

**AN AGENT-BASED MODEL OF COVID-19  
USING SIR MODEL: TRANSMISSION IN A  
PUBLIC HIGH SCHOOL CLASSROOM IN THE  
PHILIPPINES.**

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A SPECIAL PROBLEM SUBMITTED TO THE  
DEPARTMENT OF MATHEMATICS AND COMPUTER SCIENCE  
COLLEGE OF SCIENCE  
THE UNIVERSITY OF THE PHILIPPINES  
BAGUIO, BAGUIO CITY

AS PARTIAL FULFILLMENT OF THE  
REQUIREMENTS FOR THE DEGREE OF  
BACHELOR OF SCIENCE IN COMPUTER SCIENCE

JUNE 2023

This is to certify that this Special Problem entitled "**An Agent-Based Model of COVID-19 using SIR Model: Transmission in a Public High School Classroom in the Philippines.**", prepared and submitted by **Charles Vincent A. Cordial** to fulfill part of the requirements for the degree of **Bachelor of Science in Computer Science**, was successfully defended and approved on June, 2023.

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## Acknowledgments

First, I would like to thank the Almighty God for giving me wisdom and strength to finish this thesis paper despite all the circumstances. I would like to thank and acknowledge my thesis adviser, sir Joel Addawe for being so patient and guiding me throughout my thesis journey. I would also like to thank DOST-SEI and DOST-CAR for their assistance. And last but not the least, to my family and girlfriend for their unending support and understanding during my thesis journey, this one is for you Mommy and Daddy.

# Abstract

## An Agent-Based Model of COVID-19 using SIR Model: Transmission in a Public High School Classroom in the Philippines.

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This study works with Agent-Based Modelling (ABM) to simulate the COVID-19 transmission among students in a public high school classroom in the Philippines under 4 different scenarios namely SC1: Base Model, SC2: Vaccinated Scenario, SC3: Eating Healthy Scenario, and SC4: With Comorbidity Scenario. In this study, we compare the transmission of the virus in each of the 4 scenarios from the SC1:Base Model. Moreover, we conducted One Factor at a Time (OFAT) Sensitivity Analysis for each of the 4 scenarios. Lastly, using the results from OFAT Sensitivity Analysis, we determine the best and worst case by combining sensitive parameters for the Two Factor at a Time Sensitivity Analysis (2FAT). From the simulation results, SC2 produced the slowest spread of the virus with an average of 1.40 newly infected agents per day, SC3 comes second with a rate of 4.36, SC1 comes next with an average rate of 4.38, and last in the list is SC4 with an average rate of 4.44. Using OFAT and 2FAT Sensitivity Analysis, generated results showed the parameter  $Prob_{Infect}$  and  $Seat\ Distance$  as the most sensitive parameter in SC1. This suggests that increasing  $Prob_{Infect}$  by -20% and  $Seat\ Distance$  by 20% can decrease the number of infected agents by up to 14.5% in SC1. On the other hand, results also suggest that increasing  $Prob_{Infect}$  by 20% can increase the number of infected agents by up to 9.5%. In the case of scenarios SC2, SC3, and SC4, parameters  $Prob_{Cough}$  and  $Seat\ Distance$  were the most sensitive. Similar results suggest that increasing the parameters  $Prob_{Infect}$  by -20% and  $Seat\ Distance$  by 20% can decrease the number of infected by up to 20.75% and 17.25% for scenarios S2 and S4, respectively. Lastly, results suggest that increasing the parameter  $Prob_{Infect}$  by 20% and  $Seat\ Distance$  by -20% can

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# Chapter 1

## Introduction

### 1.1 Background of the Study

On January 30, 2020, the World Health Organization classified the coronavirus disease 2019 (COVID-19) epidemic as a Public Health Emergency of International Concern. As of May 3, 2023, the Philippines has reported over 4 million confirmed cases and around 66 thousand death [57] in the country. COVID-19 is a disease caused by a strain of coronavirus, namely, Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) [41], and is considered highly infectious. It is transmitted from one host to another through different modes of transmission including airborne droplets disseminated by sneezing, coughing, direct physical contact, fomites, and many more. Once infected, an individual may develop mild to severe symptoms a few days after getting infected. This delay in the onset of symptoms puts every household in a difficult position on detecting infected individuals. This nature of transmission led to an increased number of infections all over the country, forcing individuals to conduct preventive measures while authorities mandated community restrictions like lockdowns to mitigate and slow down the spread of the virus. Lockdown measures forced essential institutions and enclosed facilities like schools to close and adapt to other modes of learning (i.e. online/distance learning) which are reportedly ineffective and challenging due to various circumstances of Filipino households. [53].

To study the transmission of a particular virus, many studies have used various mathematical models to analyze and investigate its nature of transmission. There is Mechanistic-Deterministic Modeling, an approach that uses a set of Differential or Partial Differential Equations to approximate the discrete-time dynamics of a particular

disease. One common example of this is Kermack and McKendrick's Susceptible-Infected-Recovered (SIR) model [46], which structures the infected population in terms of age-of-infection while using compartments for susceptible people (S), infected (I), and recovered/removed (R). The number of compartments in this model can be extended depending on the complexity of the study. One might, for example, study a model for the evolution of the COVID-19 disease as a function of the age of the population and extend the compartments to SEIRDV (Susceptible, Exposed, Infected, Recovered, Dead, Vaccinated) as made by Bongolan [9]. On the other hand, there is a Stochastic approach where the model relaxes some hypotheses provided in deterministic modeling to add some randomness and heterogeneity to the model. One common framework being used under this model is the Markov Chain or Markov Process [46]. Next on the list are the Complex Systems/Networks, which can capture the real-life complexity of virus spread such as contact networks and host-pathogen interactions that are known to have a broad spectrum of factors [46]. And lastly, we have Agent-Based Modelling (ABM).

Agent Based Models or also known as ABM [38] is a relatively new method of computational modeling composed of interacting autonomous 'agents' with a view of assessing their effects on the system as a whole. ABM has 4 main parts: agents, actions, environment, and simulation [48]. Agents are computer objects in the model that can make decisions, act autonomously, and interact with other agents depending on their assigned behaviors that dictate how they act/behave within the system. Each agent interacts with other agents using their defined set of Actions. These Actions can impact the involved agents' attributes and behaviors or even create a global change in the system. Other models also refer to this as the Ruling Behavior, which is an algorithm that an agent follows under specific conditions. The environment is the location where the agents exist and interact. There are many types of environments depending on the interactions allowed in the model. There are Real-World environments that are usually discretized in 2-dimension(grid/plane) or 3-dimension while others use abstract environments to model complex concepts(i.e. Modelling Economic Markets). Lastly, simulation is the part that controls the situation of the first-mentioned parts. The simulation can control the initialization of the model, execution per iteration, and even vary particular behaviors on a specific iteration/time range. This provides opportunities on studying different factors

and scenarios to fully understand a particular phenomenon.

A wide number of fields and disciplines use ABM to their advantage. Applications range from the multi-agent simulation environment of Carcraft on testing algorithms for self-driving cars in the sector of technology [40], Economists using ABM to imitate the complex systems of financial markets [47], and Epidemiologists to predict threats of bio-warfare [13] and epidemics [26]. A study made by Cuevas [1] provided a basic algorithm for ABM of COVID-19 in an enclosed space facility. Despite its simple structure and algorithm, Cuevas was able to provide an overview of the nature of the COVID-19 spread in a facility under different circumstances by testing and comparing different simulation settings/parameters of the model. In another study, Shamil et. al. provides a much more complex ABM of COVID-19 to simulate the spread of the virus in Ford County Kansas, and New York City, USA [45]. Unlike Cuevas, this study presented a much more complex and realistic model while utilizing real-life demographic and physiological data of the targeted cities to fully imitate the transmission of the virus in a particular population. This study implemented 6 compartmental models, multi-layer threshold of infection, realistic set of tasks and actions, and many more. All of the factors are interconnected with each other to create a complex simulation of COVID-19 spread. Lastly, Maclinao et.al [39] presented an ABM that illustrates the COVID-19 spread in a classroom setting. This study used reported data from the Department of Health (DOH) and other studies [60] for the initial number of infected and transmission rate parameters in the model. Despite having only 1-layer of threshold for infection rule, the study emphasized the impacts of varying factors such as transmission rate, number of initial infected, and seating arrangement on the overall spread of the virus. This allowed the study to determine which sets of configurations provide the best and worst case of spreading in a classroom. These 3 studies have inspired us to study the transmission of COVID-19 in a classroom setting under different scenarios.

In this paper, we have presented an ABM intending to simulate the disease dynamics and transmission of COVID-19 in a public high school classroom in the Philippines. Our approach involves creating a model that represents the current classroom setup using reported average classroom size, number of students, seating arrangement, and class schedules to imitate the behavior of students during class hours [23, 51]. In this study,

we have focused on cough as a mode of transmission of the virus. Parameter values used for the infection behavior were gathered from multiple studies [3, 43]. Moreover, we also analyzed the transmission of COVID-19 under different scenarios namely SC1 (Base Model), SC2 (Vaccinated Scenario), SC3 (Eating Healthy Scenario), and SC4 (With Comorbidity Scenario). We compared each scenario to the SC1:Base Model to provide some comparison on performance. Each scenario was represented using data provided by various studies. Lastly, the parameters used are subjected to Sensitivity Analysis to determine their impacts on the overall spread of the virus.

## 1.2 Statement of the Problem

Ever since the implementation of localized lockdowns on March 15, 2020, the Philippine government issued a temporary closure of essential facilities and institutions including public and private schools. Social inequalities and the lack of resources at home challenged Filipino students from adjusting to the demands of the current mode of learning(online/distance learning) [53]. While the positive impact produced by the closure of schools in mitigating the spread of the virus has an effect studies blame school shutdowns to be the culprit of the increase in dropout rates and decreased literacy of children aged 10 and below, from low-and middle-income countries [27, 36].

Two years later after the first lockdown was declared last March 15, 2020, the Department of Education (DepEd) mandated the possibility of conducting blended learning in all public and private schools in the country. As of November 7, 2022, 97.5% of public schools conduct five-day face-to-face classes while easing mandatory preventive measures like wearing face masks and social distancing [31]. This was allowed due to the increased number of vaccinations on the entire population including children, creating ‘immunity’ in the major parts of the country. While most people have this misconception of equating total immunity with vaccination, in reality, ‘breakthrough infections can still occur and propagate in a population [56]. This can cause an increased number of infections and create an unnecessary burden on Filipino households, institutions, and healthcare facilities. The Philippine government and every Filipino household cannot afford to have

another lockdown in case another COVID-19 surge happens. Studying the transmission of COVID-19 in a classroom setting will help us understand the behavior of the transmission and come up with solutions to mitigate it.

Since performing human experiments to study COVID-19 spread in a particular space is considered unethical and costly [33]. Mathematical modeling can be used as a tool to observe and describe the spread of COVID-19 and come up with measures to control it. ABM is a type of modeling that can be used to model complex systems [38] like COVID-19 spread in a classroom under specific scenarios to better understand the impacts of different factors on the overall spread of the virus.

## 1.3 Objective of the Study

### 1.3.1 General Objective of the Study

The study aims to analyze the spread of the COVID-19 virus in a confined space particularly in a public high school classroom using ABM.

### 1.3.2 Specific Objective of the Study

The study aims to determine scenario/s that show the slowest and fastest spread of the virus in a classroom. Particularly, the specific objectives of the study are the following:

1. Determine the values of variables such as the average rate of newly infected from day 1 to peak, peak number of infections, number of days to reach the peak, end of infection, and slope of the generated time series for each scenario namely SC1 (Base Model), SC2 (Vaccinated Scenario), SC3 (Eating Healthy Scenario), and SC4 (With Comorbidity Scenario) through simulations of the proposed ABM.
2. Compare each of the 4 scenarios (SC1, SC2, SC3, and SC4) from SC1 using generated variables provided in item 1.
3. Determine sensitive parameters that can be controlled for each scenario by conducting One Factor at a Time(OFAT) Sensitivity Analysis.

4. Determine the best and worst configurations for each scenario by combining their respective sensitive parameters using Two Factor at a Time(2FAT) Sensitivity Analysis.

## 1.4 Significance of the Study

Since the start of the COVID-19 pandemic, many studies have used ABM to study the transmission of COVID-19 in different localities [14, 26, 45]. However, these studies have used demographic data and complicated models to fully represent the virus spread in their large target population. On the other hand, some studies have used simplified model to analyze the COVID-19 spread in smaller environments like local facilities and institutions [14, 39, 58]. So far, there are only minimal studies online that have used ABM to study the transmission of COVID-19 in a classroom setting. Although Macalinao [39] presented a study with a similar topic, her model lacks complexity, particularly in the infection mechanism. In this study, we have adapted multi-layered ruling behavior on the infection behavior of the agents that were presented from the complex studies above. In this manner, we have added some complexity to the ABM despite having a relatively smaller target environment. This also provides a much more comprehensive representation of COVID-19 spread in small facilities like classrooms where many students spend most of their time during the day. This study also determines COVID-19 factors that can be controlled within the classrooms to avoid further surges that may cause lockdowns in localities.

## 1.5 Scope and Limitation

This study focuses on analyzing the transmission of COVID-19 virus in a 7x9 meter classroom with 40 seats(two-block layout) using ABM. In this study, the SIR (Susceptible, Infected, Recovered) model has been used to compartmentalize the agents based on their infection status. Here are the following assumptions that have been considered in creating the model:

1. There are no birth and death dynamics in the model.

2. Agents will only be susceptible or infective upon entry on the classroom.
3. Infections outside the classroom are neglected
4. Cough is the only mode of transmission considered in the model.
5. COVID-19's incubation period is in effect.
6. There are no asymptomatic cases.
7. There are no reinfections in agents.
8. Outbreaks are short-lived (56 days).
9. Homogeneity in health conditions among the agents is considered depending on the scenario.
10. Other factors aside from the defined parameters in the model are neglected (i.e. Ventilation).

In real-life scenarios, student interactions can also happen outside the classroom like in cafeterias, libraries, and other common school grounds. Studying the dynamics of COVID-19 spread only inside the classroom is not enough to fully capture the complete nature of spread in a school setting. Also, we were not able to implement all the possible modes of transmission in the model due to the lack of data available online. Coughing direction was also simplified in this model, ignoring the non-linearity of the cough cloud during an event of cough. Considering these elements may add complexity to the model and differ the generated results in our study. Lastly, the generated cumulative active cases data for each simulation has been mainly used for the analysis part of the study.

# Chapter 2

## Review of Related Literature

Studies involving ABM in analyzing COVID-19 spread can be differentiated based on the number of possible states for agents and the main objectives of the study. Some studies have used SI(Susceptible, Infected) [19], SIR(Susceptible, Infected, Recovered), SEIR(Susceptible, Exposed, Infected, Recovered) [45], SEIRDV(Susceptible, Exposed, Infected, Recovered, Death, Vaccinated) [14] and many more to compartmentalize agents based on their infection status. On the other hand, ABM on COVID-19 usually has this common objective: create a model that can simulate the transmission of the virus in their target population [19]. From this, studies have been extending their objectives depending on the problem presented in the study. Large and complex ABM like [45] and [14] usually has this main goal to provide prediction and forecast of the COVID-19 transmission in their respective localities. These studies have used locally reported data such as demographic and physiological data of the particular city/town as parameters for the already complex ABM to create a much more realistic model that can accurately represent the COVID-19 spread in their target location. There are also simpler ABM like [19] and [39] that have used less complex ruling behavior and smaller environments in their studies. These studies mainly focused on identifying and assessing risk factors that significantly contribute to the spread of the virus to develop solutions that can mitigate COVID-19 provided the configurations used in the model.

In the study proposed by Cuevas [19], a simple ABM to evaluate the COVID-19 transmission risks in facilities has been presented. The proposed model was designed to simulate the spatiotemporal transmission process of COVID-19 in a facility. Cuevas has emphasized two main Ruling Behaviors to consider when creating ABM of COVID-19, Infection Behavior and Movement Behavior. These two behavior defines the health conditions and social characteristics of an agent which he considered the main driver of virus transmission. An SI(Susceptible, Infected) model was used to differentiate agents

in terms of their infection status. Cuevas used a two-dimensional space represented by a cartesian plane or a grid to discretize the facility in his model. He also assigned two main attributes for each agent that defines the behavior of an agent relative to the two mentioned ruling behaviors. These two attributes are the Probability of Infection represented by  $Pr_{in}$  and the probability of contact or mobility rate represented by  $Pr_{cm}$ . The Infection Rule has been defined by following a short algorithm. For each iteration, each susceptible agent has to analyze the existence of an infected agent within its 1-meter radius. Assuming the existence of an infected agent, a probabilistic decision process will be made by generating a random number within a uniform distribution from 0 to 1. If the generated value is less than or equal to the assigned  $Pr_{in}$ , the susceptible agent will be infected, otherwise, he/she will not be infected despite contact. This simple rule for infection has been used across different studies [14, 39, 45] to represent the virus transmission behavior from one agent to another. These studies only vary in the number of probability/thresholds used in the infection mechanism. For the movement behavior, all susceptible agents will generate a random number within a uniform distribution, if the generated value is less than the dedicated  $Pr_{cm}$  of an agent, the agent will move to a new position. There are two different movement types in the model: local and long-distance displacement which differentiate on the distance traveled by the agent. The new position will be calculated using a set of equations depending on the types of movement. The two defined Ruling Behaviors will be executed in every iteration of the model. Four experiments were also performed in the study to validate the model and test different scenarios. First, the 'Basic Performance' experiment was made to validate the actual model. Second, 'Varying size of susceptible agents', this experiment shows the maximal capacity of individuals the facility can maintain without presenting a high risk of transmission. Third, 'Varying infection probabilities', this experiment analyzes the effect of increasing and reducing  $Pr_{in}$  to the overall spread of the virus. And lastly, 'Movement Restrictions', this experiment tests the effects of restricting agents from moving further from their initial location. Despite having a relatively simple model, Cuevas was able to validate his model by showing experimental results that follow real-life expectations [55]. From this model, we have adapted the usage of the grid to discretize the classroom in our model. Moreover, we also adapted the framework of the infection Ruling Behavior

to determine the infection status of a susceptible agent using probabilities.

Shamil et. al. [45] proposed an ABM that simulates the spread of COVID-19 among the inhabitants of New York and Ford County in the USA. Their model has five main states for agents: Healthy, Not Contagious, Contagious Asymptomatic, Contagious Symptomatic, and Dead/Recovered, which is comparable to an SEIR model. Unlike [19] this model adapted the incubation period and asymptomatic nature of the COVID-19 virus. In this study, each agent was assigned to a profession that determines the set of professional tasks an agent performs each day. Each task is being performed in a particular place in the environment, allowing agents to move and interact across the city. Tasks are controlled by 3 parameters, which are the main determinant of the movement of an agent. For the Infection Rule in this model, an infected agent (contagious) can perform several actions that can contribute to the spread of the virus irrespective of the profession. These actions are the different modes of transmission adapted to model the infection mechanism of COVID-19. This adds complexity to the infection mechanism of the model as compared to [19]. These actions are controlled by 5 parameters, 4 of which are probabilities. Assuming that an agent was able to pass through all the probability parameters after performing an action, the model performs calculations that determine the infection status of the susceptible agent. This study has introduced 5 layers of thresholds for the Infection Behavior compared to Cuevas' 1-layer threshold model. This 5-layer threshold in infection behavior attempts to add complexity to COVID-19 transmission similar to real life. Compared to other studies [19, 39], this study has shown attention to detail with the Infection Behavior of the model by incorporating multiple modes of transmission of COVID-19, calculations in ruling behaviors, and multi-layer threshold on the infection process. To conduct their simulations, they collected demographics and physiological data of the inhabitants of the city to use as parameters in the model. The proposed model has been validated by comparing the generated time series data of total infection and reported data of Ford County, KS, USA. Furthermore, the study also analyzes the effect of varying the thresholds and combinations of different interventions on the trend of the virus. From this model, we have adapted the multi-layer threshold in the infection mechanism, specified mode of transmission, and the incubation period nature of COVID-19 to add complexity to our model. Moreover, we have also adapted

the process of conducting Sensitivity Analysis to parameters to determine risk factors that significantly contribute to the best and worst-case spread of the virus.

In another study, Bongolan and Celeste simulated the School Re-opening and Vaccination Scenarios in Quezon City, Philippines using their proposed ABM [14]. This study uses SEIRDV (Susceptible, Exposed, Infected, Recovered, Dead, and Vaccinated) to categorize the states of the agents in the model. The researchers used the Age-Stratified, Quarantine-Modified SEIR with Non-Linear Incidence Rates (ASQ-SEIR-NLIR) [10] compartmental model, which is composed of differential equations that describe the highly age-dependent COVID-19 transmission. Researchers were able to transcribe the compartmental model into parameters for the proposed ABM, this enables heterogeneity in the social characteristics and health conditions of the agents depending on their respective ages. The significant part of their study was the Sensitivity Analysis, in which the researchers attempted to project the change in the number of infections and death as they experiment with different coverage on School Re-opening and Vaccination in the city. Results have shown that the minimum required vaccination coverage for Quezon City, Philippines is 50% to achieve a controlled spread of the virus. Moreover, researchers suggest that students should get vaccinated first before allowing a 25% School Re-opening as a precaution. Conducting Sensitivity Analysis helps researchers to evaluate several scenarios to come up with an optimal case that can reduce viral propagation. From this study, we have adapted the process of Sensitivity Analysis to examine the effect of varying the parameters in our model.

Similar to Cuevas, a study made by Macalinao [39] implemented an ABM in Netlogo to analyze the virus transmission in a classroom setting. In this study, they have provided 4 different classroom layouts to experiment and determine which among the list produced the highest CPI (Cumulative Proportion of Infected Individuals). To represent each classroom layout, the model has used grids similar to Cuevas' model. The proposed model has 4 main parameters: Seating arrangement, number of susceptible agents, number of initially infected agents, and transmission rate. For the Infection behavior, the study has only used 1-layer threshold using the transmission rate gathered from [60]. For the Movement behavior, each agent is placed in a pre-determined seat depending on the classroom layout. Moreover, agents are not allowed to move around the classroom to

focus on the effect of different classroom layouts. For the simulation, Macalinao has also conducted Sensitivity Analysis by combining different parameter values to determine the set of configurations that produced the highest and lowest CPI. Results have shown that increasing the numeric valued parameters and utilizing the Double Horse Shoe classroom layout produced the highest CPI among the experiments. On the other hand, decreasing numeric valued parameters and using One seat apart classroom layout produced lower CPI relative to other experiments. This study has inspired us to further study the transmission of COVID-19 within a classroom setting and emphasize the Sensitivity Analysis to determine configurations that produced the fastest and slowest spread of the virus.

The studies discussed above show the possibility of simulating COVID-19 transmission in different types of environments using ABM. They also show the importance of the data availability and proper implementation of ruling behaviors, particularly infection and movement behaviors in creating decent ABM that simulates COVID-19 transmission in a target population. These studies have provided us with key insights and techniques on implementing our ABM in this study.

