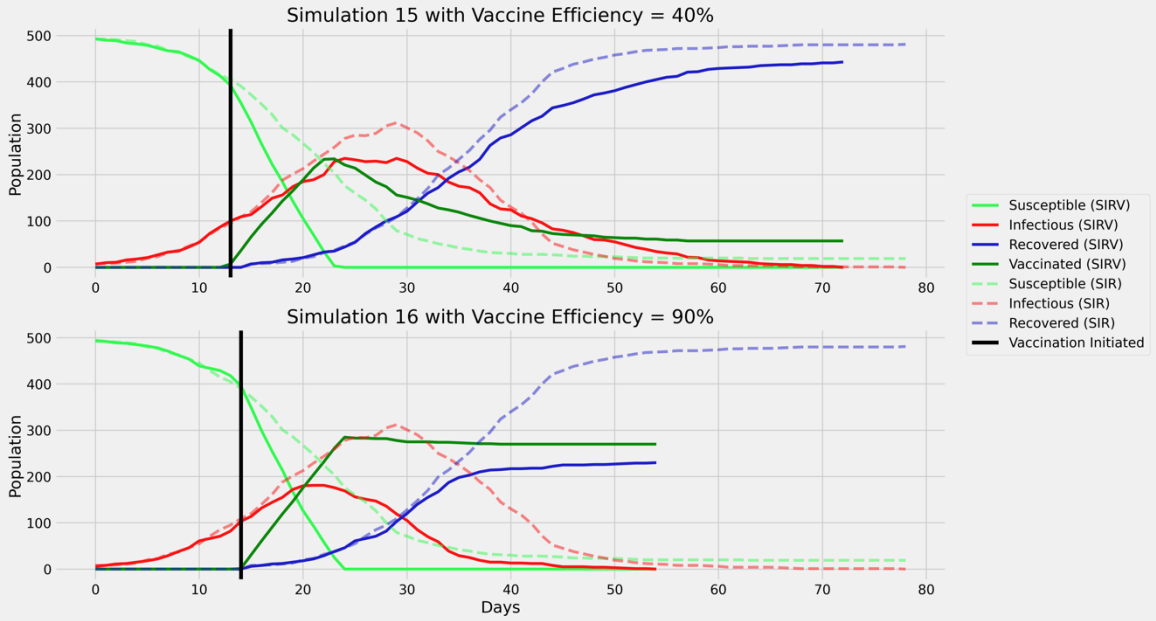


*Figure 23 - Data Visualization for Simulations with Different Vaccine Efficiency*

Simulations 15 and 16 implemented a vaccination program, commencing on days 13 and 14 respectively. In Simulation 15, all individuals who had not contracted the disease were vaccinated by day 23. However, despite this intervention, the vaccine exhibited low efficacy, resulting in 88% of the population becoming infectious over the course of the 73-day simulation period. In contrast, Simulation 16 demonstrated a significant reduction in the number of infections, with only 46% of the population contracting the disease compared to the original simulation (Simulation 6), where 96% were infected. Remarkably, the virus was eradicated in a mere 54 days. The predefined vaccine effectiveness of 90% in this simulation elucidates the critical role of vaccination as an effective intervention strategy against epidemics. These findings underscore the importance of high vaccine efficacy in achieving substantial control over disease transmission. The results also underscore the importance of rigorous vaccine testing and ensuring its effectiveness to ensure a successful intervention against infectious diseases.

One of the gathered data from running a simulation is the practical probability of infection; Figure 24 visualizes the effect of the vaccination on this metric.

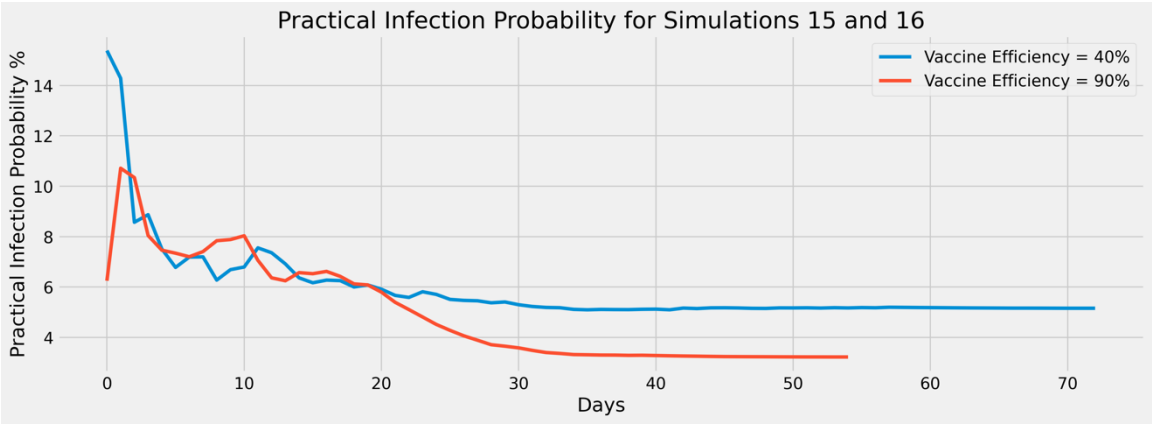


*Figure 24 - Practical Infection Probability for Simulations with Different Vaccine Efficiency*

This graph illustrates the effect of vaccination on the likelihood of individuals contracting the disease in real-world scenarios. The data clearly shows that simulation 6 with higher vaccination efficiency exhibit significantly reduced practical probabilities of infection, indicating the effectiveness of vaccination in lowering the risk of contracting the disease. Conversely, simulation 15 with lower vaccine efficiency demonstrate notably higher probabilities of infection.

### Central Place

Within the Central Place scenario, which emulates real-world dynamics by incorporating a central location with a higher population density, we conducted two simulations to examine the impact of a central place compared to a basic simulation environment. Building upon simulations 3 and 4, simulations 17 and 18 were specifically designed to explore the effects of the central place in terms of disease spread dynamics. Hypothetically, we expected that the presence of a central place would result in a more rapid and extensive transmission of the disease, given the higher population density and increased interactions within this central hub. Through the analysis of these simulations, we aimed to assess whether the central place indeed influences the spread of the disease, providing valuable insights into the role of densely populated central locations in epidemic scenarios.

*Table 9 - Parameters for Simulations in Central Place Scenario*

| | Simulation 17 | Simulation 18 |
|---|---|---|
| Population Size | 500 | 500 |
| Infection Radius | 8 pixels | 24 pixels |
| Initially Infectious | 1% | 1% |
| Infection Duration | 10 days | 10 days |
| Infection Probability | 7% | 7% |