# Chapter 3

## Preliminaries

### 3.1 Agent-Based Modelling

As mentioned in the previous sections, many different fields of study have already used ABM to answer their scientific inquiries [13, 26, 40, 47]. This section discusses ABM and its parts in the context of the COVID-19 spread. The 4 main parts of ABM are Agents, Actions or Ruling Behavior, Environment, and Simulation. We have defined and discussed the representations of each part of ABM using [19].

#### 3.1.1 Agents

Agents in ABM are the collection of autonomous decision-making entities that interacts with one another in a particular environment that is governed by a set of rules [19]. ABM studies have used state models to categorize agents based on their infection status. The SIR (Susceptible, Infected, and Recovered) state model is one of the most common state models used in modeling epidemiology using ABM.

**Susceptible Agent** - A non-infected type of agent that is capable of contracting a virus upon interaction with infected agents.

**Infected Agents** - An infected type of agent that is capable of infecting susceptible agents upon interaction.

**Recovered Agents** - A non-infected agent that develops immunity after surviving a prior infection.

Originally, the SIR model is a mathematical model that consists of differential equations that use rates of transition from one compartment to another [45]. In this study, we have used SIR to compartmentalize the agents and to determine the current number

of susceptible, infected, and recovered agents in the model at a particular period. Figure 3.1 shows the transition order for an SIR state model, where  $\beta$  and  $\gamma$  are the infection and recovery rate.

Cuevas has represented each compartment of SIR in his study using a mathematical set. In this case, we modify some assigned variables to follow the SIR states. Suppose we let the cardinalities of the sets  $|S(k)|$ ,  $|I(k)|$ , and  $|R(k)|$  be the number of susceptible, infected, and recovered agents respectively at iteration  $k \in \mathbb{Z}^+$ . Adopting Cuevas' model, we let

$$S(k) = \{s_j, s_{j+1}, \dots, s_{|S(k)|}\}$$

be a set containing  $|S(k)|$  susceptible agents at iteration  $k$  where  $s_j$  is a particular susceptible agent in set  $S(k)$  and  $j \in \mathbb{Z}^+$ . For the infected agents, we let

$$I(k) = \{i_j, i_{j+1}, \dots, i_{|I(k)|}\}$$

be a set containing  $|I(k)|$  infected agents at iteration  $k$  where  $i_j$  is a particular infected agent in set  $I(k)$ . Lastly, for the recovered agents, we let

$$R(k) = \{r_j, r_{j+1}, \dots, r_{|R(k)|}\}$$

be a set containing  $|R(k)|$  infected agents at iteration  $k$  where  $r_j$  is a particular recovered agent in set  $R(k)$ . In a closed population model,  $|S(k)| + |I(k)| + |R(k)| = N$  at any  $k$  where  $N$  is the total population.

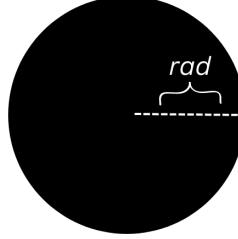


**Figure 3.1:** Sequence of transition for Susceptible-Infected-Recovered (SIR) State Model

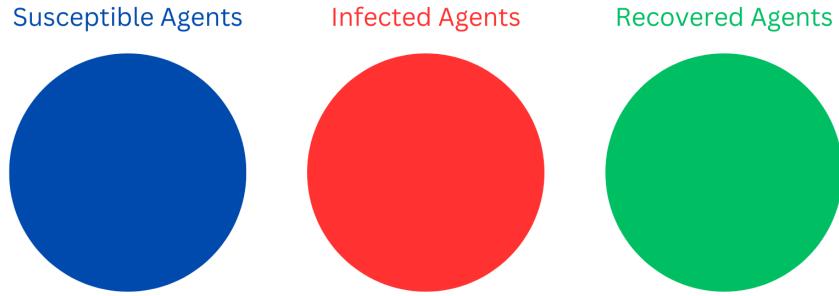
### 3.1.1.1 Representation of Agents

In some ABM platforms like GAMA [24] and NetLogo [42], COVID-19 agents are visually represented with 2-dimensional circular icons with fixed radius  $rad \in \mathbb{R}^+$  (i.e 0.25 meter) [17] as shown in Figure 3.2. To differentiate susceptible, infected, and recovered

agents in the model, all susceptible agents will be represented with blue-colored circles, infected agents will have red-colored circles, and recovered agents will have green-colored circles as shown in Figure 3.3.



**Figure 3.2:** Representation of an agent in ABM for COVID-19

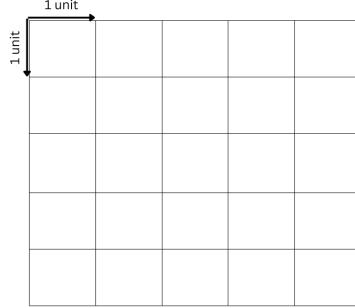


**Figure 3.3:** Agents representation based on their infection status (Left: Susceptible Agent, Middle: Infected Agent, Right: Recovered Agent)

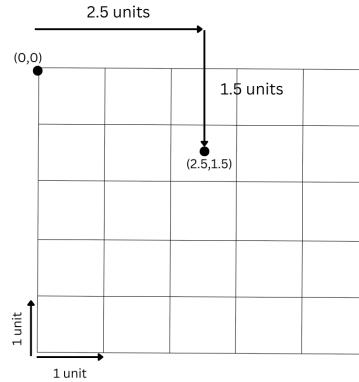
### 3.1.2 Environment

In this study, we use Cuevas' model to represent the facility using a two-dimensional space like a cartesian plane. Moreover, we will use a Grid to discretize our target environment. Grid [12] refers to a collection of intersections of 2 sets of evenly-spaced parallel lines at a 90-degree angle in  $\mathbb{R}^2$  as shown in Figure 3.4. Each small square in the grid is called the *grid cell* with equal lengths of sides (i.e. 1 unit) that can be modified depending on how discrete an environment will be in a model. Figure 3.4 shows an example of a 5x5 (width x length) Grid with a 5 unit width and 5 unit length where each *grid cell* has a side length equal to 1 unit. To navigate through the grid, we need to set the upper left corner of the grid to be the origin or point (0,0). Each point/location in the

Grid can be identified uniquely by means of ordered pair or real coordinates denoted by  $(\bar{x}, \bar{y}) \in \mathbb{R}^+ \times \mathbb{R}^+$  where  $\bar{x}$  corresponds to the distance to the right from the vertical line passing origin to the point  $(\bar{x}, \bar{y})$  and  $\bar{y}$  correspond to the downward distance from the horizontal line passing origin to the point  $(\bar{x}, \bar{y})$  as shown in the example in Figure 3.5.



**Figure 3.4:** Example of a 5x5 (width x length) Grid Environment



**Figure 3.5:** Example of locating points  $(2.5,1.5)$  in a 5x5 Grid

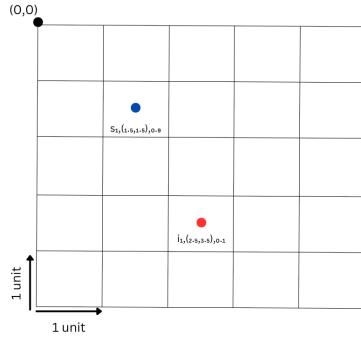
### 3.1.2.1 Position of Agents

In this model, agents can be placed at any given point  $(\bar{x}, \bar{y})$  given that  $\bar{x} \in [0, m]$  and  $\bar{y} \in [0, n]$  where  $m \in \mathbb{R}^+$  and  $n \in \mathbb{R}^+$  are the width and length of the facility. A particular agent's current position will be represented as coordinates denoted by  $(x_i, y_i)$  which will be placed as a subscript on the rightmost part of a particular agent (i.e  $s_{j,(x_i,y_i)}$ ). Figure 3.6 shows a 5x5 grid environment containing agent  $s_1$  and  $i_1$  located at points  $(1.5, 1.5)$  and  $(2.5, 3.5)$ . Note that the geometric center of the agents is exactly placed in their

respective locations as shown in the figure. The distance between two agents will be measured using *Euclidean Distance Formula* [18] denoted by

$$d_{euc} = \sqrt{(x_i - x_j)^2 + (y_i - y_j)^2}$$

where  $d_{euc}$  is the distance between the points  $(x_i, y_i)$  and  $(x_j, y_j)$ .



**Figure 3.6:** Example of 5x5 Grid environment with agents  $s_1$  and  $i_1$  located at points  $(1.5, 1.5)$  and  $(2.5, 3.5)$  respectively

### 3.1.3 Ruling Behaviors

Agents ruling behaviors are the materialization of agent decision-making that is usually expressed through actions performed which can lead to a change in the system. The changes could affect the individual agent performing the action, other involved agents, and even the environment of the model [48]. According to Cuevas [19], in order for agents to simulate the COVID-19 transmission, agents in  $S(k)$ ,  $I(k)$ , and  $R(k)$  should acquire two main behaviors: Infection Behavior and Movement Behavior. These two behaviors are usually represented through probabilistic tests as discussed in the next subsections.

#### 3.1.3.1 Movement Behavior

In Cuevas' model, each agent will determine whether they will move or not through a single probabilistic decision. Each agent acquires an attribute named  $Pr_{cm} \in [0, 1]$  which is placed beside the agent's current location (i.e.  $s_i, (x_i, y_i), Pr_{cm}$ ). This attribute represents the probability of an agent to move to another location for every iteration. A high value

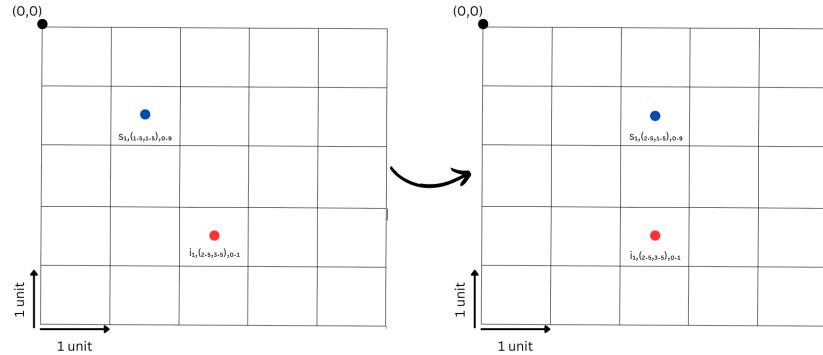
of  $Pr_{cm}$  indicates a higher chance for an agent to move every iteration, and vice versa. For this process, a random number will be generated within a uniform distribution  $U[0, 1]$ . If the generated value is less than or equal to the agent's  $Pr_{cm}$  value, an agent will move to a new position, otherwise not. Agent's next position is determined by calculating the next values for  $x_i$  and  $y_i$  using the given formula:

$$\begin{aligned}x_i &= 0 + \text{rand}(0, 1) * (m) \\y_i &= 0 + \text{rand}(0, 1) * (n)\end{aligned}$$

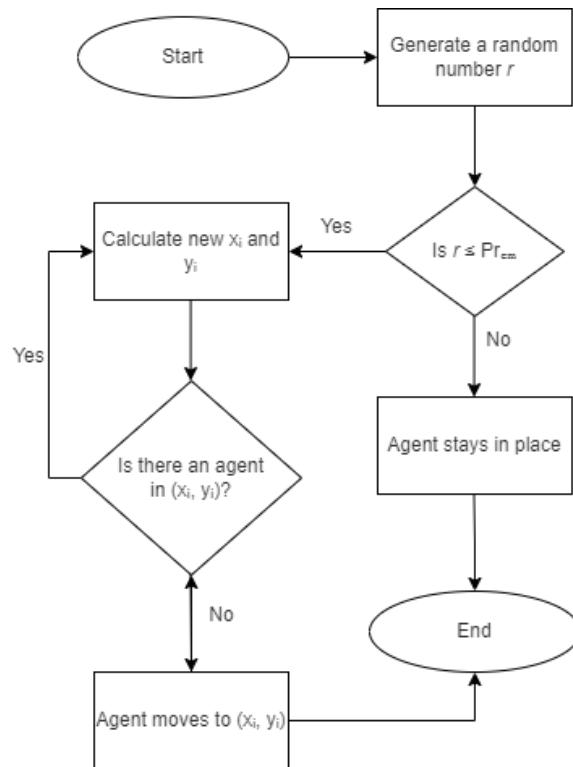
Figure 3.8 shows the summary of the movement behavior in a flowchart form. This behavior is being performed by all agents for every iteration. Suppose we use the example provided in Figure 3.6 to represent the movement behavior of the two agents, but this time we have to assign the  $Pr_{cm}$  for agent  $s_1$  and  $i_1$  to be equal to 0.9 and 0.1 respectively. Supposed that only agent  $s_1$  will move due to its high  $Pr_{cm}$ , we now calculate the next position for agent  $s_1$ :

$$\begin{aligned}x_i &= 0 + \text{rand}(0, 1) * (5) \\&= 0 + 0.5 * (5) \\&= 2.5 \\y_i &= 0 + \text{rand}(0, 1) * (5) \\&= 0 + 0.3 * (5) \\&= 1.5\end{aligned}$$

Using the formula, agent  $s_{1,(1.5,1.5),0.9}$  will be moved to coordinates (2.5, 1.5) for the iteration while agent  $i_{1,(2.5,3.5),0.1}$  stays at coordinates (2.5, 3.5) as shown in Figure 3.7. If another agent is located to the calculated values, the model will recalculate a new set of coordinates until an empty one is found. Take note that the movement behavior in this model does not follow a specific pathway to move to another location, all agents transport across a distance instantaneously. This behavior applies to all agents in the model for every iteration.



**Figure 3.7:** Example of 5x5 Grid environment with agents  $s_1$  and  $i_1$  where agent  $s_1$  moves to a new position following the movement behavior.



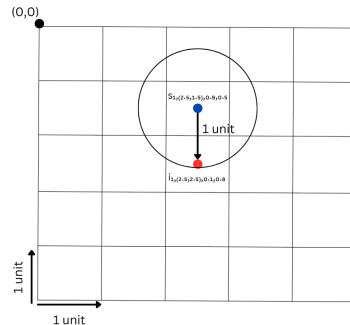
**Figure 3.8:** Flowchart of the Movement Behavior proposed by Cuevas

### 3.1.3.2 Infection Behavior

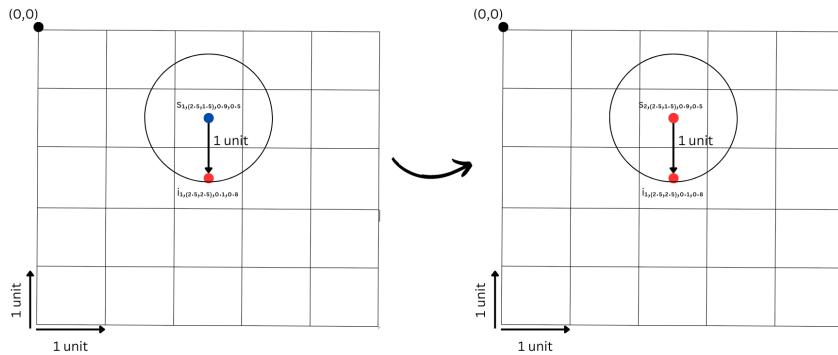
COVID-19 virus is transmitted from one host to another through different modes of transmission including airborne droplets disseminated by sneezing, coughing, direct

physical contact, fomites, and many more [41]. In Cuevas' [19] model, he simplified the infection mechanism by summing up all the transmission modes into a single probabilistic decision. Each agent acquires an attribute named  $Pr_{in} \in [0, 1]$  which is placed beside the agent's current probability of moving (i.e.  $s_{i,(x_i,y_i),Pr_{cm},Pr_{in}}$ ). This attribute represents the probability of an agent on getting infected upon interacting with an infected. A high value of  $Pr_{in}$  indicates a higher chance of getting infected upon interaction with an infected while a lower value indicates a lower chance of getting infected from the virus.

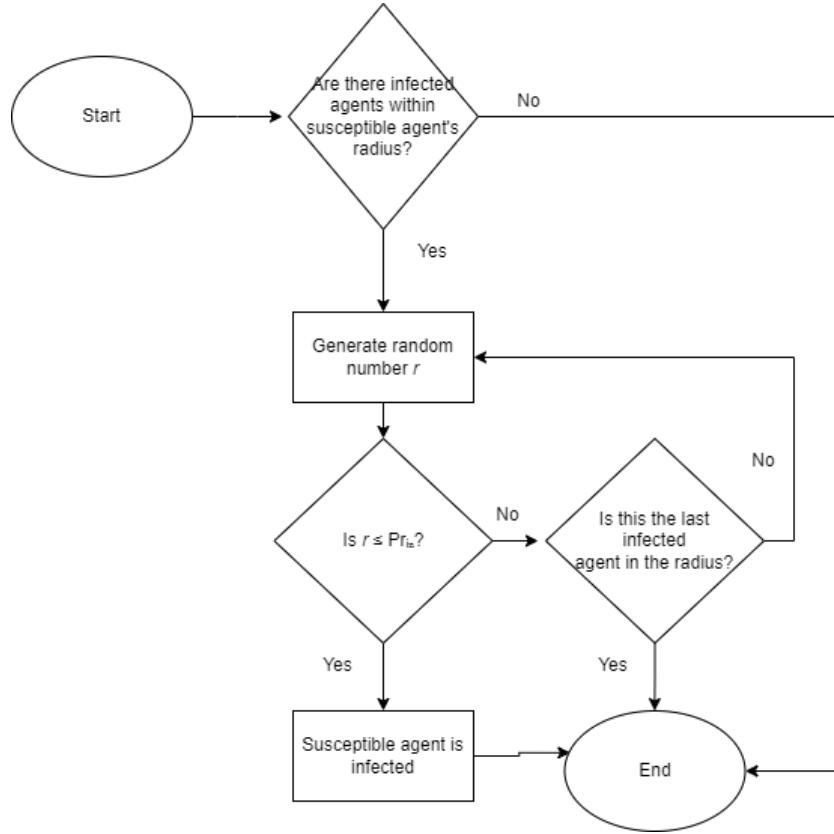
For this process, every susceptible agent will analyze the existence of an infected agent within its 1 unit radius as shown in Figure 3.9. This radius can be modified depending on the model's behavior (i.e. 1.5 meter radius). Also, the *Euclidean Distance* between the geometric center of two agents will be used to determine the distance of two agents. Suppose that a susceptible agent detected an infected agent within its radius, a probabilistic decision will be made in the model. A random number will be generated within a uniform distribution  $U[0, 1]$  which will be compared to the susceptible agent's  $Pr_{in}$  value. If the generated random number is less than or equal to the susceptible agent's  $Pr_{in}$ , the susceptible agent will become infected as shown in Figure 3.10, otherwise not. Newly infected agents will be transferred from set  $S(k)$  to  $I(k)$  for counting. In case a susceptible agent detects multiple infected agents, the susceptible agent will perform the infection behavior  $\bar{n}$  times where  $\bar{n}$  is the number of infected agents within its radius. For the recovery behavior, if an agent has been infected for 14 days, the agent will be transferred to the recovery compartment  $R(k)$  and acquire immunity. Note that all infected and recovered agents will not undergo the checking and probabilistic decision, only susceptible agents. This behavior applies to all agents in the model for every iteration. Figure 3.11 shows the summary of Infection Behavior in a flowchart form which susceptible agents follow for every iteration.



**Figure 3.9:** Example of Infection Behavior in the model where susceptible  $s_1$  detects the existence of infected agent  $i_2$  in its 1 unit radius.



**Figure 3.10:** Example of Infection Behavior in the model where susceptible  $s_1$  was successfully infected by infected agent  $i_1$  due to its high  $Pr_{in}$  value



**Figure 3.11:** Flowchart of the Infection Behavior proposed by Cuevas

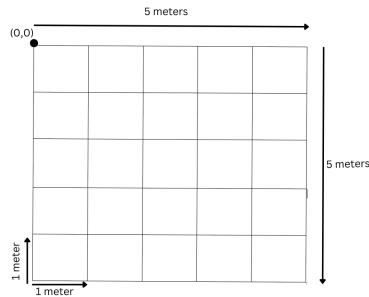
### 3.1.4 Simulation

Simulation is the aspect of the model that is responsible for controlling the 3 defined parts (Agent, Actions or Ruling Behavior, and Environment) programmatically. First, the model requires input values for all the parameters for each part discussed above. For the environment, we have to assign values for the 4 parameters such as the maximum number of iterations, representation of 1 iteration, width and length of the facility, radius of infection, and length of a *grid cell*. Note that iteration always starts at 0 in every simulation. Figure 3.12 shows an environment following the inputs provided in Table 3.1. For the agents, the following parameters that need input values are the initial number of susceptible agents  $|S(0)|$ , initial number of infected agents  $|I(0)|$ , initial number of recovered agents  $|R(0)|$ , probability of an agent to move  $Pr_{cm}$ , probability of an agent of getting infected  $Pr_{in}$ , and agents' initial positions. The probability attributes and

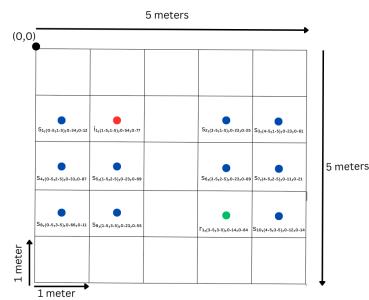
Parameter	Value	Units	Description
$maxiter$	500	iterations	maximum number of iteration in the model
$interval$	1	day/iteration	real life equivalent of 1 iteration in the model
$m$	5	meter	width of facility: the total horizontal distance between the outermost edges of the building
$n$	5	meter	length of facility: the total vertical distance between the outermost edges of the building
$grid_{cell}$	1	meter	side length of each <i>grid cell</i>
$rad_{infect}$	1	meter	radius of infection for Infection Behavior
$ S(0) $	10	agents	number of susceptible agents at iteration 0
$ I(0) $	1	agents	number of infected agents at iteration 0
$ R(0) $	1	agents	number of recovered agents at iteration 0

**Table 3.1:** Input parameters required for the model simulations

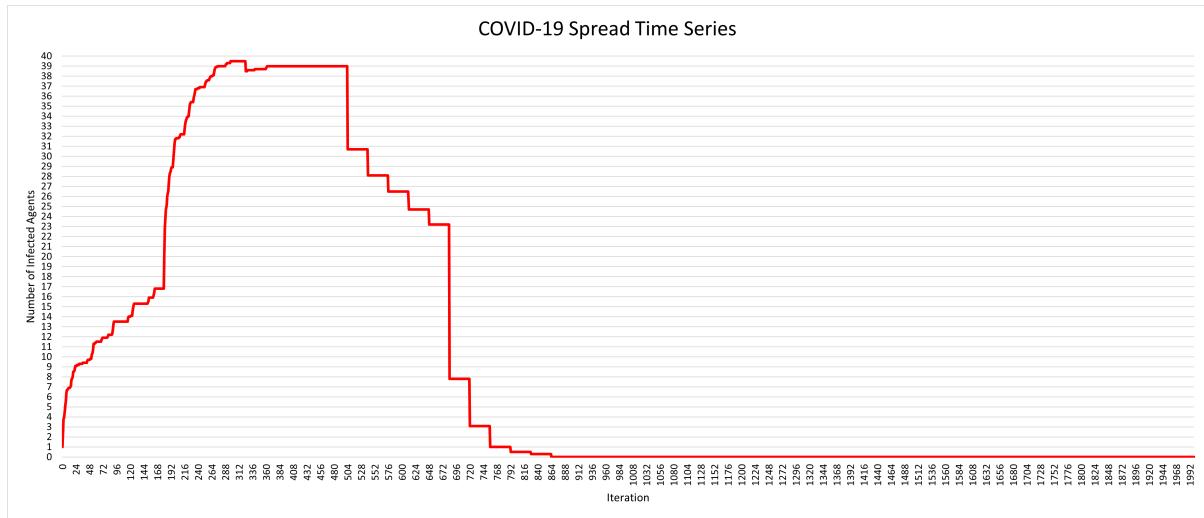
initial positions for each agent will be randomly generated at the start of the model. Table 3.1 now contains the necessary parameters for agents and environment with their corresponding values for the simulation. For the actions or ruling behavior, the model will adapt the two behaviors defined in Section 3.1.3. Figure 3.13 shows an example of an initialized model using the parameters provided in Table 3.1. For the output, the model is expected to generate a time series containing the cumulative number of infected agents per iteration similar to Figure 3.13. Lastly, Algorithm 1 summarizes an example of the sequence of the model from initialization of parameters to actual simulation of COVID-19 transmission of agents in a facility.



**Figure 3.12:** Environment generated in the model using the parameters provided in Table 3.1



**Figure 3.13:** Example of initialized model using the parameters provided in Table 3.1



**Figure 3.14:** Example of Time Series of Cumulative Number of Infected per iteration

---

**Algorithm 1** Pseudo-code for the COVID-19 transmission in a facility

---

**Input:**  $k = 0, maxiter, interval, m, n, grid_{cell}, rad_{infect}, |S(0)|, |I(0)|, |R(0)|$

**Output:** Time Series graph containing Cumulative Number of Infected agents per iteration.

```

1:  $S(k) \leftarrow \text{GenerateSusceptibleAgents}(|S(0)|);$ 
2:  $I(k) \leftarrow \text{GenerateInfectedAgents}(|I(0)|);$ 
3:  $R(k) \leftarrow \text{GenerateRecoveredAgents}(|R(0)|);$ 
4:  $\text{AssignPr}_{in}(S(k), I(k), R(k));$ 
5:  $\text{AssignPr}_{cm}(S(k), I(k), R(k));$ 
6:  $\text{GenerateGrid}(m, n, grid_{cell});$ 
7:  $\text{InitializedAgentsPosition}(S(k), I(k), R(k))$ 
8: _____
9: while  $k < maxiter$  do
10: _____
11:   for each  $a_j \in S(k), I(k), R(k)$  do                                 $\triangleright$  Rule I: Movement Behavior START
12:     if  $\text{rand}(0, 1) \leq Pr_{cm}$  then
13:        $\text{moveAgent}(a_i);$                                           $\triangleright$  Rule I: Movement Behavior END
14: _____
15:   for each  $s_j \in S(k)$  do                                 $\triangleright$  Rule II: Infection Behavior START
16:      $T \leftarrow \text{FindAllInfected}(rad_{infect});$ 
17:     if  $|T| == 0$  then
18:       skip
19:     else
20:       for  $i \leftarrow 1$  to  $|T|$  do
21:         if  $\text{rand}(0, 1) \leq Pr_{in}$  then
22:            $\text{ConvertToInfected}(s_j, I(k));$ 
23:   for each  $i_j \in I(k)$  do
24:     if  $\text{isInfectedFor14Days}(i_j)$  then
25:        $\text{ConvertToRecovered}(i_j, R(k));$                                  $\triangleright$  Rule II: Infection Behavior END
26:    $\text{store}(|I(k)|, k);$ 
27:    $k \leftarrow k + 1$ 
28:  $\text{generateTimeSeries}();$ 

```

---

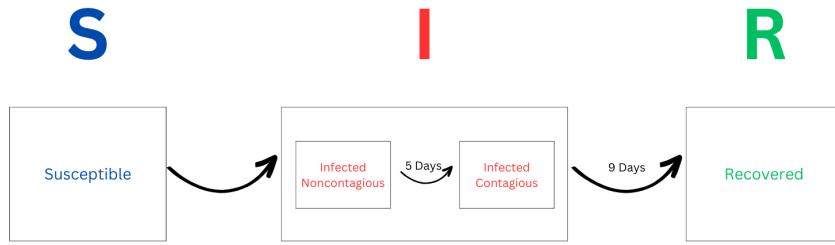
# Chapter 4

## Methodology

In this study, we have attempted to simulate the transmission of the COVID-19 virus among students in a public high-school classroom. We have also tested 4 different scenarios such as the SC1: Base Model, SC2: Vaccinated Scenario where all students are vaccinated, SC3: Eating Healthy Scenario where students follow a healthy diet, and SC4: With Comorbidity where all students suffer from comorbidities. This section discusses the representations of ABM parts and their configurations to achieve our desired model. We have used Section 3 as a reference for the model structure, some changes in the parts have been made to situate our ABM based on our target population and environment.

### 4.1 Agents: Students

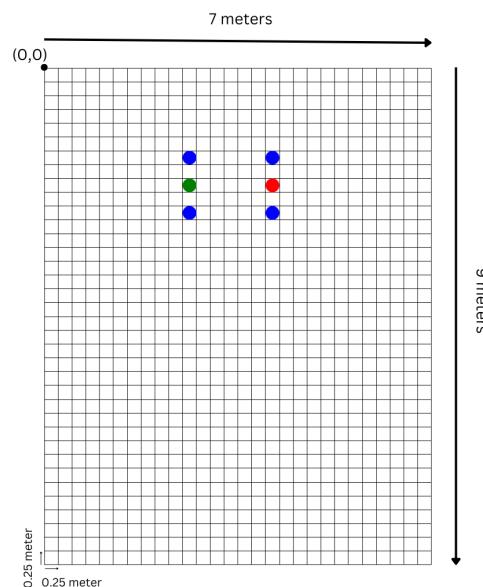
In this model, the main agents are the students in a public high-school classroom. All students are categorized based on their infection status, we adjusted the SIR model by integrating the incubation period (4 days) [34] and the average duration (14 days) [9] of the COVID-19 virus resulting in a sequence of infection as shown in Figure 4.1. In this process, a newly infected agent will be noncontagious for 4 days before becoming contagious 5 days after infection. Moreover, an agent has to be infected for 14 days before recovering and acquiring immunity from the virus. All infected agents whether contagious or noncontagious are considered under the infected compartment. Similar to Cuevas [19], all agents are displayed as a color-coded circle (radius = 0.125 meters) depending on their infection status as shown in Figure 3.3.



**Figure 4.1:** Sequence of infection for Susceptible-Infected-Recovered(SIR) in our ABM

## 4.2 Environment: Classroom

In this model, we have used 1 classroom environment where agents are placed to analyze the transmission of the COVID-19 virus. According to the Department of Education [23], a standard classroom in the Philippines has a width of 7 meters and a length of 9 meters. This was represented in the model using a 7x9 meters grid where each *grid cell* has a side length equal to 0.25 meters as shown in Figure 4.2. Note that agents are only allowed to be placed and navigate inside the grid. The process of navigating the grid discussed in Section 3.1.2 was adapted in this model.



**Figure 4.2:** A 7x9 Classroom Environment represented as a grid with 0.25 *grid cell* length

## 4.3 Gathering of Parameters

In this model, we have adapted the multi-layer threshold of [45] in the Infection Behavior by specifying cough as the mode of COVID-19 transmission and implementing two probability parameters such as the probability of coughing and probability of infection through cough denoted by  $Prob_{Cough}$  and  $Prob_{Infect}$ , respectively. As much as we want to cover all the modes of COVID-19 transmission, we were not able to find data regarding other modes besides cough. For the classroom environment, we have used the two-block-layout for the seating arrangement [39] where agents have their designated seats separated by 0.5 meters from the front, back, and sides of each seat.

### 4.3.1 Probability of Coughing: $Prob_{Cough}$

This section discusses how we gathered the value of the probability of coughing using a Poisson Distribution [52] and a study that measures the cough frequency of a person suffering from acute cough. In the study presented by Sunger et. al [49], the researchers measured the frequency of cough from 54 healthy volunteers suffering from acute cough ( $\leq 3$  weeks) associated with upper respiratory tract infections (URTIs). All subjects performed a 24-hour ambulatory cough monitoring using a modified recording device. The study has reported that a person suffering from acute cough has an average rate of 16 coughs per hour during the daytime, which is equivalent to 4 coughs per 15 mins. Given this data, we have determined the probability of an agent performing 1,2,3 or 4 cough/s in 15 minutes using the Poisson Distribution [52] as shown in equation 4.1

The formula for the Poisson distribution function is given by:

$$P(x) = \frac{e^{-\lambda} \lambda^x}{x!} \quad (4.1)$$

where:  $P(x)$  = Probability of a cough event

$e$  = Euler's constant

$x$  = number of times an event(cough) occur

$\lambda$  = average number of times an event (cough) occur

We now let  $\lambda = 4$  and  $x$  to be equal to 1,2,3, and 4. Hence, we now solve for  $P(1 \leq x \leq 4)$  given by:

$$P(1 \leq x \leq 4) = P(x = 1) + P(x = 2) + P(x = 3) + P(x = 4) \quad (4.2)$$

$$P(1 \leq x \leq 4) = \frac{e^{-4} * 4^1}{1!} + \frac{e^{-4} * 4^2}{2!} + \frac{e^{-4} * 4^3}{3!} + \frac{e^{-4} * 4^4}{4!} \quad (4.3)$$

$$P(1 \leq x \leq 4) = 0.61 \quad (4.4)$$

Note that we have simplified the cough transmission by considering the chances of 1,2,3, or 4 coughs as 1 cough event. Using the data given above, we can conclude that a contagious agent has a 61% chance of performing a cough every 15 minutes.

### 4.3.2 Probability of Infection from Cough: $Prob_{Infect}$

In the works of Agrawal and Bhardwaj [3], the researchers have estimated the probability of an infected person infecting another person in an enclosed space through cough in the context of COVID-19. The analysis has used Wells Riley Theorem [50] denoted by the Poisson probability distribution in the Equation 4.5 where  $\mu$  is the *quanta*, a measured number of infectious airborne particles required to infect a person. This study used the physics of fluids (Volume coughed, Volume inhaled, Radius of inhalation, and Duration of inhalation) of cough to determine the parameters needed to calculate the value for *quanta* in their model. Wells Riley Theorem [50] utilizes Poisson Distribution to measure the probability of a person inhaling one or more doses of *quanta*, which can result in an infection.

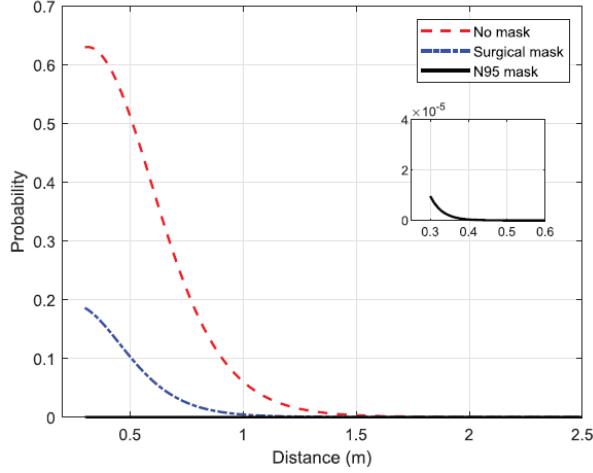
$$P = 1 - exp^{(-\mu)} \quad (4.5)$$

where:  $P$  = Probability of inhaling one or more doses of *quanta*

$exp$  = exponential function

$\mu$  = *quanta* [50]

In their results, the study determined different probability values for cases of no mask, with surgical mask, and with N95 mask at different distances from the source. Figure 4.3 shows the variation in the probability of infection based on the distance in the three cases mentioned

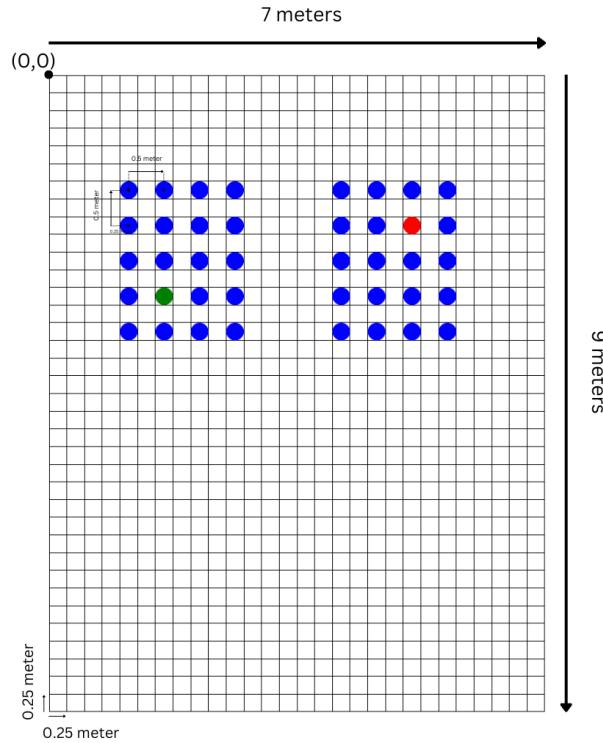


**Figure 4.3:** Distance-variation of the probability of COVID-19 infection for three cases, namely, no mask, surgical mask, and N95 mask

### 4.3.3 Classroom Environment Setting/Configuration

One of the common seating arrangement layout that has been used in the Philippines classrooms today is the two-block layout [39]. In a two-block layout, each block has 4 columns and 5 rows of seating capacity, divided by an aisle where each student in a block is separated by 0.5 meters as shown in Figure 4.4. According to a report [37], public schools in the Philippines have an average of 40 students per classroom. Using the data provided, we have implemented a classroom model that has 40 seats for 40 students. Each agent has a designated seat which will be assigned randomly in the initialization. Here are the following exact coordinates for all the 40 seats in the model:  $\{(1.125, 1.625), (1.625, 1.625), (2.125, 1.625), (2.625, 1.625), (4.125, 1.625), (4.625, 1.625), (5.125, 1.625), (5.625, 1.625), (1.125, 2.125), (1.625, 2.125), (2.125, 2.125), (2.625, 2.125), (4.125, 2.125), (4.625, 2.125), (5.125, 2.125), (5.625, 2.125), (1.125, 2.625), (1.625, 2.625), (2.125, 2.625), (2.625, 2.625), (4.125, 2.625), (4.625, 2.625), (5.125, 2.625), (5.625, 2.625), (1.125, 3.125)\}$

$(1.625, 3.125), (2.125, 3.125), (2.625, 3.125), (4.125, 3.125), (4.625, 3.125), (5.125, 3.125),$   
 $(5.625, 3.125), (1.125, 3.625), (1.625, 3.625), (2.125, 3.625), (2.625, 3.625), (4.125, 3.625),$   
 $(4.625, 3.625), (5.125, 3.625), (5.625, 3.625)\}.$



**Figure 4.4:** Two-block layout classroom where each block has 4 columns and 5 rows, each seat is separated by 0.5 meters

## 4.4 Ruling Behaviors: Infection and Movement Behavior

Similar to Cuevas [19], we have implemented two behaviors of agents particularly the Infection Behavior and Movement Behavior that determines the health condition and social characteristics of an agent. For each iteration (equivalent to 15 minutes), an agent checks whether he/she will perform a particular action discussed in the next subsections.

#### 4.4.1 Movement Behavior

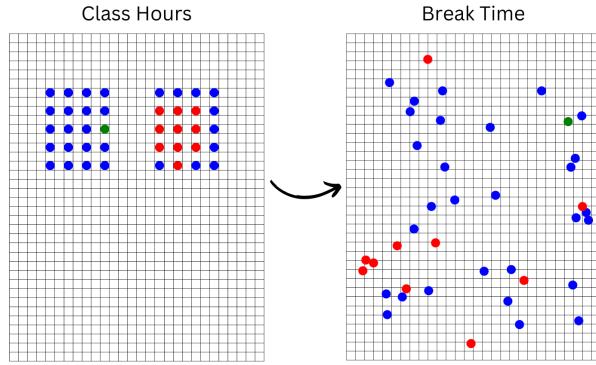
For the movement behavior, we have implemented the 9-hour class with 2 breaks (30 minutes after the end of the 2nd hour and 1 hour after the end of the 4th hour) schedule that has been used in most of the public high schools in the Philippines [51]. In this model, all agents are placed in their designated seats throughout the simulation and are only allowed to move during the scheduled breaks. Agents will be placed again in their designated seats every after breaks. To determine the next position of an agent during a break, the model will calculate a random coordinates for the next position of each agent using the *Random Distance Movement* equation for each iteration:

$$x_i = 0 + \text{rand}(0, 1) * (m) \quad (4.6)$$

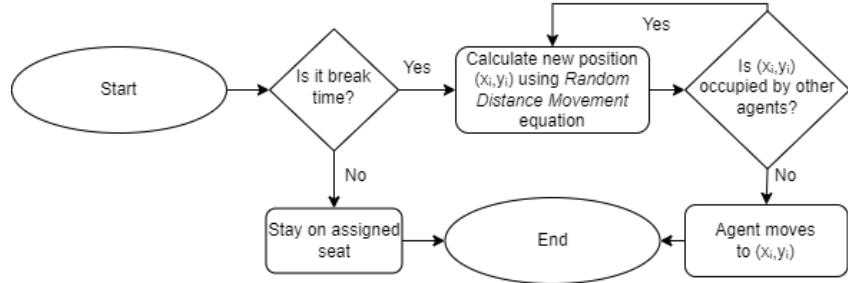
$$y_i = 0 + \text{rand}(0, 1) * (n) \quad (4.7)$$

where:  $m = 7$  = width of the classroom in meters  
 $n = 9$  = length of the classroom in meters  
 $(x_i, y_i)$  = target coordinates for the next position of an agent  
 $\text{rand}(0, 1)$  = function that generates random real number between 0 and 1

The model recalculates a new position in case an agent is already placed in the newly calculated coordinates. Figure 4.5 shows an example of agents moving from their assigned seats to a random location in the classroom during a break using *Random Distance Movement* equation. Figure 4.6 shows the summary of Movement Behavior in a flowchart form that agents follow for each iteration.



**Figure 4.5:** Examples of agents moving from their designated seat to random positions during break time using *Random Distance Movement* equation



**Figure 4.6:** Algorithm of Movement Behavior which all agents perform every iteration

#### 4.4.2 Infection Behavior

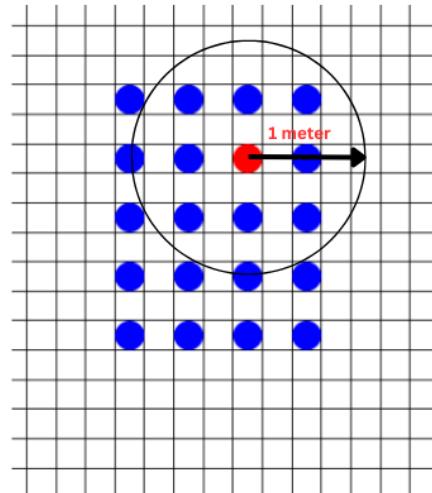
In this model, we have implemented a 2 layer probabilistic decision similar from [45] for the Infection Behavior using the  $Prob_{Cough}$  and  $Prob_{Infect}$  parameters discussed in Section 4.3 to determine the infection status of a susceptible agent upon interaction with an infected. Recall that the parameter  $Prob_{Cough}$  is the probability of an agent performing a cough every 15 minutes while the parameter  $Prob_{Infect}$  is the probability of a susceptible agent of getting infected from a cough of an infected agent. Unlike Cuevas' model [19], each agent does not have dedicated values for the two parameters, hence, a general value was used in this case. For the  $Prob_{Cough}$ , we have used 0.61 as the value gathered in Section 4.3.1. For the  $Prob_{Infect}$ , we used the no mask category from Figure 4.3. Aside from that, we have estimated the following probability values extracted from

Figure 4.3 [3] to simplify the distribution as shown in Table 4.1.

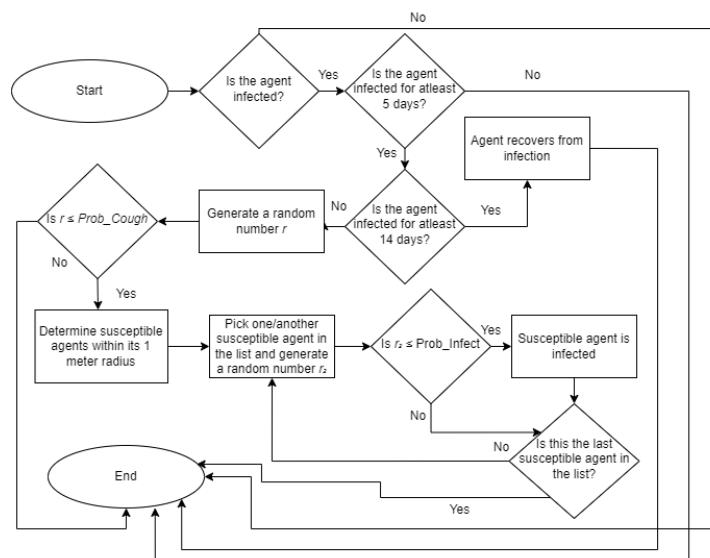
For every iteration, all contagious infected agents will determine whether they will cough or not through a probabilistic decision. For each contagious agent, a random number will be generated within the uniform distribution  $U[0, 1]$  which will be compared to the universal  $Prob_{Cough}$  value. If the generated random number is less than or equal to  $Prob_{Cough}$ , this indicates that a contagious agent will perform cough. By this time, the contagious agent analyzes the existence of susceptible agents within its 1-meter radius Figure 4.7. All susceptible agents within the 1-meter radius will now check whether they will be infected or not by generating another random number within the uniform distribution  $U[0, 1]$ , which will be compared to the  $Prob_{Infect}$ . If the generated random number is less than or equal to the  $Prob_{Infect}$ , the susceptible agent will be considered noncontagious infected, otherwise not. Note that the  $Prob_{Infect}$  value varies depending on the *Euclidean distance* between the susceptible agent and the contagious infected agent. Newly infected agents will be represented with red color circles in the model, these agents remain noncontagious for 4 days. After that, they will eventually become contagious after 5 days prior to infection [34]. For the recovery process, an infected agent will acquire immunity and recover 14 days after getting infected. Figure 4.8 shows the algorithm of Infection Behavior in a flowchart form in which all agents check every iteration.