Figure 25 visualizes the obtained results

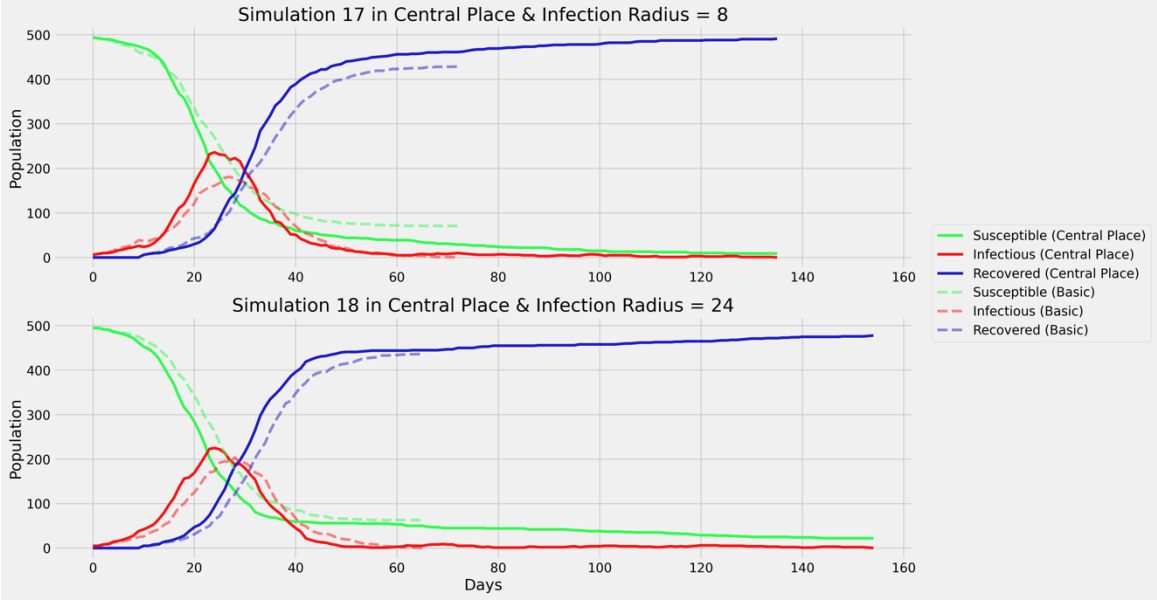


*Figure 25 - Data Visualization for Simulations in Central Place Scenario*

Figure 25 illustrates the results of Simulations 17 and 18, which reveal a higher transmission rate compared to Simulations 3 and 4, respectively. In both Simulations 17 and 18, a slightly larger number of infections is observed, with over 98% of the population being infectious. The use of a central place in these simulations implies a higher population density; Hence, more interactions that results in more infections, confirming the findings from Simulations 1 and 2. The denser population in the central place in Simulations 17 and 18 contributes to a faster transmission rate and a greater number of infections. These results provide further evidence supporting the correlation between community density and disease transmission, emphasizing the significance of accounting for crowded locations when formulating strategies to effectively manage and mitigate the propagation of infectious diseases.

## 3.3 Real-World Application

To further validate the effectiveness of our interactive epidemic simulation tool, we conducted an in-depth analysis of a dataset capturing the daily progression of the Covid-19 pandemic. By some investigation and data collection about Covid-19 and leveraging the capabilities of our developed tool, we performed a simulation that closely mirrored the observed rate of transmission, reproducing the propagation patterns of the virus and aligning them with empirical data. This empirical validation not only demonstrated the efficacy of our tool but also provided a deeper understanding of the underlying mechanisms governing the spread of Covid-19.

### Dataset Description

The COVID-19 Daily Progression dataset, sourced from the World Health Organization (WHO) [59], provides a concise and reliable overview of the daily progression of COVID-19 in 237 countries. It serves as a valuable resource for researchers, analysts, and policymakers seeking up-to-date and credible information to track the global impact of the pandemic and inform decision-making processes. The dataset is organized as shown in Table 10

*Table 10 - Description of Variables in Covid-19 Dataset*

| Field name | Type | Description |
|---|---|---|
| Date_reported | Date | Date of reporting to WHO |
| Country_code | String | ISO Alpha-2 country code |
| Country | String | Country, territory, area |
| WHO_region | String | Regional Office for Africa (AFRO), Regional Office for the Americas (AMRO), Regional Office for South-East Asia (SEARO), Regional Office for Europe (EURO), Regional Office for the Eastern Mediterranean (EMRO), Regional Office for the Western Pacific (WPRO) |
| New_cases | Integer | New confirmed cases. Calculated by subtracting previous cumulative case count from current cumulative cases count |
| Cumulative_cases | Integer | Cumulative confirmed cases reported to WHO to date |
| New_deaths | Integer | New confirmed deaths. Calculated by subtracting previous cumulative deaths from current cumulative deaths |
| Cumulative_deaths | Integer | Cumulative confirmed deaths reported to WHO to date |

### Data Preprocessing & Assumptions

In order to focus our analysis on a specific country, namely Algeria, we filtered the extensive dataset comprising Covid-19 statistics from 237 different countries. Our objective was to extract the daily progression of the pandemic within Algeria and compare it with the simulated outcomes generated by our tool. To facilitate this comparison, we required the values for three key variables: susceptible, infectious, and recovered individuals. By employing appropriate feature engineering techniques on the available "Cumulative cases" data and under the assumptions that the duration of infection for Covid-19 is 15 days [60] and the total susceptible population in Algeria during the early stages of the virus is approximately 20,000 individuals. We successfully derived these essential variables using the formulas in Equations 8, 9 and 10.

$$Infectious = Cumulative\ cases - Cumulative\ cases\ (shifted\ by\ 15\ days) \quad (11)$$

$$Recovered = Cumulative\ cases\ (shifted\ by\ 15\ days) \quad (12)$$

$$Susceptible = 20000 - (Infectious + Recovered) \quad (13)$$

As the simulation tool does not support over 1000 individuals. A population size of 500 individuals was selected for similar population density. We sliced the first 100 days after the first Covid-19 case in Algeria. The obtained results are shown on Figure 26.