Distance	Probability(No Mask)
0 - 0.25 meter	0.61
0.26 - 0.50 meter	0.55
0.51 - 0.75 meter	0.38
0.76 - 1.0 meter	0.15
> 1 meter	0.03

**Table 4.1:** Estimated Distance-Variation Probability of COVID-19 infection via cough for two cases, namely, no mask and with surgical mask



**Figure 4.7:** Example of a contagious infected analyzing the existence of susceptible agents within 1 meter radius



**Figure 4.8:** Algorithm of Infection Behavior for all agent in every iteration

## 4.5 Simulations

After defining all the parts (Agents, Behavior, and Environment) in our ABM, this section discusses the sequence of the behaviors and the final list of parameters that were used in the model. Moreover, this section also discusses the model configurations for the 4 scenarios namely SC1 (Base Model), SC2 (Vaccinated Scenario), SC3 (Eating Healthy Scenario), and SC4 (With Comorbidity Scenario) mentioned in the objectives. For the global time setting in the model, since 1 day of class is equivalent to 9 hrs according to [51], this indicates that 1 whole day class is equivalent to 36 iterations (1 iteration is equivalent to 15 mins) in the model. Since we are only considering the infection within the classroom setting, we will skip/ignore the remaining time of the day after class and start with next day. In that 36 iterations per day, agents are only allowed to move on iterations 8 to 9 and 16 to 20 as discussed in Section 4.4.1. On the other hand, all agents check their Infection Behavior for every iteration. This process repeats every day(36 iterations) in the model until the model reaches *maxiter* as shown in Algorithm 2.

### 4.5.1 4 Scenarios

This section discusses the configurations of the 4 different scenarios namely SC1 (Base Model), SC2 (Vaccinated Scenario), SC3 (Eating Healthy Scenario), and SC4 (With Comorbidity Scenario) that were used in the experiments to analyze the transmission of COVID-19 virus in a classroom under different conditions. All scenario has the same set of behaviors, parameters (except *multiplier*), and algorithm. Due to different *multiplier* values, the 4 scenarios varies in the *ProbInfect* values based on different studies discussed in the next subsections.

#### 4.5.1.1 SC1: Base Model

This experiment used the parameters provided in Table 4.2 and the ABM algorithm in Algorithm 2. This model was also used as the basis for the performance produced by the other 3 scenarios. SC1 represents a traditional classroom setting with 40 students that have no certain health or social conditions besides the defined behaviors.

#### 4.5.1.2 SC2: Vaccinated Scenario

A study from the Center for Disease Control and Prevention (CDC) [15] found that mRNA COVID-19 vaccines such as Pfizer and Moderna reduce the risk of infection by 90% for fully vaccinated people compared to unvaccinated. This was represented in the model by incorporating a *multiplier* in the  $Prob_{Infect}$  parameter. A *multiplier* is a factor that amplifies or increases the base value [28]. Note that in this experiment, we assume that all agents in the classroom are vaccinated. To achieve that, we will set the *multiplier* to be equal to -0.90, this indicates that vaccination reduced the  $Prob_{Infect}$  value by 90% in all agents. The new value of  $Prob_{Infect}$  is then calculated using the Equation 4.8 given by:

$$Prob_{Infect} = Prob_{Infect} + Prob_{Infect} * multiplier \quad (4.8)$$

This experiment used the parameters provided in Table 4.3 and the ABM algorithm in Algorithm 2.

#### 4.5.1.3 SC3: Eating Healthy Scenario

A study from Harvard [25] found that people who reported following a healthy diet by eating healthy foods had a 9% lower risk of getting COVID-19. In this scenario, we set the *multiplier* to be equal to -0.1 to represent the reported data. This value applies to all agents in the model, assuming that all agents in the classroom eat healthy foods. The new  $Prob_{Infect}$  in this scenario will be calculated using Equation 4.8. This experiment used the parameters provided in Table 4.4 and the ABM algorithm in Algorithm 2.

#### 4.5.1.4 SC4: With Comorbidity Scenario

In this scenario, we assumed that all agents in the classroom suffer from comorbidities like cancer, chronic lung diseases, chronic liver disease, hypertension, obesity, and diabetes. According to studies [2, 4], the relative risk ratio of a person suffering from comorbidities ranges from 1.3 to 1.9. This means that person suffering from medical conditions has a 30% to 90% more chance of getting infected compared to people without these conditions. Since we are considering various sicknesses in this model, we will just

Parameter	Value	Units	Description
$maxiter$	2000	iteration	maximum number of iteration in the model
$iter_{val}$	15	minutes/iteration	real life equivalent of 1 iteration in the model
$m$	7	meter	width of the classroom: the total horizontal distance between the outermost edges of the classroom
$n$	9	meter	length of the classroom: the total vertical distance between the outermost edges of the classroom
<i>Seat Distance</i>	0.5	meter	front, back, and sides distance of seats in the classroom
$grid_{cell}$	0.25	meter	side length of each <i>grid cell</i> in the grid
$rad_{infect}$	1	meter	radius of infection for Infection Behavior
$Prob_{Cough}$	0.61	-	infected agent's probability of coughing per iteration
$Prob_{Infect}$	see Table 4.1	-	susceptible agent's probability of getting infected from a cough
<i>multiplier</i>	0	-	percentage increase or decrease of the $Prob_{Infect}$ 's base value
$S$	39	agents	initial number of susceptible agents
$I$	1	agents	initial number of infected agents
$R$	0	agents	initial number of recovered agents

**Table 4.2:** Final list of parameters required for the SC1 model

simplify the increase by setting the *multiplier* to be equal to 0.5. The new  $Prob_{Infect}$  in this scenario will be calculated using Equation 4.8. This experiment used the parameters provided in Table 4.5 and the ABM algorithm in Algorithm 2.

Parameter	Value	Units	Description
$maxiter$	2000	iteration	maximum number of iteration in the model
$iter_{val}$	15	minutes/iteration	real life equivalent of 1 iteration in the model
$m$	7	meter	width of the classroom: the total horizontal distance between the outermost edges of the classroom
$n$	9	meter	length of the classroom: the total vertical distance between the outermost edges of the classroom
<i>Seat Distance</i>	0.5	meter	front, back, and sides distance of seats in the classroom
$grid_{cell}$	0.25	meter	side length of each <i>grid cell</i> in the grid
$rad_{infect}$	1	meter	radius of infection for Infection Behavior
$Prob_{Cough}$	0.61	-	infected agent's probability of coughing per iteration
$Prob_{Infect}$	see Table 4.1	-	susceptible agent's probability of getting infected from a cough
$multiplier$	-0.90	-	percentage increase or decrease of the $Prob_{Infect}$ 's base value
$S$	39	agents	initial number of susceptible agents
$I$	1	agents	initial number of infected agents
$R$	0	agents	initial number of recovered agents

**Table 4.3:** Final list of parameters required for the SC2 model

Parameter	Value	Units	Description
$maxiter$	2000	iteration	maximum number of iteration in the model
$iter_{val}$	15	minutes/iteration	real life equivalent of 1 iteration in the model
$m$	7	meter	width of the classroom: the total horizontal distance between the outermost edges of the classroom
$n$	9	meter	length of the classroom: the total vertical distance between the outermost edges of the classroom
<i>Seat Distance</i>	0.5	meter	front, back, and sides distance of seats in the classroom
$grid_{cell}$	0.25	meter	side length of each <i>grid cell</i> in the grid
$rad_{infect}$	1	meter	radius of infection for Infection Behavior
$Prob_{Cough}$	0.61	-	infected agent's probability of coughing per iteration
$Prob_{Infect}$	see Table 4.1	-	susceptible agent's probability of getting infected from a cough
<i>multiplier</i>	-0.10	-	percentage increase or decrease of the $Prob_{Infect}$ 's base value
$S$	39	agents	initial number of susceptible agents
$I$	1	agents	initial number of infected agents
$R$	0	agents	initial number of recovered agents

**Table 4.4:** Final list of parameters required for the SC3 model

Parameter	Value	Units	Description
$maxiter$	2000	iteration	maximum number of iteration in the model
$iter_{val}$	15	minutes/iteration	real life equivalent of 1 iteration in the model
$m$	7	meter	width of the classroom: the total horizontal distance between the outermost edges of the classroom
$n$	9	meter	length of the classroom: the total vertical distance between the outermost edges of the classroom
<i>Seat Distance</i>	0.5	meter	front, back, and sides distance of seats in the classroom
$grid_{cell}$	0.25	meter	side length of each <i>grid cell</i> in the grid
$rad_{infect}$	1	meter	radius of infection for Infection Behavior
$Prob_{Cough}$	0.61	-	infected agent's probability of coughing per iteration
$Prob_{Infect}$	see Table 4.1	-	susceptible agent's probability of getting infected from a cough
<i>multiplier</i>	0.50	-	percentage increase or decrease of the $Prob_{Infect}$ 's base value
$S$	39	agents	initial number of susceptible agents
$I$	1	agents	initial number of infected agents
$R$	0	agents	initial number of recovered agents

**Table 4.5:** Final list of parameters required for the SC4 model

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**Algorithm 2** Pseudo-code for the COVID-19 transmission in a classroom setting

---

**Input:**  $k = 0, maxiter, interval, m, n, grid_{cell}, rad_{infect}, Prob_{Cough}, Prob_{Infect}[], S, I, R$

**Output:** Time Series graph containing Cumulative Number of Infected agents per iteration.

```

1:  $S(k) \leftarrow \text{GenerateSusceptibleAgents}(S);$ 
2:  $I(k) \leftarrow \text{GenerateInfectedAgents}(I);$ 
3:  $R(k) \leftarrow \text{GenerateRecoveredAgents}(R);$ 
4:  $\text{generateGrid}(m, n, grid_{cell});$ 
5:  $\text{assignSeat}(S(k), I(k), R(k));$ 
6:  $multiplier \leftarrow 0$ 
7:  $counter \leftarrow 0$ 
8: _____
9: while  $k < maxiter$  do
10: _____
11:   if  $counter == 36$  then
12:      $counter = 0$ 
13:   for each  $a_j \in S(k), I(k), R(k)$  do                                 $\triangleright$  Rule I: Movement Behavior
14:     if ( $counter \geq 8$  AND  $counter \leq 9$ ) OR ( $counter \geq 16$  AND  $counter \leq 20$ ) then
15:        $\text{moveAgent}(a_j);$ 
16:     else
17:        $\text{goBackSeat}(a_j);$ 
18: _____
19:   for each  $i_j \in I(k)$  do                                 $\triangleright$  Rule II: Infection Behavior
20:     if  $\text{isInfectedfor5Days}(i_j);$  then
21:        $i_j.\text{state} \leftarrow \text{"Contagious Infected"}$ 
22:     if  $\text{isInfectedfor14Days}(i_j);$  then
23:        $\text{convertToRecovered}(i_j, R(k));$ 
24:     if  $\text{isContagious}(i_j);$  then
25:       if  $\text{rand}(0, 1) \leq Prob_{Cough}$  then
26:          $T \leftarrow \text{findAllSusceptible}(i_j, rad_{infect});$ 
27:         if  $|T| == 0$  then
28:           skip
29:         else
30:           for each  $s_j \in T$  do
31:              $dist \leftarrow \text{getDistance}(i_j, s_j);$ 
32:              $Prob_{Infect} \leftarrow \text{getProbInfect}(dist, Prob_{Infect}[], multiplier);$ 
33:             if  $\text{rand}(0, 1) \leq Prob_{Infect}$  then
34:                $\text{convertToInfected}(s_j, I(k));$ 
35:    $\text{store}(|I(k)|, k);$ 
36:    $counter \leftarrow counter + 1$ 
37:    $k \leftarrow k + 1$ 
38:  $\text{generateTimeSeries}();$ 

```

---

### 4.5.2 Model Output

To eliminate bias in the results, average output data from 10 runs were collected for each experiment/scenario. Each scenario (SC1, SC2, SC3, SC4) generated the following data below at the end of the simulations. These data were used in the analysis section discussed in Chapter 5.

1. Record of cumulative number of infected agents per iteration
2. Time Series containing cumulative number of infected agents per iteration
3. Day with highest number of infection (peak day)
4. Number of Infected agents during peak
5. Average rate of newly infected agents from day 1 to peak day
6. Day when the infection ends

# Chapter 5

## Results and Discussion

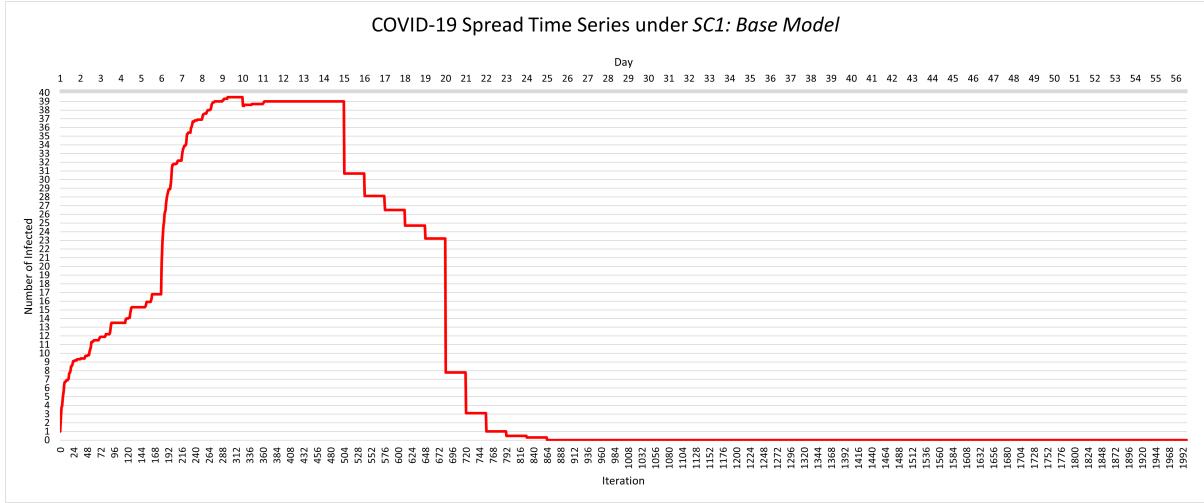
This section discusses the multiple experiments conducted to generate necessary data provided in Section 4.5.2 that could explain the nature of COVID-19 transmission in a classroom under various scenarios. The data presented in this section are the result of the simulations of the proposed ABM using the *GAMA Platform*. This section discusses the results obtained from the simulations of the 4 different scenarios (SC1, SC2, SC3, and SC4) defined in Section 4.5.1. Aside from that, an analysis using key variables such as the average rate of newly infected agent, peak day of the infection, number of infected agents at peak, end of infection, and the overall trend of the series was made to determine the difference of SC2, SC3, and SC4 from SC1. Sensitivity analysis was also performed to analyze the effect of increasing/decreasing parameter values in the overall transmission of virus. This helped us determine the sensitive parameters and identify the combinations of parameter values that can provide the fastest and slowest COVID-19 transmission for each scenario.

### 5.1 Simulation of the 4 Scenarios

#### 5.1.1 SC1: Base Model

In this experiment, we used the input parameters defined in Table 4.2 for our simulation. Notice from Figure 5.1, the spread of the virus from Day 1 to 5 started slow with an average of 3.36 newly infected per day, resulted in an increasing concave downward movement on the time series. This delay happened due to the model's configuration where we set the number of initially infected individuals to 1 across all the simulations. Furthermore, the incubation period of COVID-19 restrict newly infected agents on Day 1 to 5 from infecting susceptible agents in the area, resulting in infection delay despite of

their infection status. 12 newly infected agents from Day 1 are expected to be contagious by Day 6 due to incubation period (5 days after infection). The incubation period nature of COVID-19 resulted in an increased rate of virus transmission on Day 6 to 9, reporting 5.67 newly infected agent per day, 68.75% increase on the rate compared to Day 1 to 5 (3.36). This can also be attributed to the fact that the initial infected agent was able to infect 30% (12 agents) of the population during Day 1. SC1 hit a peak of infected at the end of Day 9, infecting 98.75%(39.5 agents) of the population. After that, the number of infected agents decreased from Day 10 and reached zero by Day 25.

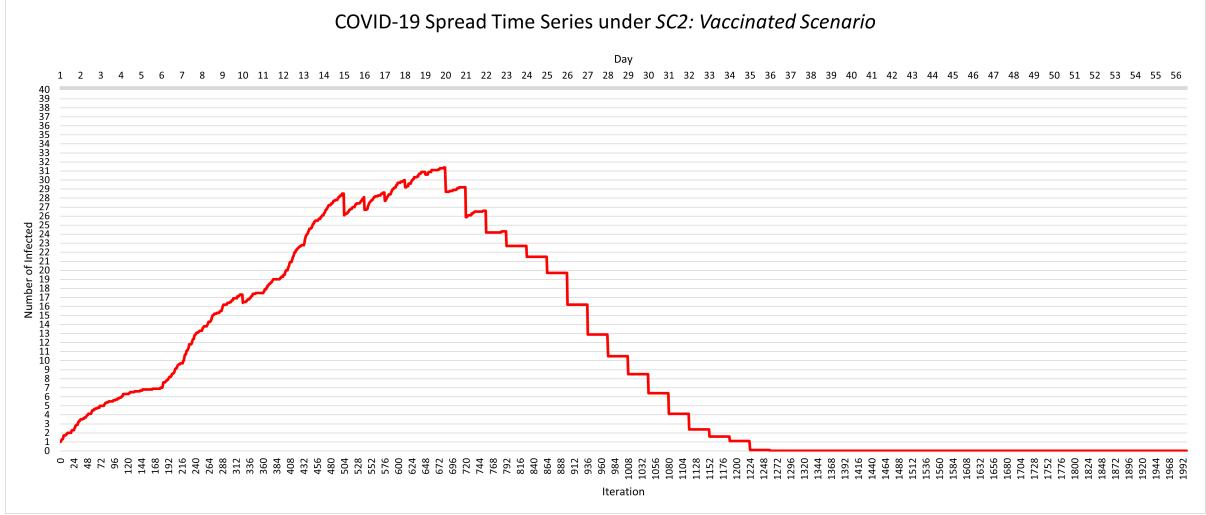


**Figure 5.1:** Time series graph of the number of infected agents generated from SC1 using the parameters provided in Table 4.2 from Day 1 to 56

### 5.1.2 SC2: Vaccinated Scenario

During Day 1 to Day 2, SC2 shows a slow increase in the number of infected agents with an average of 2.25 newly infected agent per day compared to SC1(3.36) as shown in Figures 5.2 and 5.5. In this experiment, the initial infected agent infects 7 susceptible agents from Day 1 to 5, 58% lower than the SC1(16.8 agents) for that time period. This decrease can be attributed to the vaccination's effect on reducing the probability of infection for all the vaccinated susceptible agents. During Days 6 to 14, the rate of newly infected agent increases partially to 2.38, a slight increase compared to Day 1 to 5 (2.25) as

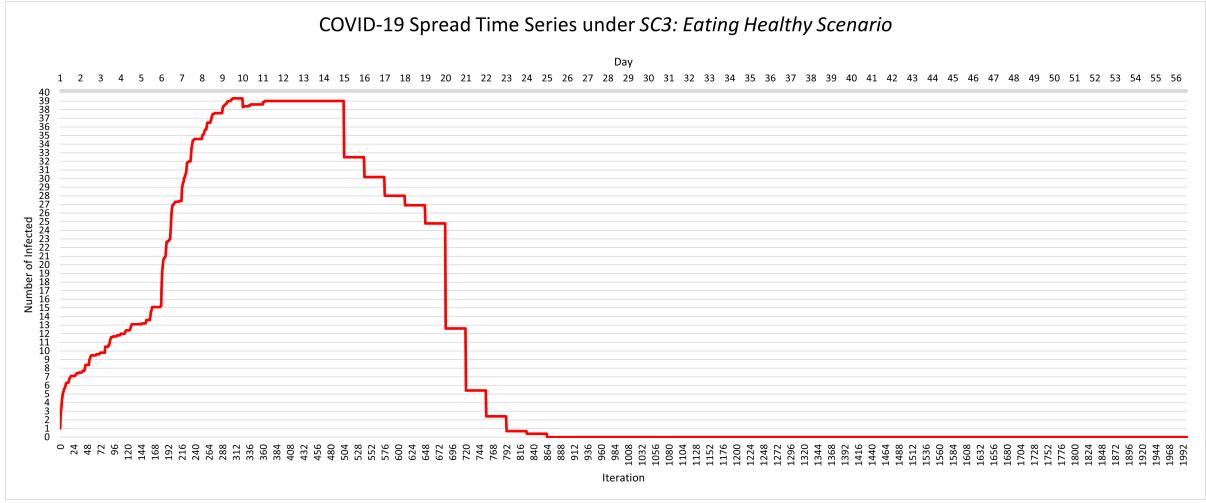
newly infected individuals from Days 1 to 6 become contagious. Multiple infected agents began to recover on Days 9 and 14 even before the time series reached the peak infection, as opposed to SC1, in which we reached the peak first before infected agents began to recover. SC2 reached a peak of infection at the end of Day 19, infecting 78% (31.4 agents) of the population, 20% lower than the peak infection of SC1 (39.5 agents). Furthermore, the peak of infection in SC2 (Day 19) occurred 10 days later than the SC1 (Day 9). In totality, a much more spread and flat curve COVID-19 spread can be observed from SC2 when compared to the SC1 as shown in Figure 5.5. This shows the impact of vaccines on delaying the spread of the virus by reducing the peak number of infected agents and shifting the peak to the right as much as possible, resulting in a much flatter epidemic curve. On a larger scale (i.e. COVID 19 spread in a country), flattening the curve by spreading out the rate of infection is the primary objective in order to keep our healthcare system and infrastructure from getting overwhelmed [29], SC2 was able to illustrate that as shown in Figure 5.5.



**Figure 5.2:** Time series graph of Number of Infected agents generated from SC2 using the parameters provided in Table 4.3 from Day 1 to 56

### 5.1.3 SC3: Eating Healthy Scenario

In this simulation, we look at how a healthy diet affects the overall distribution of COVID-19 in a classroom context. Upon inspection of the graph, SC3 generated a time series graph that is similar to SC1 than SC2 as shown in Figure 5.3 and 5.5. The initial infected agent was able to infect 15.2 susceptible individuals from Day 1 to 5, which is 9.52% lower than the SC1(16.8). Similar to the previous scenarios, the rate of newly infected agent in SC3 rises from 3.04 on Day 1 to 5 to 6.02 on Day 6 to Day 10, a 98% increase in rate as the newly infected individuals become contagious starting Day 6. SC3 caused a slight delay in the overall spread as the overall curve in the time series was slightly pushed to the right compared to SC1 as shown in Figure 5.5. This can be verified using the rates of newly infected agent per day of the two scenarios where SC1 and SC3 had 4.38 and 4.36 respectively from Day 1 to peak day(Day 9). The peak number of infected agents was reached at the end of Day 9 infecting 98.25% (39.3 agents) of the population. On Day 10, some infected agents began to recover, and by Day 25, the number of infected agents dropped to zero. This simulation demonstrates that despite the benefits an agent can receive from eating healthy as discussed in Section 4.5.1.3, this may not have a significant influence in a population like a classroom unlike SC2. Nonetheless, while eating well may slightly slow the spread of COVID-19 at the start (Day 1 to 9), it will certainly still reach a substantial number of infected agents at the peak as in the SC1.

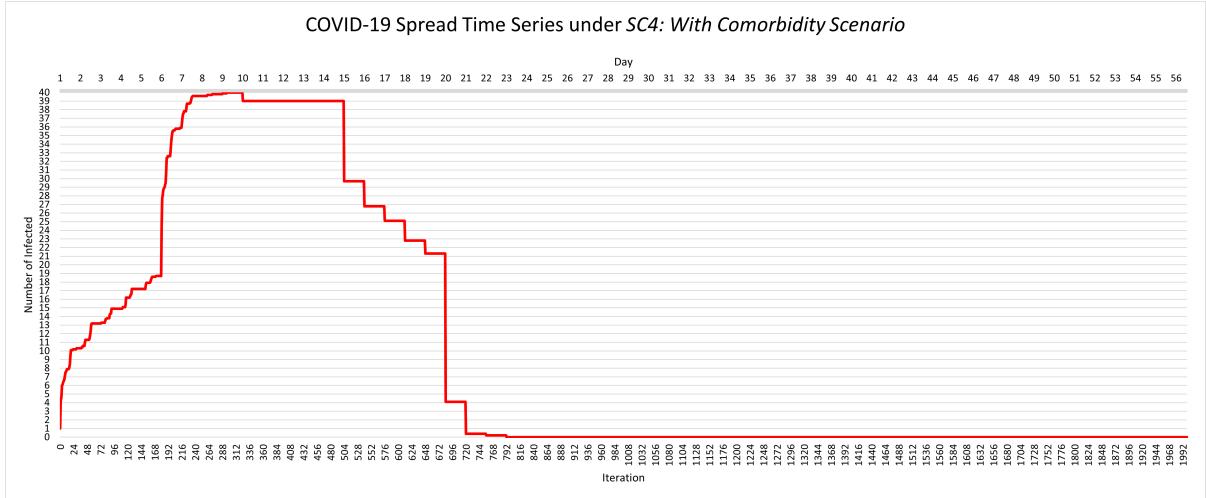


**Figure 5.3:** Time series graph of Number of Infected agents generated from SC3 using the parameters provided in Table 4.4 from Day 1 to 56

#### 5.1.4 SC4: With Comorbidity Scenario

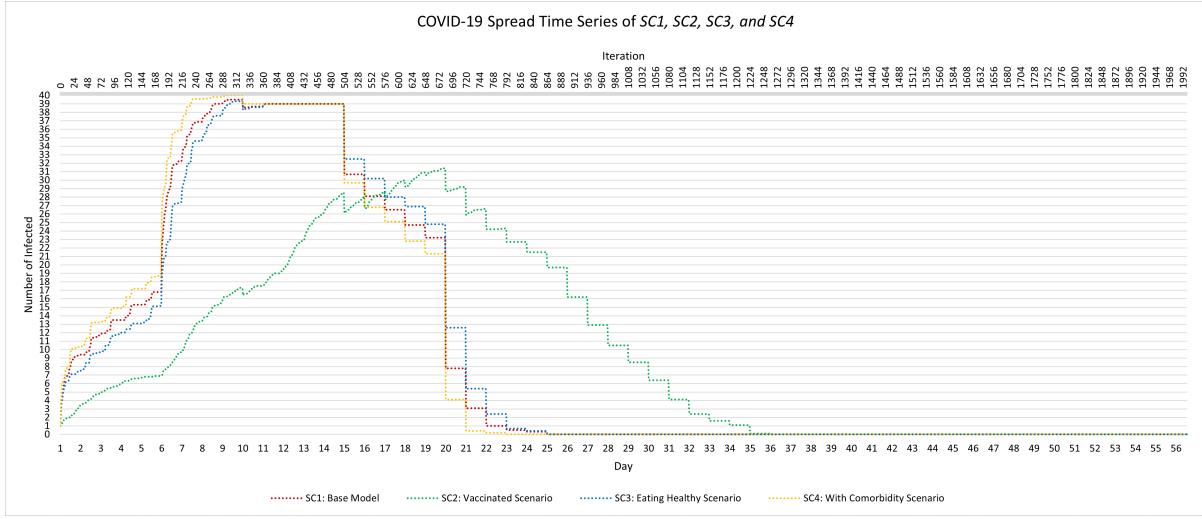
Among the four scenarios, SC4 exhibits the highest number of newly infected agent from Day 1 to 5, infecting 18.7 susceptible agents, an 11.30% more than SC1(16.8). This is due to the substantially higher probability of infection caused by comorbidities, putting vulnerable agents at a higher risk of infection as discussed in Section 4.5.1.4. The collective high risk of all susceptible agents suffering from comorbidity caused the fastest rate of infection among the other scenario recording an average of 3.74 newly infected agent per day (SC1=3.36, SC2=1.40, SC3=3.04, SC4=3.74) from Day 1 to 5 as shown in Figure 5.5. The highest rate of infection in SC4 can be seen during Days 6 infecting 17.2 agents per day (SC1=15.4, SC2=2.7, SC3=12.2, SC4=17.2) as the newly infected from Day 1 to 5 become contagious. Peak infection was reached on Day 9 infecting all the susceptible agents in the classroom. Similar to the SC1 and SC3, SC4 reached the peak infection first before some infected agents began to recover. The time series produced SC4 slightly shifts to the left and produced a steeper slope from Day 1 to peak (Day 9) when compared to the SC1 as shown in Figure 5.5. This implies a faster spread of virus for SC4 as infected agents were able to infect more susceptible agents every iteration due

to the high value of the probability of infection relative to the SC1.



**Figure 5.4:** Time series graph of Number of Infected agents generated from SC4 using the parameters provided in Table 4.5 from Day 1 to 56

Figure 5.5 and Table 5.1 shows that the SC2 attained the slowest COVID-19 transmission among the list as it lowers the peak number of infected agents by 8.1 agents and delay the peak day by up to 10 days when compared to S1. Moreover, SC2 was able to flatten the overall curve producing an average of 1.65 newly infected agent per day (SC1=4.38, SC2=1.65 SC3=4.36, SC4=4.44) from Day 1 to peak. SC3 comes in second place considering the slight decrease in the rate of newly infected agent from Day 1 to peak (SC1=4.38, SC2=1.65 SC3=4.36, SC4=4.44) that caused a slight tilt to the right in the graph relative to the SC1; despite having a close value of the peak number of infections and peak day to SC1 as shown in Figure 5.1, SC3 reported a lower value of infected agents for every iteration, causing a slight delay in virus spread. SC1 comes next in the rank. Lastly, SC4 Scenario resulted as the worst-case scenario as it produced an average of 4.44 newly infected agents from Day 1 to peak, fastest among other scenarios(SC1=4.38, SC2=1.65 SC3=4.36, SC4 = 4.44). Furthermore, the overall curve slightly tilts to the left of the SC1 which indicates a faster rate of infection.



**Figure 5.5:** Time Series graphs of the number of infected agents of the 4 Scenarios namely SC1:Base Model, SC2:Vaccinated Scenario, SC3:Eating Healthy Scenario, and SC4:With Comorbidity Scenario.

Scenarios	Peak Day (Day)	Number of Infected Agents at Peak Day (agents)	End of Infection Day (Day)
SC1	9	39.5	25
SC2	19	31.4	36
SC3	9	39.3	25
SC4	9	40	23

**Table 5.1:** Generated values of Peak day, Number of Infected at peak, and End of infection day for the 4 Scenarios (SC1, SC2, SC3, SC4) using the proposed ABM.

## 5.2 Sensitivity Analysis

Sensitivity Analysis is a statistical tool to analyze the effects of variations and uncertainty in input on the resulting output of the model [44]. Most studies conduct Sensitivity Analyses of their ABM for various reasons, including but not limited to a.) Quantify the variability in ABM outcomes resulting from changes in model parameters b.) Validate the Model by comparing the output to real-life scenarios or reported real data and c.)

Examine the Robustness of the Model which were used as the goal of the Sensitivity Analysis conducted in the studies presented in [39], [30], and [26] respectively. Depending on the objective and structure of the model, there are various sensitivity analysis methodologies, including but not limited to a.) One-factor-at-a-time b.) Global Sensitivity Analysis and c.) Regression-based Methods. Some research concentrates largely on wider global behavior, such as movement settings and external policies [19], while others concentrate on a more quantitative input parameter like infection rate, initial number of infected agents, etc. In this section, we will conduct One Factor at a time (OFAT) and Two Factor at a time (2FAT) analysis to measure the impact of changing single or multiple input parameter values defined in Section 4.5.1 particularly the  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  on the overall trend of the COVID-19 spread in a classroom under a particular scenario. With the help of Sensitivity Analysis, we can be able to determine which parameter/s are the most sensitive and need to be controlled in order to come up with a setting/scenario that produces the slowest and fastest COVID-19 transmission.

### 5.2.1 One Factor at a Time Sensitivity Analysis

For each scenario, we subjected our 3 parameters namely  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  to OFAT Sensitivity Analysis. The process starts off by increasing each parameter value by -20%, -10%, -5%, 0%, 5%, 10%, and 20%, we will refer to each of the increases as an experimental case (i.e -20% increased  $Prob_{Cough}$  in SC1 experimental case). Average values of 10 runs for each experimental case were collected to avoid biased data. We also set the 0% case as the Base Case for each scenario. After that, we collected the difference between the number of infected agents per iteration of the Base Case and each of the experimental cases (-20%, -10%, -5%, 0%, 5%, 10%, or 20% increase) in order to quantify the change in the number of infected agents per iteration. For each experimental case (i.e -20% increased  $Prob_{Cough}$  vs Base Case), we manually take the Maximum Increase and Maximum Decrease of the simulation by taking the lowest and highest difference value respectively. These two variables measure the largest deviation/change in the number of infected agents across all iteration of an experimental case from the Base Case. Difference in peak day, peak number of infected agents, and end

of infection day were also gathered to analyze the effect of particular parameter increase on the model output.

### 5.2.1.1 OFAT SC1: Base Model

In this section, we analyze the responses of the model output from varying one parameter at a time under SC1. Figure 5.6 shows the data for the Maximum Decrease, Maximum Increase, Minimum Decrease, and Minimum Increase in the number of infected agents generated by performing OFAT on the three parameters in this Scenario. On the other hand, Table 5.2 presents the list of parameters that produced the Highest Decrease and Increase in number of infected agents for each experimental case from Figure 5.6.

First, we discuss the parameters that resulted in the Highest Decrease in the number of infected agents for each experimental case in Table 5.2. Out of the three parameters,  $Prob_{Infect}$  and  $Prob_{Cough}$  are the two most sensitive to increases of -5%, -10%, and -20%. Each of the mentioned parameter increase results in an 8%, 9.5%, and 14.75% decreases in the number of infected agents compared to the Base Case as shown in Figure 5.6. Maximum Decreases in the number of infected agents occurred at the start of the spread particularly on Days 5 to 6 as shown in Figures 5.7, 5.8, and 5.9.

This might be a result of  $Prob_{Infect}$ 's dependency on the distance between susceptible agent and infected agent. The model result also suggests that increasing  $Seat\ Distance$  value by -5% and -10% has no effect in the number of exposed seatmates (12 agents) and its corresponding probability of infection during class hours compared to Base Case. However, increasing  $Seat\ Distance$  by -20% increased the number of affected seatmates to 20 agents. Those 8 newly added exposed agent has a relatively low probability value (0.15) due to their distant location from the infected agent based on their seating arrangement, making it insignificant in this instance. This shows how increasing  $Seat\ Distance$  by -5% to -20% does not provide much change in the overall trend of the virus under SC1. Making  $Prob_{Infect}$  as the most sensitive among the three when increased by -5% to -20%.

This implies that the impact of decreased  $Prob_{Infect}$  value on reducing the number of infected agent at the start of the spread (Day 5 to 6) is greater than the impact of decreased  $Seat\ Distance$  on increasing the number of infected agent and decreased  $Prob_{Cough}$  on decreasing the number of infected agent as shown in Figures 5.13.

On the other hand, *Seat Distance* is the most sensitive to 5%, 10%, and 20% increases as shown in Table 5.2. Each of the increases results in a 7.5%, 7.25%, and 9.25% decrease in the number of infected agents compared to the Base Case provided in Figure 5.6. In contrast to decreased *Seat Distance*, increasing *Seat Distance* by 5%, 10%, and 20% significantly reduced the number of exposed seatmates from 12 to 8 agents per cough event during class hours. This results in a much lower probability of infection for the seatmates of an infected agent as shown in Table 4.1 as opposed to the case of decreased *Seat Distance* discussed above.

The second row of Table 5.2 contains the parameters that produced the highest increase in number of infected agents for all percentage increases.  $Prob_{Infect}$  produced the highest increase in the number of infected agents when subjected to -5%, -10%, and -20% increases. Each of the increases results in a 5.5%, 8.5%, and 13.5% increase in the number of infected agents compared to the Base Case as shown in Figure 5.6. This indicates that directly decreasing the value of  $Prob_{Infect}$  results in a significant decrease in the number of infected agents per iteration as compared to the impacts of decreased  $Prob_{Cough}$  or decreased *Seat Distance*. Moreover, this resulted in a delay in the peak of infection by up to 3 days as shown in Table 5.3.

In the case of 5%, 10%, and 20% increases,  $Prob_{Infect}$  remained as the most sensitive parameter producing 6.75%, 5.25%, and 9.5% increases in the number of infected agents which occurred on Day 6 to 7. This shows that at the start of spread, the impact of an increased  $Prob_{Infect}$  is much greater than the impact of increased  $Prob_{Cough}$  on increasing the number of infected agent and the impact of increased *Seat Distance* on decreasing the number of infected agent as shown in Figure 5.10, 5.11, and 5.12 respectively.

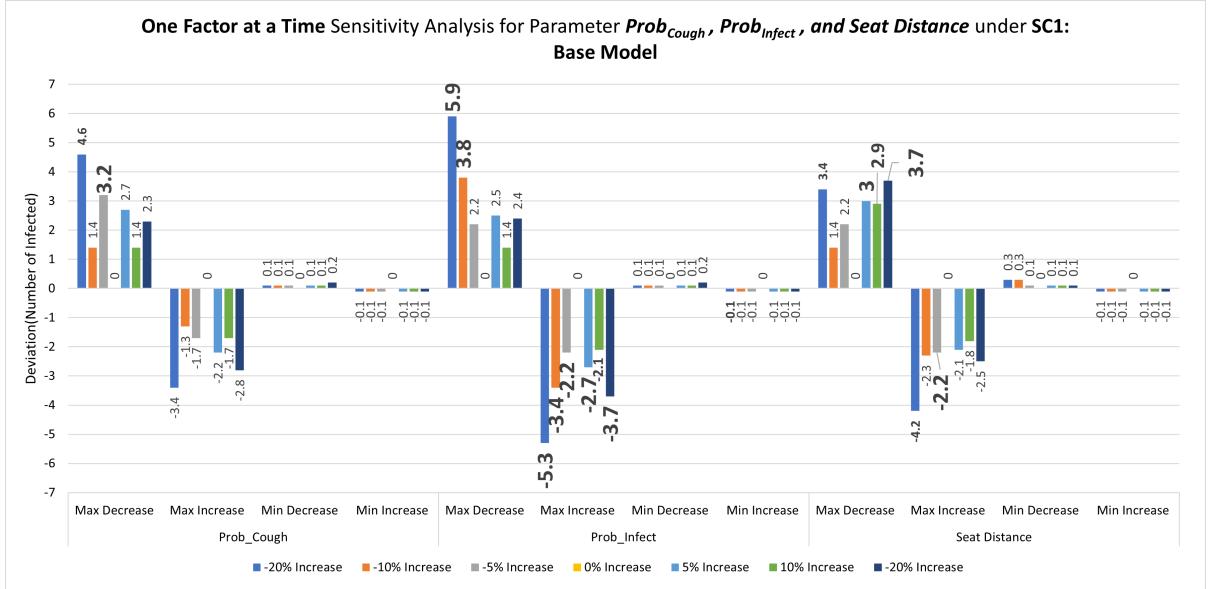
The overall findings imply that we should aim for the lower value of  $Prob_{Infect}$  as it causes the highest decrease in the number of infected agents among all the decreased parameter values both at the beginning and end of infection. This indicates a more distributed and slow transmission of virus within the area. Likewise, an increased value of *Seat Distance* can also effectively delay the spread of the virus by reducing the number of infected agents, particularly at the end of the spread. On the other hand, an increased value of  $Prob_{Infect}$  led to a significant increase in the number of infected agents, indicating that a high value of  $Prob_{Infect}$  should be avoided to prevent further increase in the

	-20% Increase	-10% Increase	-5% Increase	0% Increase	5% Increase	10% Increase	20% Increase
Parameter With Highest Decrease	$Prob_{Infect}$	$Prob_{Infect}$	$Prob_{Cough}$	-	$Seat\ Distance$	$Seat\ Distance$	$Seat\ Distance$
Parameter With Highest Increase	$Prob_{Infect}$	$Prob_{Infect}$	$Prob_{Infect}$	-	$Prob_{Infect}$	$Prob_{Infect}$	$Prob_{Infect}$

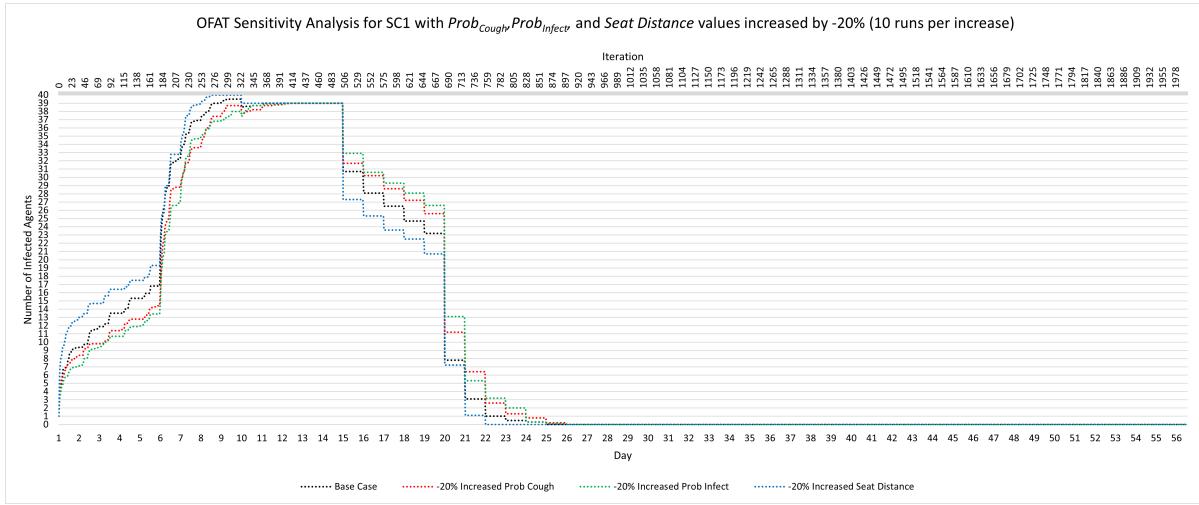
**Table 5.2:** List of parameters that generated Highest Decrease and Highest Increase for each experimental case (-20%, -10%, -5%, 0%, 5%, 10%, 20% Increase) from conducting OFAT Sensitivity Analysis on parameters namely  $Prob_{Infect}$ ,  $Prob_{Cough}$ , and  $Seat\ Distance$  under SC1.

transmission of COVID-19 virus.

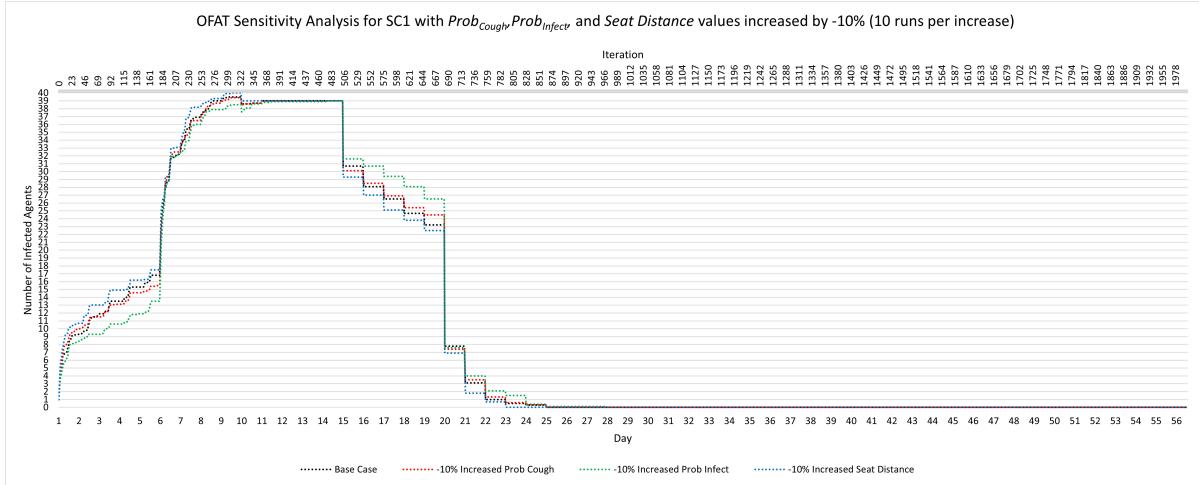
Lastly, this part of the result validates the model as it follows the same principle in real life [54], where having a low  $Prob_{Infect}$  value and increased  $Seat\ Distance$  can result in a much slower spread virus while increasing  $Prob_{Infect}$  and decreasing  $Seat\ Distance$  do otherwise.