### Simulation

To simulate the breakthrough of Covid-19 in Algeria, the following parameters in Table 11 were used.

*Table 11 - Parameters for Simulation of Covid-19 Outbreak in Algeria*

| | Covid Simulation |
|---|---|
| Population Size | 500 |
| Infection Radius | 5 pixels |
| Initially Infectious | 1% |
| Infection Duration | 15 days |
| Infection Probability | 3% |

The results of the simulation are shown in Figure 26

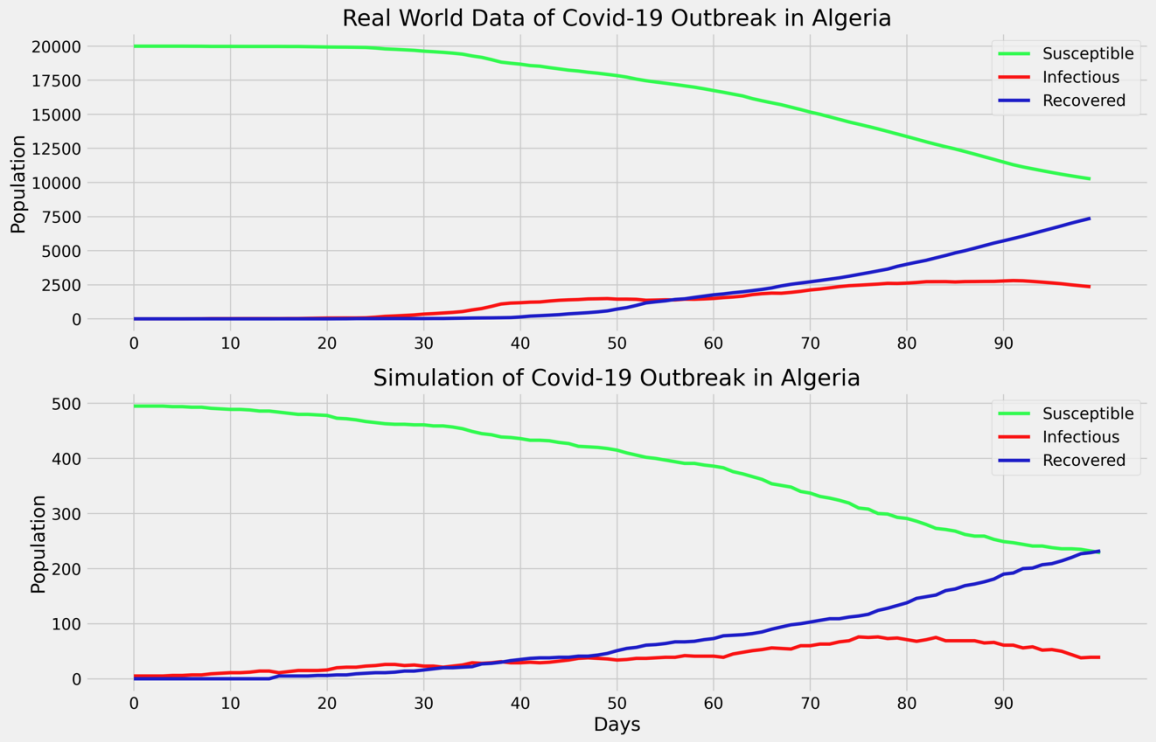


*Figure 26 - Data Visualization for Real World and Simulation of Covid-19 Outbreak in Algeria*

The findings presented in Figure 26 demonstrate a remarkable similarity between the rate of transmission of Covid-19 in Algeria, as observed in real-world data, and the outcomes derived from a simulation model. Notably, both scenarios depict a gradual and consistent progression of transmission throughout a 100-day period. Moreover, the final tally of infections in both instances approximates slightly less than 50% of the total population. These similar patterns provide compelling evidence to support the assertion that our simulation tool possesses the capacity to effectively emulate the spread of actual diseases when equipped with appropriate parameters and informed assumptions as foundational elements. This validation of the simulation tool's efficacy offers researchers and policymakers a valuable resource for forecasting and assessing disease dynamics, thereby contributing to enhanced preparedness and response strategies.