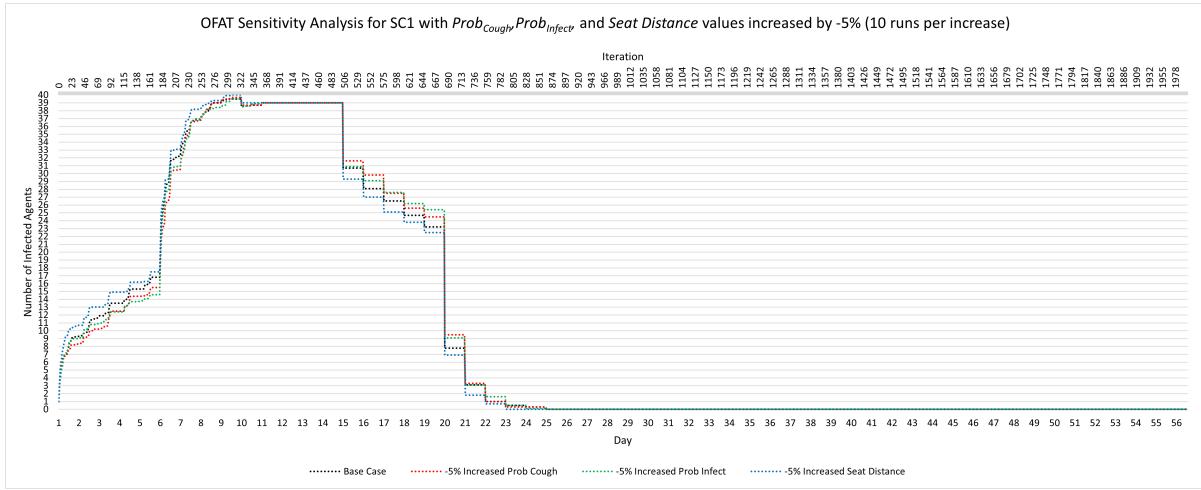
**Figure 5.6:** Generated Maximum Decrease, Maximum Increase, Minimum Decrease, and Minimum Increase in number of infected individuals produced from conducting OFAT Sensitivity Analysis on the three parameters namely  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  under SC1



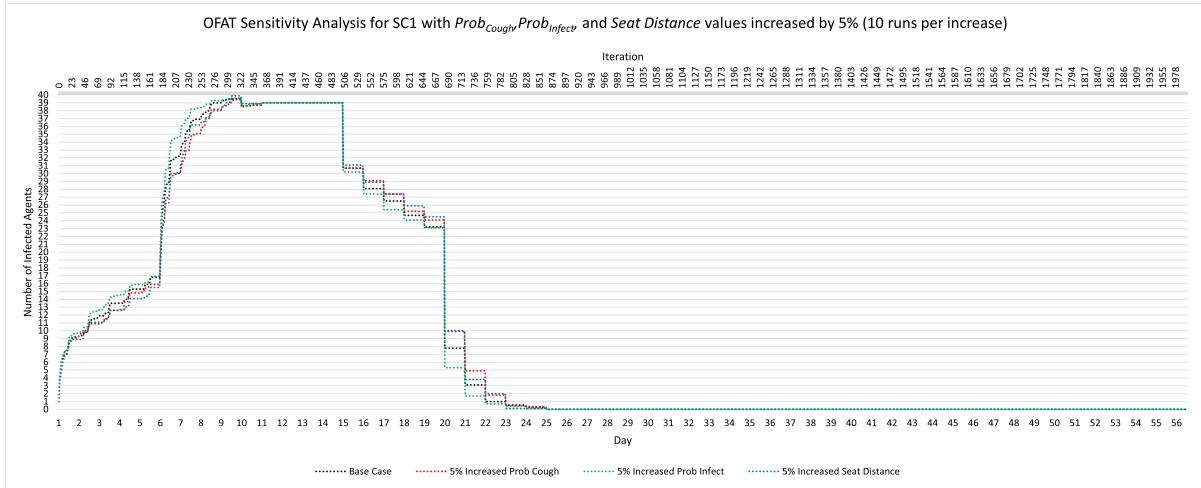
**Figure 5.7:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by -20% under SC1



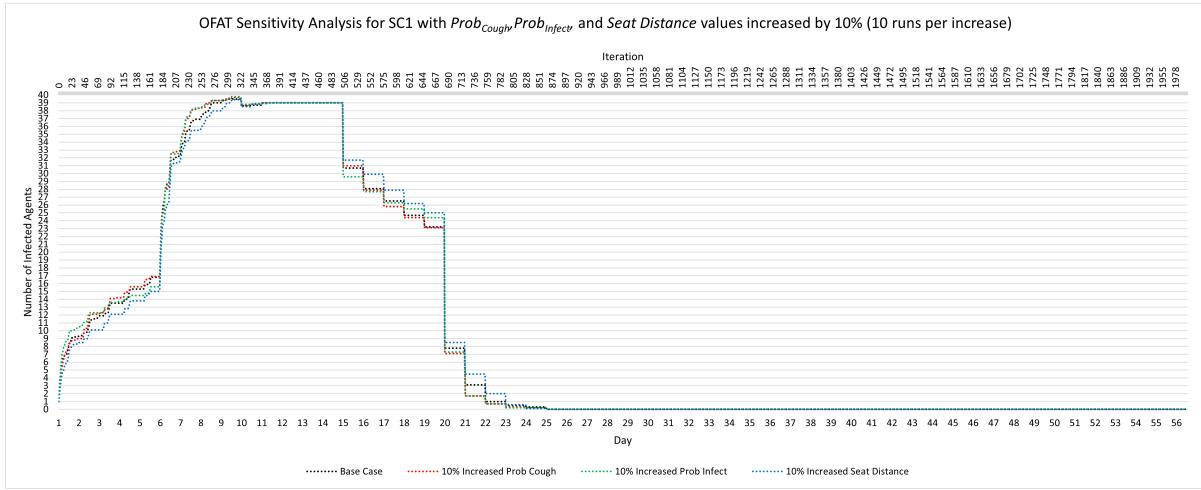
**Figure 5.8:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by -10% under SC1



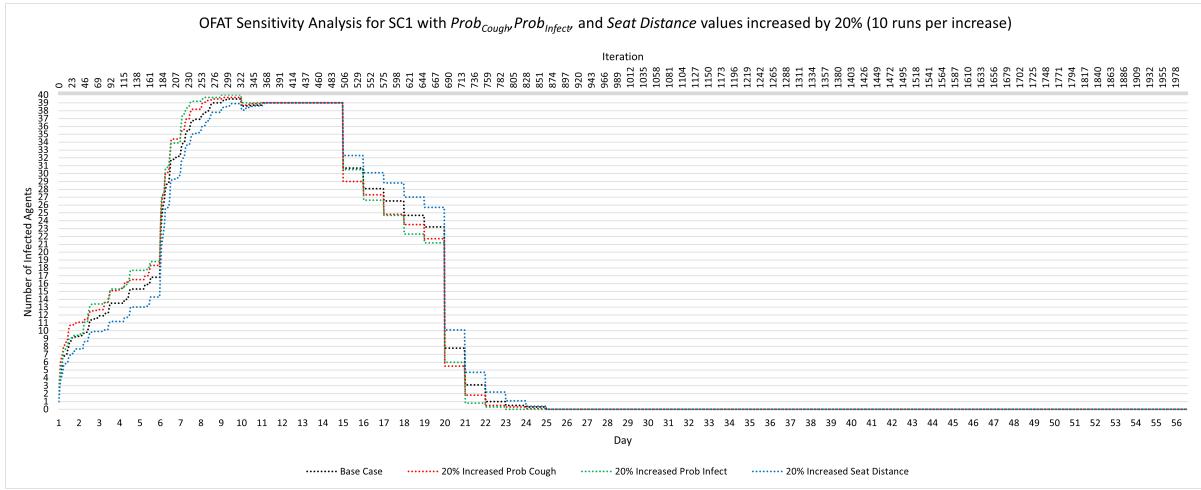
**Figure 5.9:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by -5% under SC1



**Figure 5.10:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by 5% under SC1



**Figure 5.11:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by 10% under SC1



**Figure 5.12:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by 20% under SC1

Parameter	Parameter Increase													
	-20%		-10%		-5%		0%		5%		10%		20%	
	Peak Day	Peak Number of Infected	Peak Day	Peak Number of Infected	Peak Day	Peak Number of Infected	Peak Day	Peak Number of Infected	Peak Day	Peak Number of Infected	Peak Day	Peak Number of Infected	Peak Day	Peak Number of Infected
$Prob_{Cough}$	12	39	9	39.4	9	39.7	9	39.5	9	39.4	9	39.7	9	39.7
$Prob_{Infect}$	12	39	14	39	9	39.5	9	39.5	9	39.6	9	39.8	9	40
$Seat Distance$	8	40	9	40	9	39.5	9	39.5	9	39.5	9	39.4	11	39

**Table 5.3:** Peak Day and Number of Infected at Peak per experimental case (-20%, -10%, -5%, 0%, 5%, 10%, 20% increase) of the three parameters namely  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat Distance$  subjected to OFAT Sensitivity Analysis under SC1

### 5.2.1.2 OFAT SC2: Vaccinated Scenario

This section discusses the results of the model from varying one parameter at a time under SC2. Figure 5.13 shows the data for the Maximum Decrease, Maximum Increase, Minimum Decrease, and Minimum Increase in the number of infected agents for this scenario. Table 5.4 presents the list of parameters that produced the Highest Decrease and Increase in the number of infected agents for each experimental case from Figure 5.13.

Unlike SC1,  $Seat Distance$  and  $Prob_{Cough}$  produced the Highest Decrease in the number of infected agents when increased by -5%, -10%, and -20% as shown in Table 5.4. Each of the parameter increase results in a 6.5%, 12.25%, and 20.5% decreases in the number of infected agents compared to the Base Case. These increases occurred around Days 17, 25, and 26 as shown in Figure 5.13.

Notice how close the Maximum Decrease values of  $Prob_{Infect}$  and  $Seat Distance$  when increased by 5% in Figure 5.13; this shows that  $Seat Distance$  responded most sensitively to increases of 5%, 10%, and 20% by producing 16%, 11%, and 14.25% decrease in the number of infected agents, respectively. It can be observed that directly increasing the  $Prob_{Infect}$  value produced a relatively smaller deviation in number of infected agent compared to other parameters due to its low value. The summary results in Table 5.5 shows the change in peak day and peak number of infections of each increase, validating the sensitivity of  $Seat Distance$  in the experimental cases where low  $Prob_{Infect}$  can also be attributed to this result.

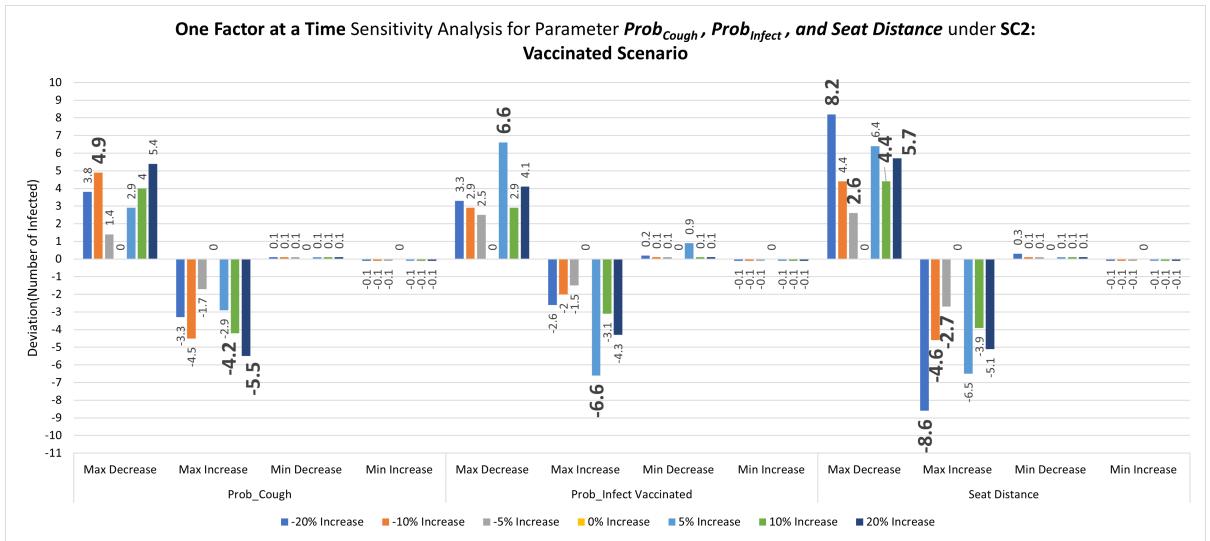
On the other hand,  $Seat Distance$  also produced the highest increase in the number of infected agents from increases of -5%, -10%, and -20%, producing 6.75%, 11.5%, and

21.5% increases in the number of infected. However,  $Prob_{Cough}$  and  $Prob_{Infect}$  became the sensitive parameter on increases 5%, 10%, and 20%. Each parameter increase results in a 13.75%, 1.5%, and 16.5% increase in the number of infected agents compared to the Base Case which can be found on Days 12 to 14 as presented in Figures 5.17, 5.18, and 5.19, respectively. Despite the change, it can be observed that *Seat Distance* was able to maintain a significant increase in the number of infected relative to  $Prob_{Cough}$  and  $Prob_{Infect}$  as shown in Figure 5.13.

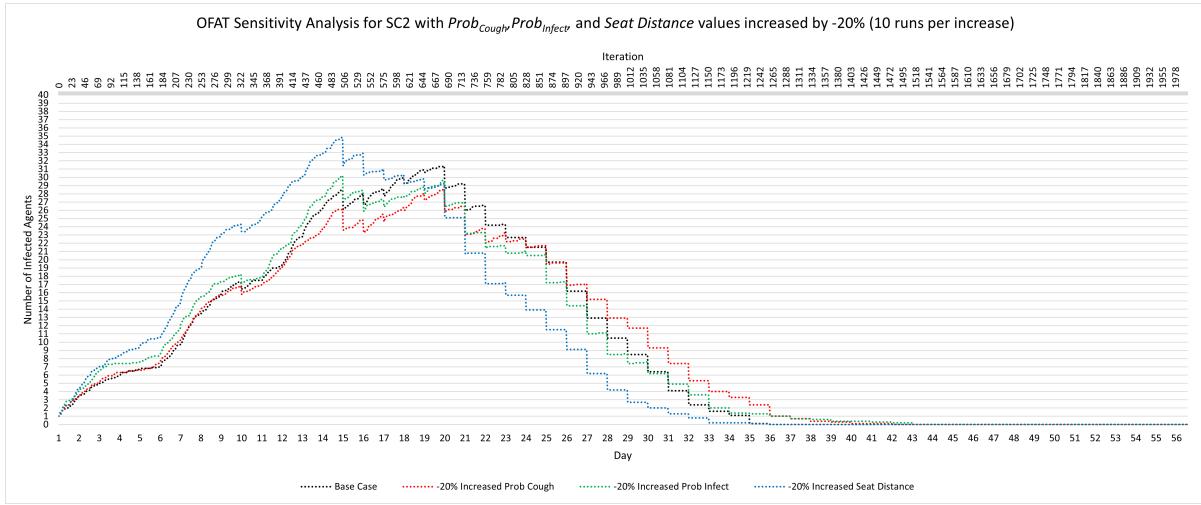
The findings above imply that  $Prob_{Infect}$ 's relatively low value does not significantly affect the model output when increased/decreased compared to the Base Case. Decreasing the *Seat Distance* or increasing  $Prob_{Cough}$  can pose a significant effect on the transmission by increasing the number of infected agent at the start and end of the spread as shown in Figures 5.14 and 5.19, respectively. However, increasing *Seat Distance* can effectively reduce the transmission by reducing the number of infected agent per iteration. Thus, a combination of an increased *Seat Distance* and decreased  $Prob_{Cough}$  may significantly reduce the spread of the virus even more than the decreased *Seat Distance* alone.

	-20% Increase	-10% Increase	-5% Increase	0% Increase	5% Increase	10% Increase	20% Increase
<b>Parameter With Highest Decrease</b>	<i>Seat Distance</i>	$Prob_{Cough}$	<i>Seat Distance</i>	-	$Prob_{Infect}$	<i>Seat Distance</i>	<i>Seat Distance</i>
<b>Parameter With Highest Increase</b>	<i>Seat Distance</i>	<i>Seat Distance</i>	<i>Seat Distance</i>	-	$Prob_{Infect}$	$Prob_{Cough}$	$Prob_{Cough}$

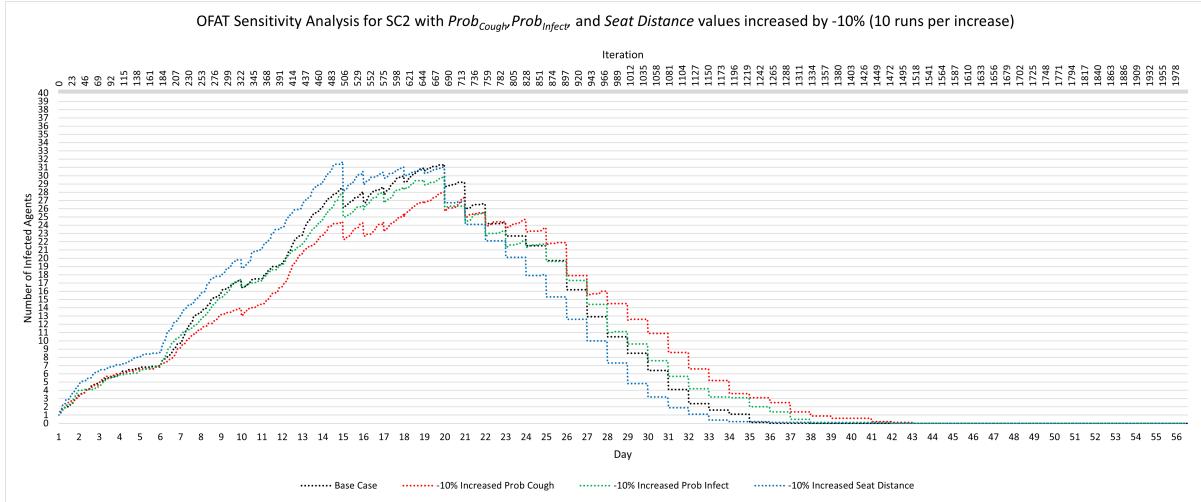
**Table 5.4:** List of parameters that generated Highest Decrease and Highest Increase for each experimental case (-20%, -10%, -5%, 0%, 5%, 10%, 20% Increase) from conducting OFAT Sensitivity Analysis on parameters namely  $Prob_{Infect}$ ,  $Prob_{Cough}$ , and *Seat Distance* under SC2.



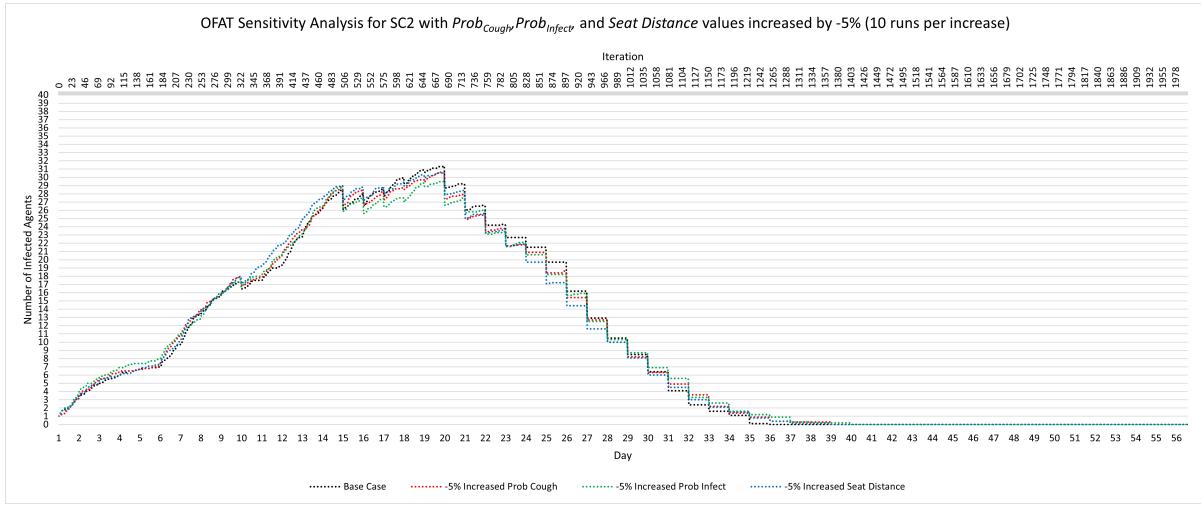
**Figure 5.13:** Generated Maximum Decrease, Maximum Increase, Minimum Decrease, and Minimum Increase in number of infected individuals produced from conducting One Factor at a Time Sensitivity Analysis on the three parameters namely  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and *Seat Distance* under SC2



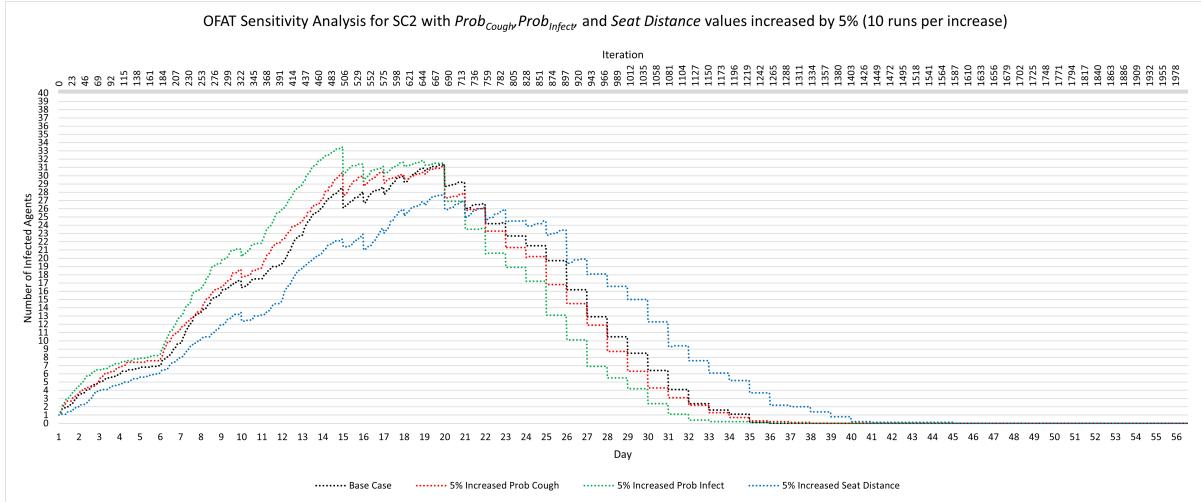
**Figure 5.14:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by -20% under SC2



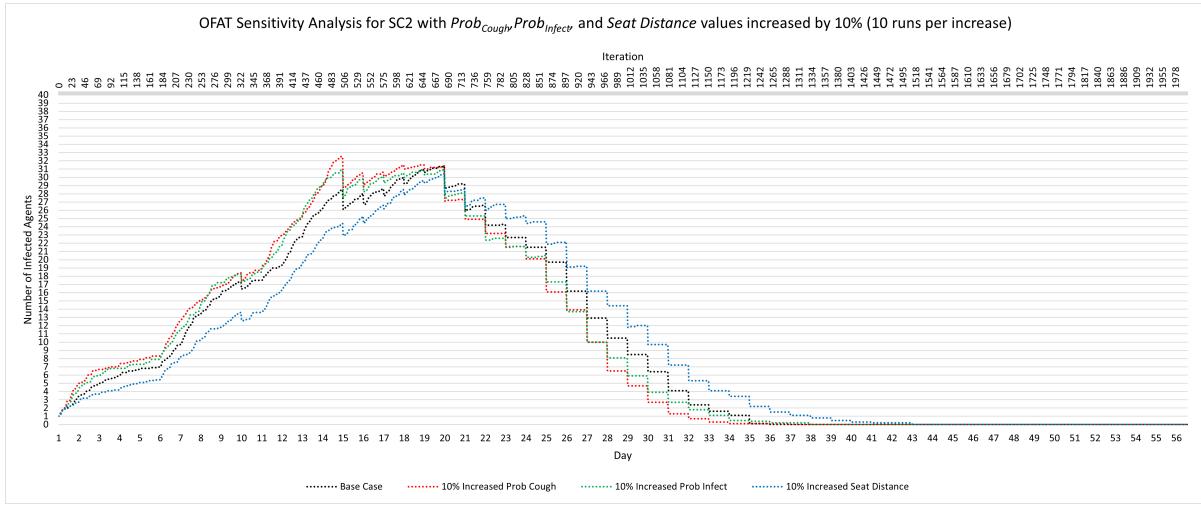
**Figure 5.15:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by -10% under SC2



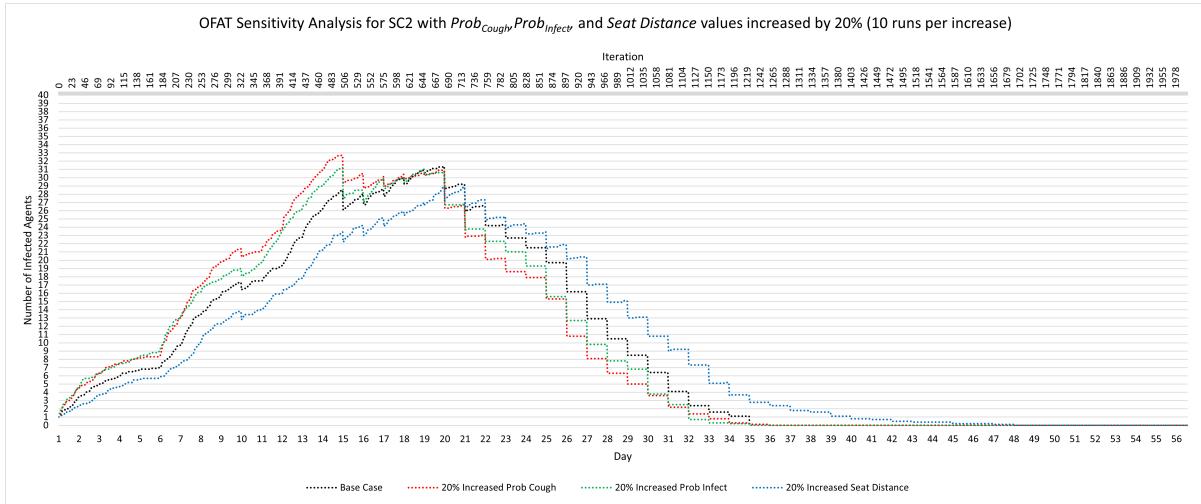
**Figure 5.16:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by -5% under SC2



**Figure 5.17:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by 5% under SC2



**Figure 5.18:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by 10% under SC2



**Figure 5.19:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by 20% under SC2

Parameter	Parameter Increase											
	-20%		-10%		-5%		0%		5%		10%	
	Peak Day	Peak Number of Infected	Peak Day	Peak Number of Infected	Peak Day	Peak Number of Infected	Peak Day	Peak Number of Infected	Peak Day	Peak Number of Infected	Peak Day	Peak Number of Infected
$Prob_{Cough}$	19	28.5	19	28	19	30.6	19	31.4	19	31.1	14	32.5
$Prob_{Infect}$	14	30.2	19	29.9	19	29.5	19	31.4	15	33.5	19	31
$Seat Distance$	14	34.8	15	31.7	19	30.6	19	31.4	19	27.8	20	30.5
											19	28.9

**Table 5.5:** Peak Day and Number of Infected at Peak per experimental case (-20%, -10%, -5%, 0%, 5%, 10%, 20% increase) of the three parameters namely  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat Distance$  subjected to OFAT Sensitivity Analysis under SC2

### 5.2.1.3 OFAT SC3: Eating Healthy Scenario

In this section, we analyze the results of the model by varying one parameter at a time under SC3. Figure 5.20 shows the data for the Maximum Decrease, Maximum Increase, Minimum Decrease, and Minimum Increase in the number of infected agents for this scenario. Table 5.6 presents the list of parameters that produced the Highest Decrease and Increase in the number of infected individuals for each experimental case from Figure 5.20.

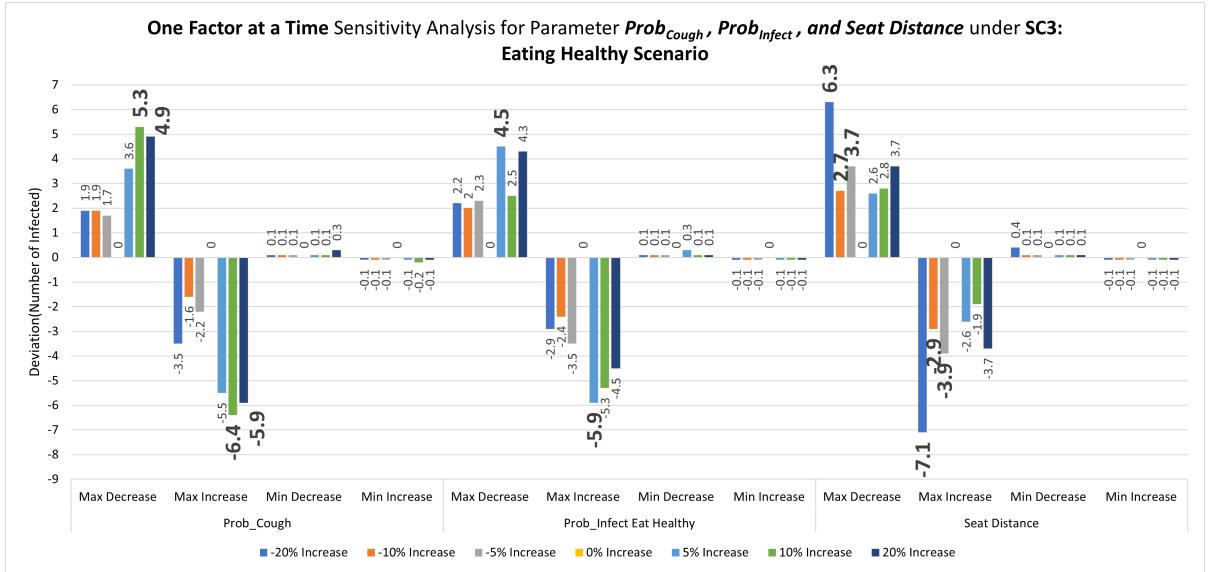
Similar to SC2, increasing the  $Seat Distance$  by -5% to -20% led to the highest decrease in the number of infected agent which can be found at the end of infection (Day 25 to 26). Each of the increases results in a 9.25%, 6.75%, and 15.25% decrease in the number of infected agents compared to the Base Case as shown in Figure 5.20. This suggests that reducing  $Seat Distance$  can speed up the transmission of virus by increasing the number of infected agent, this has a larger impact than decreased  $Prob_{Cough}$  or  $Prob_{Infect}$  does. However, the two probability parameters particularly the  $Prob_{Cough}$  produced the highest decrease in number of infected agent when increased by 5% to 20%, producing 11.25%, 13.25%, and 12.25% decrease respectively. This decrease indicates faster spread of virus as the produced time series shifts to the left of the Base Case as shown in Figure 5.24, 5.25, and 5.26. This shows that a higher value of  $Prob_{Cough}$  outperforms increased  $Prob_{Infect}$  on increasing the spread of the virus and increased  $Seat distance$ 's capability to reduce the spread under SC3.

The same result can be observed under the Highest Increase in the 2nd row of Table 5.6, where  $Seat Distance$  remained as the most sensitive when decreased by -5% to -20%, resulting in a 9.75%, 7.25%, and 17.75% increase in number of infected agents

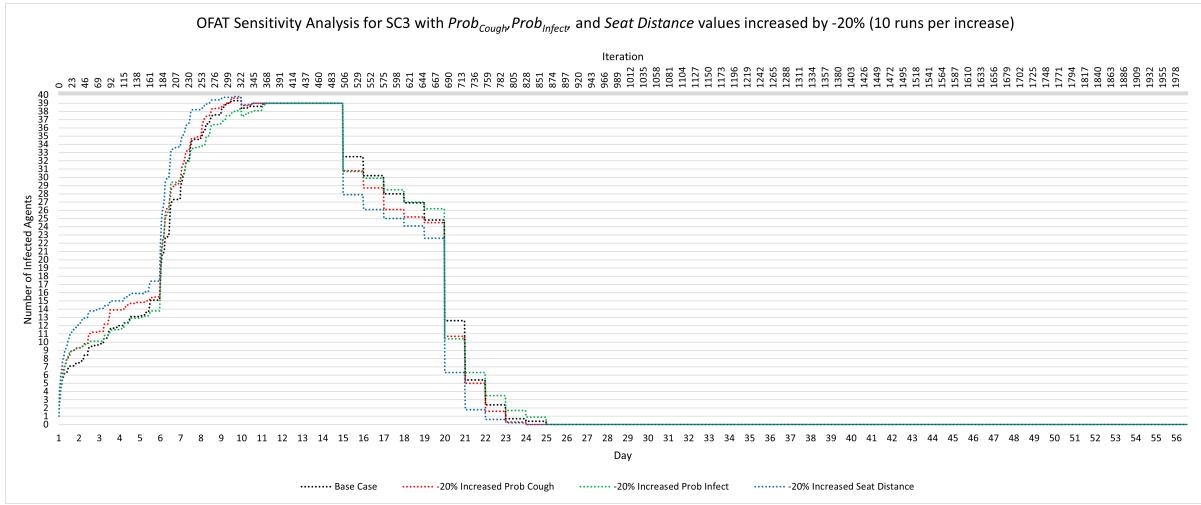
	-20% Increase	-10% Increase	-5% Increase	0% Increase	5% Increase	10% Increase	20% Increase
Parameter With Highest Decrease	<i>Seat Distance</i>	<i>Seat Distance</i>	<i>Seat Distance</i>	-	$Prob_{Infect}$	$Prob_{Cough}$	$Prob_{Cough}$
Parameter With Highest Increase	<i>Seat Distance</i>	<i>Seat Distance</i>	<i>Seat Distance</i>	-	$Prob_{Infect}$	$Prob_{Cough}$	$Prob_{Cough}$

**Table 5.6:** List of parameters that generated Highest Decrease and Highest Increase for each experimental case (-20%, -10%, -5%, 0%, 5%, 10%, 20% Increase) from conducting OFAT Sensitivity Analysis on parameters namely  $Prob_{Infect}$ ,  $Prob_{Cough}$ , and *Seat Distance* under SC3.

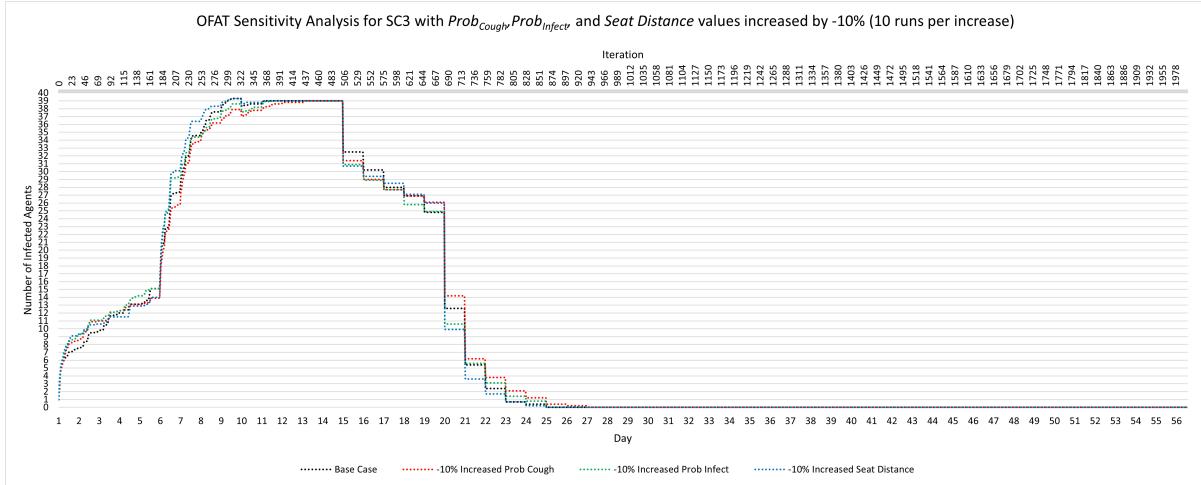
respectively, confirming our initial analysis above. Furthermore, increased  $Prob_{Cough}$  by 5% to 20% also produced the highest increase number of infections in this scenario. Our results suggest that decreasing *Seat Distance* and increasing  $Prob_{Cough}$  should be avoided in this Scenario as it produced a significant increase in the number of infected agent as shown in Figures 5.21 and 5.26 respectively.



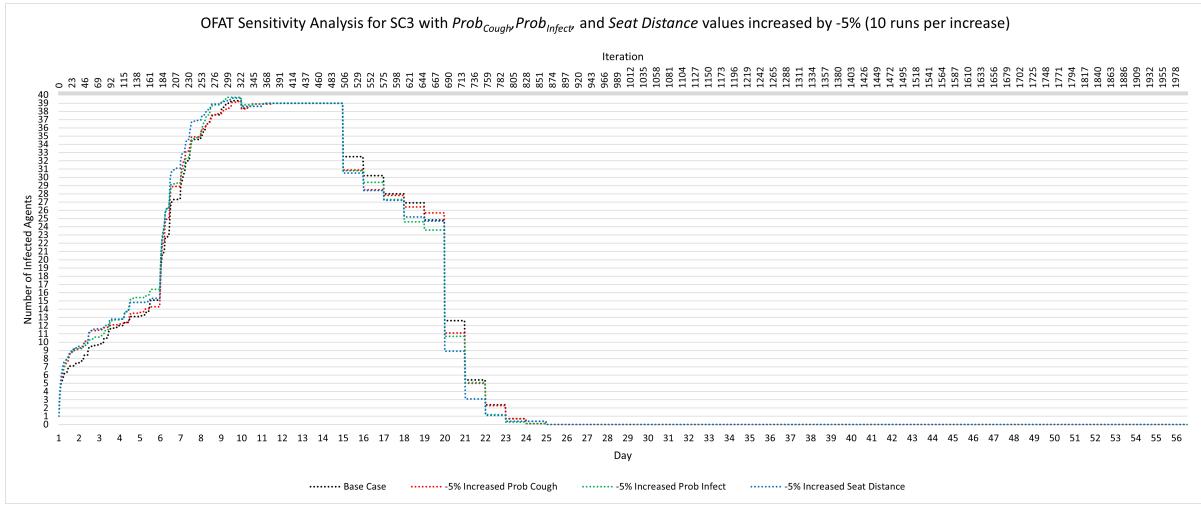
**Figure 5.20:** Generated Maximum Decrease, Maximum Increase, Minimum Decrease, and Minimum Increase in number of infected individuals produced from conducting One Factor at a Time Sensitivity Analysis on the three parameters namely  $Prob_{Infect}$ ,  $Prob_{Cough}$ , and *Seat Distance* under SC3



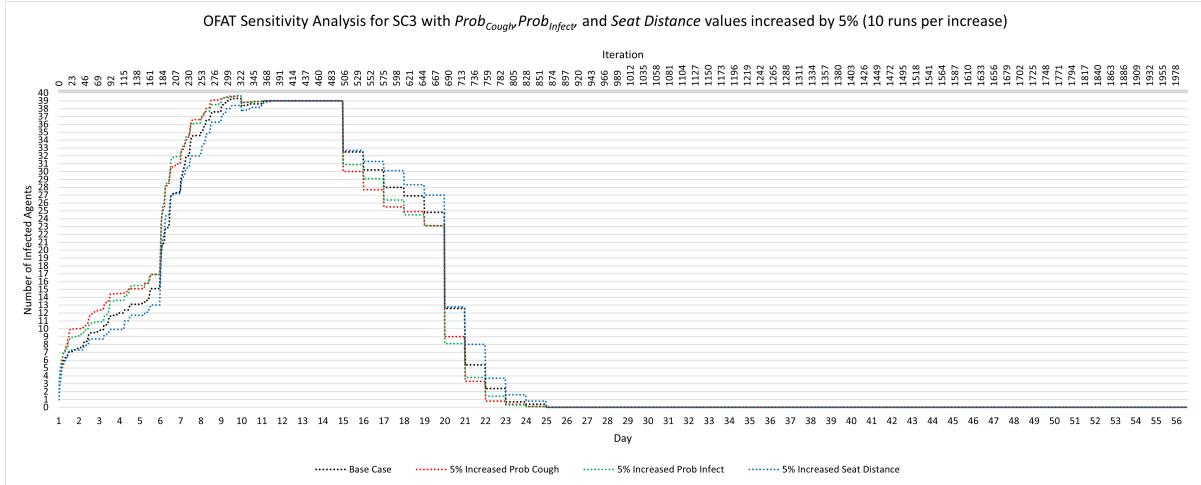
**Figure 5.21:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by -20% under SC3



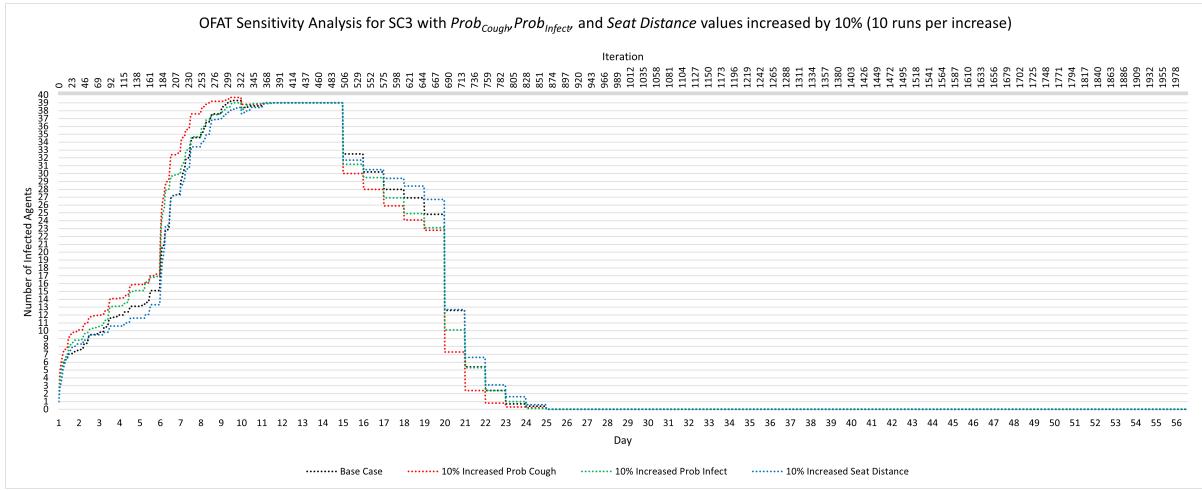
**Figure 5.22:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by -10% under SC3



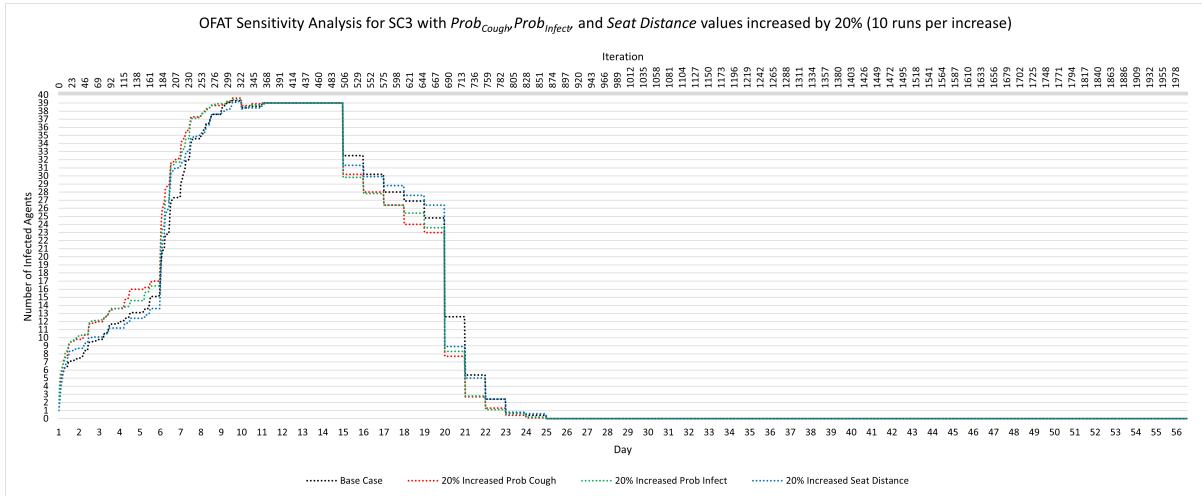
**Figure 5.23:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by -5% under SC3



**Figure 5.24:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by 5% under SC3



**Figure 5.25:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by 10% under SC3



**Figure 5.26:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by 20% under SC3

Parameter	Parameter Increase											
	-20%		-10%		-5%		0%		5%		10%	
	Peak Day	Peak Number of Infected	Peak Day	Peak Number of Infected	Peak Day	Peak Number of Infected	Peak Day	Peak Number of Infected	Peak Day	Peak Number of Infected	Peak Day	Peak Number of Infected
$Prob_{Cough}$	10	39.7	13	39	9	39.3	9	39.3	9	39.6	9	39.7
$Prob_{Infect}$	11	39	11	39	9	39.7	9	39.3	9	39.7	9	39
$Seat Distance$	9	39.8	9	39.3	9	39.6	9	39.3	11	39	11	39
											9	39.2

**Table 5.7:** Peak Day and Number of Infected at Peak per experimental case (-20%, -10%, -5%, 0%, 5%, 10%, 20% increase) of the three parameters namely  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat Distance$  subjected to OFAT Sensitivity Analysis under SC3

#### 5.2.1.4 OFAT SC4: With Comorbidity Scenario

We now analyze the data results produced by varying one parameter at a time under SC4. Figure 5.27 shows the data for the Maximum Decrease, Maximum Increase, Minimum Decrease, and Minimum Increase in the number of infected agents for this Scenario. Table 5.8 presents the list of parameters that produced the Highest Decrease and Increase in the number of infected individuals for each experimental case from Figure 5.27.

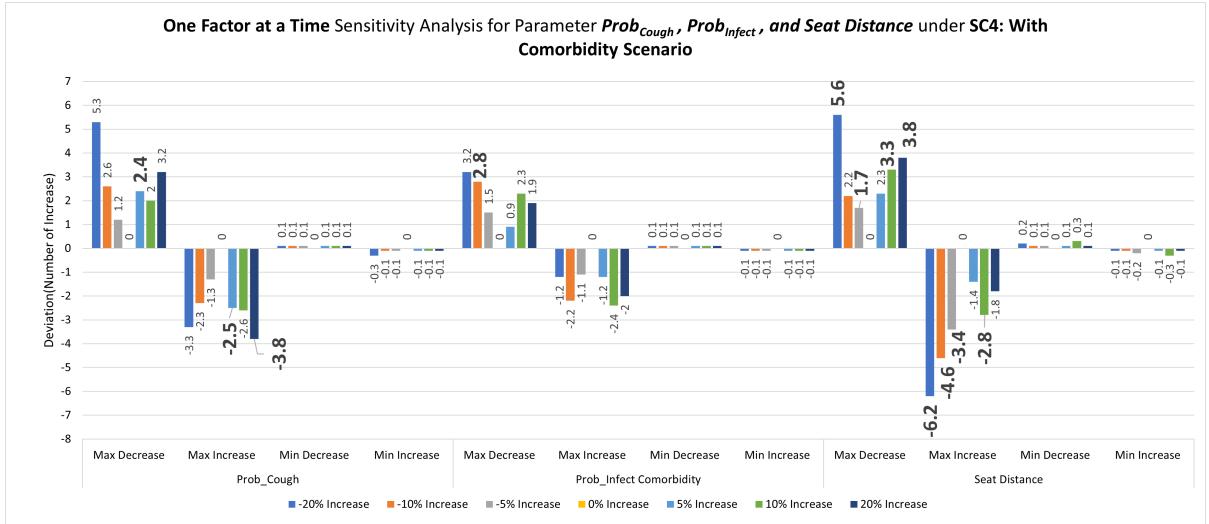
In this experiment, the  $Seat Distance$  parameter produced the highest decrease in the number of infected agents when increased by -5% and -20%, producing 4.25% and 14% decreases in infection, while  $Prob_{Infect}$  had the -10% increase case resulting in a 7% decrease in infection. However, it can be observed in Figure 5.27 that  $Prob_{Cough}$  produced larger values of decrease/increase across all the experimental cases, making it more sensitive than the  $Prob_{Infect}$ . On the other hand,  $Seat Distance$  maintains the highest decrease in infection when increased by 10% and 20% with 8.25% and 9.5% decreases in infection while  $Prob_{Cough}$  had the 5% increase producing a 6% decrease in the number of infections.