## 3.4 Conclusion

In conclusion, the 'Results, Analysis & Discussions' chapter provided a comprehensive evaluation of an epidemic simulation framework and its effectiveness in modeling the spread of infectious diseases. Through the implementation of various simulations and analysis of the generated data, several key findings emerged.

Firstly, population size was found to have a significant impact on disease transmission. Simulations showed that a larger population size led to a faster and more extensive spread

of the disease, highlighting the importance of population density and interactions between individuals.

Secondly, the infection radius parameter played a crucial role in the propagation of the disease. Simulations demonstrated that a larger infection radius resulted in a faster spread of the disease over longer distances, making it more difficult to control through traditional interventions.

Thirdly, the duration of infection was found to be a critical factor in disease transmission rates. Simulations showed that a longer infection duration led to a higher transmission rate and a more extensive spread of the disease, emphasizing the need for timely intervention measures to reduce the duration of infection.

Fourthly, the infection probability parameter had a significant impact on disease transmission. Higher infection probability resulted in a faster and more extensive spread of the disease, highlighting the importance of public health interventions aimed at reducing infection probability, such as social distancing measures and the use of personal protective equipment such as hygiene and facemasks.

Additionally, the effectiveness of control measures was evaluated. Simulations showed that early detection and swift response, along with effective implementation of quarantine measures, played a crucial role in mitigating the spread of infectious diseases.

Furthermore, the presence or absence of symptoms had a considerable impact on disease spread and severity. Simulations demonstrated that a significant proportion of asymptomatic cases could undermine quarantine efforts and lead to a higher overall transmission rate.

Lastly, the role of public awareness and collective collaboration in implementing control measures was highlighted. The success of interventions such as quarantine relied on individuals' understanding and adherence to guidelines, emphasizing the need for public education campaigns and clear communication.

Overall, the findings from this chapter underscore the complex dynamics of disease transmission and the importance of various parameters and control measures in shaping the spread of infectious diseases. The simulation framework proved to be a valuable tool for modeling and analyzing the impact of different scenarios, providing insights that can inform public health policy and future research efforts.

## Conclusion

This project aimed at proposing and evaluating an Interactive Epidemic Simulation Framework for modeling the spread of infectious diseases based on SIR model. The tool successfully provided a platform for simulating various scenarios and manipulating parameter values to analyze the impact of population and infection parameters on disease transmission dynamics.

The simulations conducted using the tool highlighted the crucial role of population size in disease propagation. Larger populations were found to facilitate a rapid spread of infections due to higher population densities and increased interactions between individuals. Conversely, smaller populations exhibited limited disease spread, indicating that reduced opportunities for contact between infectious and non-infectious individuals can help contain outbreaks.

Moreover, the investigation into infection parameters underscored the significance of the infection radius. Simulations with smaller infection radii demonstrated more controlled spread, while larger radii resulted in a substantial escalation of infections. These findings emphasize the importance of interventions that limit contact between infectious and susceptible individuals in curbing the spread of infectious diseases.

The Interactive Epidemic Simulation Tool proved to be an effective resource for modeling disease dynamics and analyzing epidemic trends. By providing the ability to simulate different scenarios and manipulate parameter values, the tool facilitated a deeper understanding of the complex relationship between population dynamics, infection parameters, and disease transmission patterns. This enhanced understanding has practical implications for public health policy and intervention strategies.

However, it is important to acknowledge the limitations of the tool and the study. The simulations were based on specific assumptions and simplifications, and real-world scenarios may involve additional complexities and factors. Future improvements could explore the incorporation of more realistic parameters and consider the impact of other variables, such as vaccination rates, mobility patterns, and behavioral factors, to further enhance the tool's accuracy and applicability.

In conclusion, this project successfully developed and evaluated an Interactive Epidemic Simulation Tool that demonstrated its effectiveness in modeling the spread of infectious diseases. The tool's capability to simulate various scenarios and manipulate parameter

values provided valuable insights into the impact of population and infection parameters on disease transmission. This project contributes to the field of public health by offering a practical tool for designing effective strategies to prevent and control epidemics. By further refining and expanding upon simulation tools like this, we can improve our preparedness and response to future disease outbreaks, ultimately safeguarding public health and well-being.

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