The data in the second row of Table 5.8 verifies the first findings above, as increasing  $Seat Distance$  by -5% to -20% resulted in the highest increase in the number of infected agents, garnering an 8.5%, 11.5%, and 15.5% increase. Furthermore, when increased by 5% and 20%,  $Prob_{Cough}$  provided the largest increase in infection with 6.25% and 9.5% infection increase, whereas  $Seat Distance$  had the 10% increase case. In this scenario, little to no changes can be observed in the peak days and the number of infected during peaks of the experimental cases when compared to the Base Case as shown in Table 5.9.

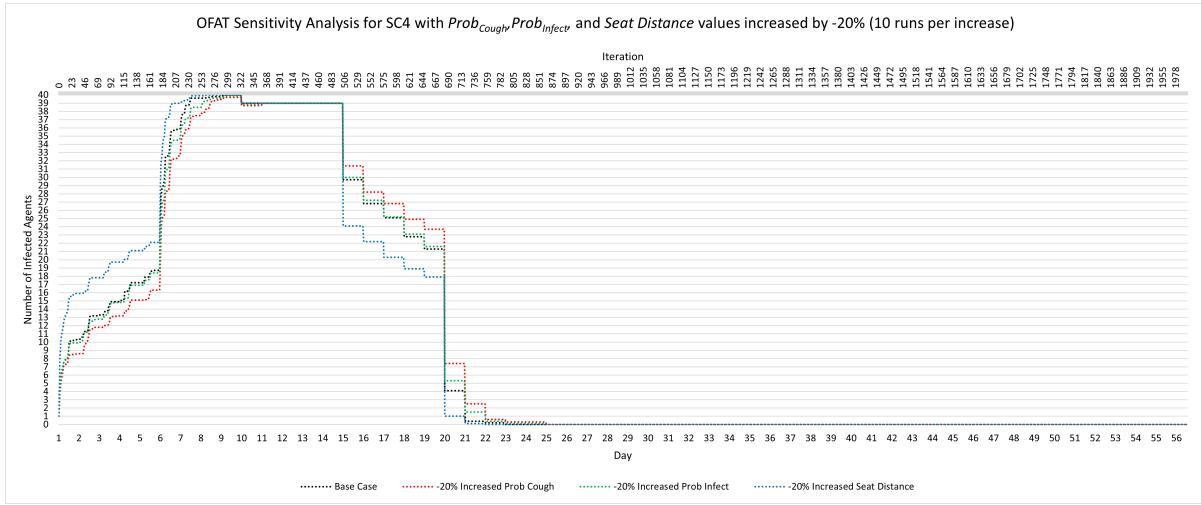
	-20% Increase	-10% Increase	-5% Increase	0% Increase	5% Increase	10% Increase	20% Increase
Parameter With Highest Decrease	<i>Seat Distance</i>	$Prob_{Infect}$	<i>Seat Distance</i>	-	$Prob_{Cough}$	<i>Seat Distance</i>	<i>Seat Distance</i>
Parameter With Highest Increase	<i>Seat Distance</i>	<i>Seat Distance</i>	<i>Seat Distance</i>	-	$Prob_{Cough}$	<i>Seat Distance</i>	$Prob_{Cough}$

**Table 5.8:** List of parameters that generated Highest Decrease and Highest Increase for each experimental case (-20%, -10%, -5%, 0%, 5%, 10%, 20% Increase) from conducting OFAT Sensitivity Analysis on parameters namely  $Prob_{Infect}$ ,  $Prob_{Cough}$ , and *Seat Distance* under SC4.

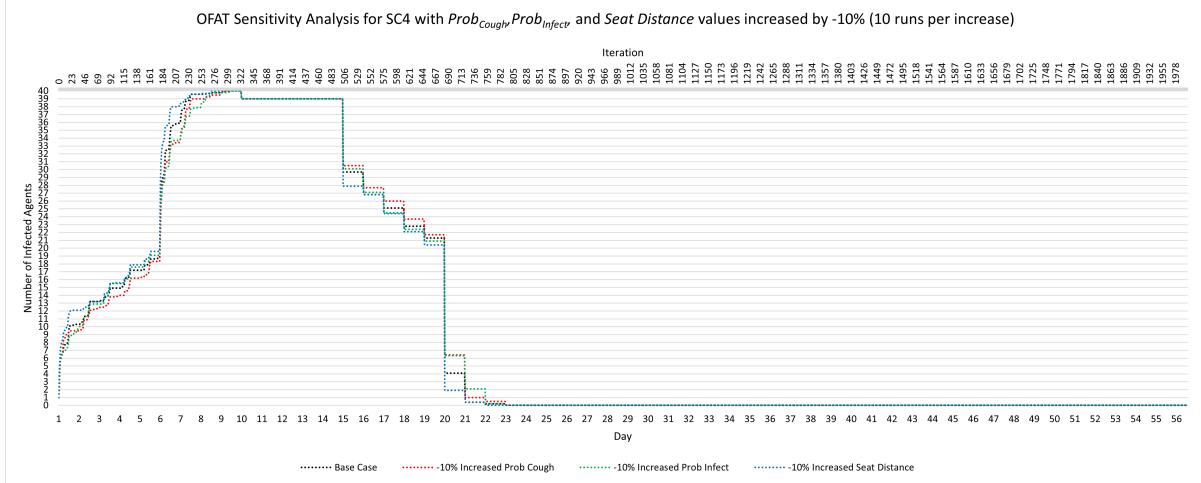
The data results imply that reducing the  $Prob_{Cough}$  and increasing *Seat Distance* provides a significant impact on the reducing the number of infected agents in this scenario, as demonstrated in Figures 5.28 and 5.33, respectively. In contrast, it is advised to avoid reducing the *Seat Distance* or increasing the  $Prob_{Cough}$  value as these conditions produced the highest increase the number of infected agents among the experimental cases.



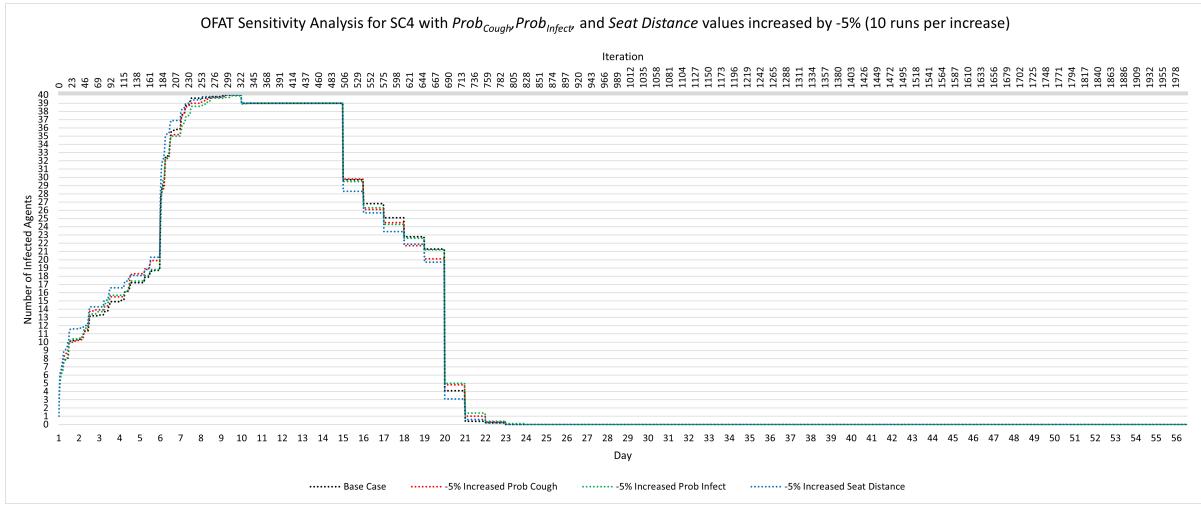
**Figure 5.27:** Generated Maximum Decrease, Maximum Increase, Minimum Decrease, and Minimum Increase in number of infected individuals produced from conducting One Factor at a Time Sensitivity Analysis on the three parameters namely  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and *Seat Distance* under SC4



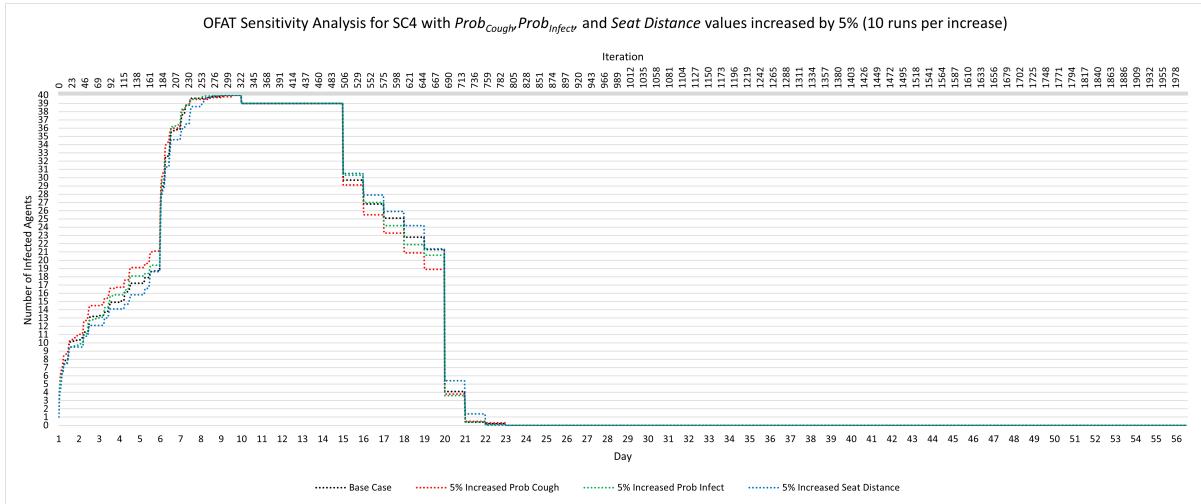
**Figure 5.28:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by -20% under SC4



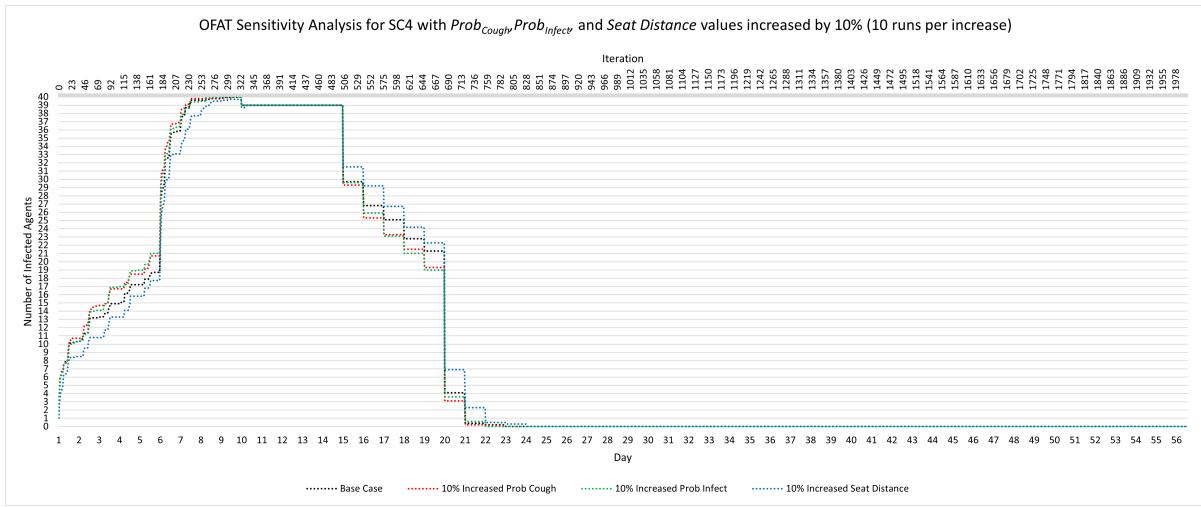
**Figure 5.29:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by -10% under SC4



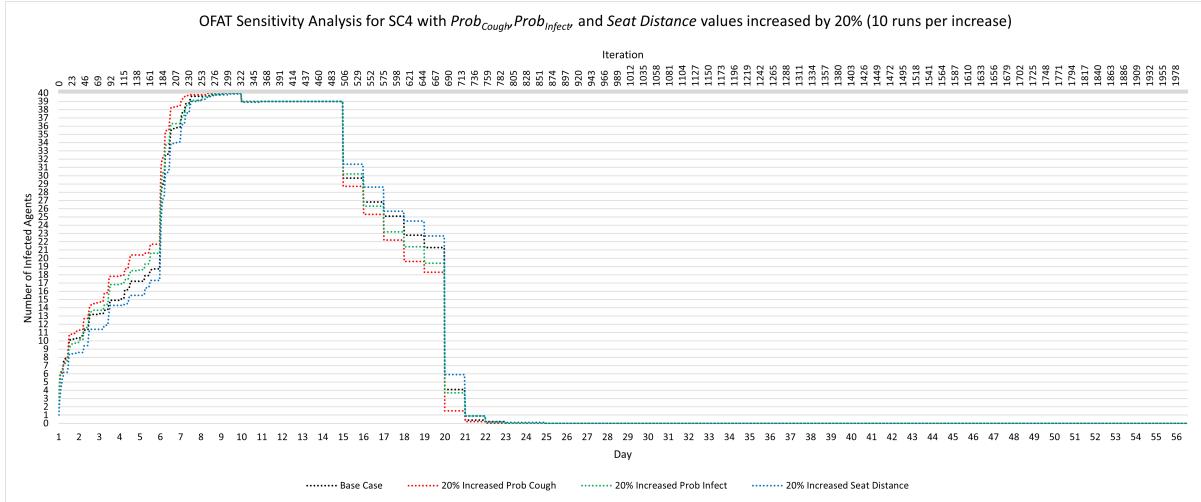
**Figure 5.30:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by -5% under SC4



**Figure 5.31:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by 5% under SC4



**Figure 5.32:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by 10% under SC4



**Figure 5.33:** Generated Time Series data from increasing the value of parameters  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$  by 20% under SC4

Parameter	Parameter Increase											
	-20%		-10%		-5%		0%		5%		10%	
	Peak Day	Peak Number of Infected	Peak Day	Peak Number of Infected	Peak Day	Peak Number of Infected	Peak Day	Peak Number of Infected	Peak Day	Peak Number of Infected	Peak Day	Peak Number of Infected
$Prob_{Cough}$	9	39.7	9	40	9	40	9	40	9	40	9	40
$Prob_{Infect}$	9	39.9	9	40	9	39.9	9	40	8	40	8	40
$Seat Distance$	8	40	8	40	9	40	9	40	9	39.7	9	39.9

**Table 5.9:** Peak Day and Number of Infected at Peak per experimental case (-20%, -10%, -5%, 0%, 5%, 10%, 20% increase) of the three parameters namely  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat Distance$  subjected to OFAT Sensitivity Analysis under SC4

### 5.2.2 Two Factor at a Time Sensitivity Analysis

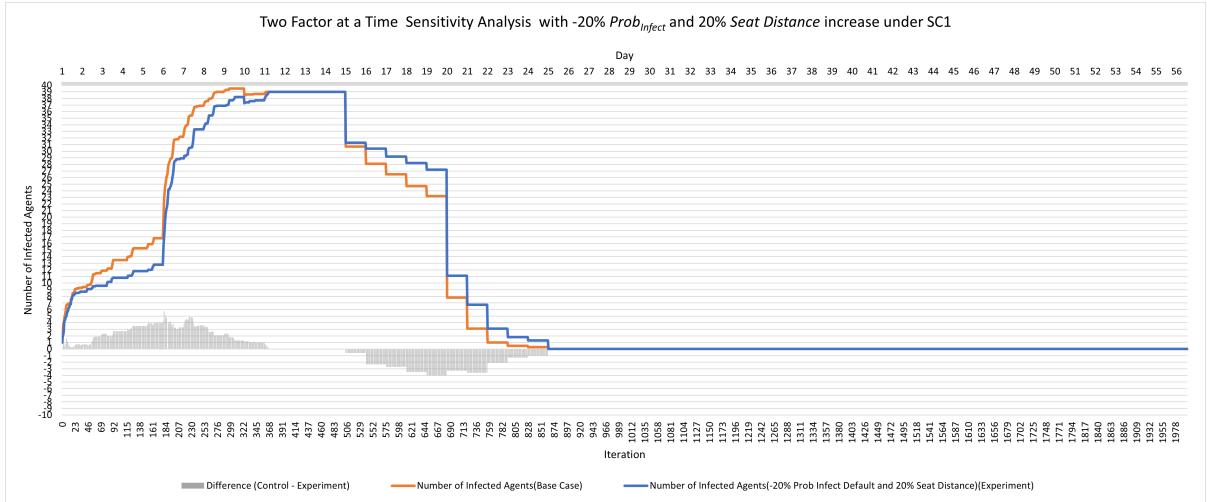
In this section, we conducted 2FAT Sensitivity Analysis on each scenario by combining the resulting sensitive parameters in Section 5.2.1. We combined the sensitive parameters that produced the highest decrease in number of infected agent to come up with the best-case experiment for each scenario. Similarly, the worst-case experiments were simulated by combining the sensitive parameters that produced the highest increase in number of infected agent. Note that in Section 5.2.1, we were unable to determine a worst-case scenario for S1 and best-case for S2. This part of the experiment attempts to validate the initial analysis and recommendations discussed in Section 5.2.1 and illustrate the best and worst case by controlling the sensitive parameters for each scenario.

#### 5.2.2.1 2FAT SC1: Base Model

Under SC1, we have found that decreasing  $Prob_{Infect}$  or increasing  $Seat Distance$  significantly produced the highest decrease in the number of infected agents as shown in Table 5.2. For the best-case experiment, we performed a simulation where we combined the two configurations, increasing the value of  $Prob_{Infect}$  and  $Seat Distance$  by -20% and 20%, respectively. Figure 5.34 shows the time series produced by the best-case experiment together with the Base Case (control) in this scenario. The best-case experiment produced a 14.5% highest decrease in the number of infections on Day 6 while an 8% highest increase occurred on Days 19 to 21. Despite combining the two positive configurations for our best-case experiment, the model simulation only produced a slight difference in the highest decrease and increase compared to the positive OFAT experimental cases particularly on the -20% increased  $Prob_{Infect}$  as shown in Table 5.10. In

this simulation, the -20% increased  $Prob_{Infect}$  experimental case outperformed our best-case experiment by producing a larger increase and decrease in the number of infections when compared to the best-case, indicating that reducing  $Prob_{Infect}$  alone already has a significant impact on reducing the spread of the virus under the SC1.

However, the best-case configuration was still able to delay and distribute the spread of the virus compared to the Base Case by decreasing the rate of newly infected agent by 19.17% where best-case had an average rate of 3.54 newly infected agent per day and Base Case had 4.38 newly infected agent per day from Day 1 to peak. On the other hand, Figure 5.12 shows the worst-case experiment where we increase the  $Prob_{Infect}$  by 20%, this resulted in a 9.5% highest increase in the number of infected agents as discussed in Section 5.2.1.1.



**Figure 5.34:** Generated Time Series from the best-case experiment (-20%  $Prob_{Infect}$  and 20%  $Seat\ Distance$  increase) vs Base Case under SC1.

### 5.2.2.2 2FAT SC2: Vaccinated Scenario

According to Section 5.2.1.2, increasing  $Prob_{Cough}$  by -20% or  $Seat\ Distance$  by 20% results in a highest deviation in number of infected agent relative to other parameter increases. In this experiment, we combined the two to simulate the best-case experiment

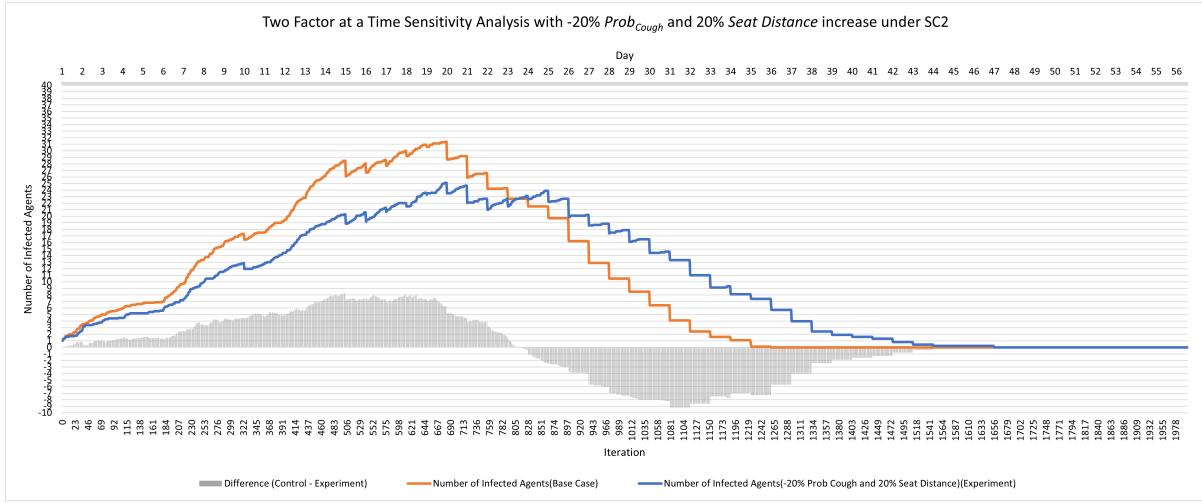
2FAT Experiments				Positive OFAT Cases				Negative OFAT Cases	
2FAT Best-case Experiment (-20% $Prob_{Infect}$ and 20% $Seat\ Distance$ Increase)		2FAT Worst-case Experiment (20% $Prob_{Infect}$ Increase)		-20% $Prob_{Infect}$ Increase		20% $Seat\ Distance$ Increase		20% $Prob_{Infect}$ Increase	
Highest Decrease (%)	Highest Increase (%)	Highest Decrease (%)	Highest Increase (%)	Highest Decrease (%)	Highest Increase (%)	Highest Decrease (%)	Highest Increase (%)	Highest Decrease (%)	Highest Increase (%)
14.5% @ Day 6	8% @ Day 19 to 21	9.25% @ Day 18 to 19	6% @ Day 6	14.75% @ Day 6	13.25 @ Day 6	9.25% @ Day 6	6.25% @ Day 19 to 20	6% @ Day 18 to 19	9.25% @ Day 7

**Table 5.10:** Highest Decrease and Highest Increase in number of infected agents produced by the experimental case with sensitive parameters from OFAT Sensitivity Analysis together with the Best-Case experiment and Worst-Case Experiment under SC1.

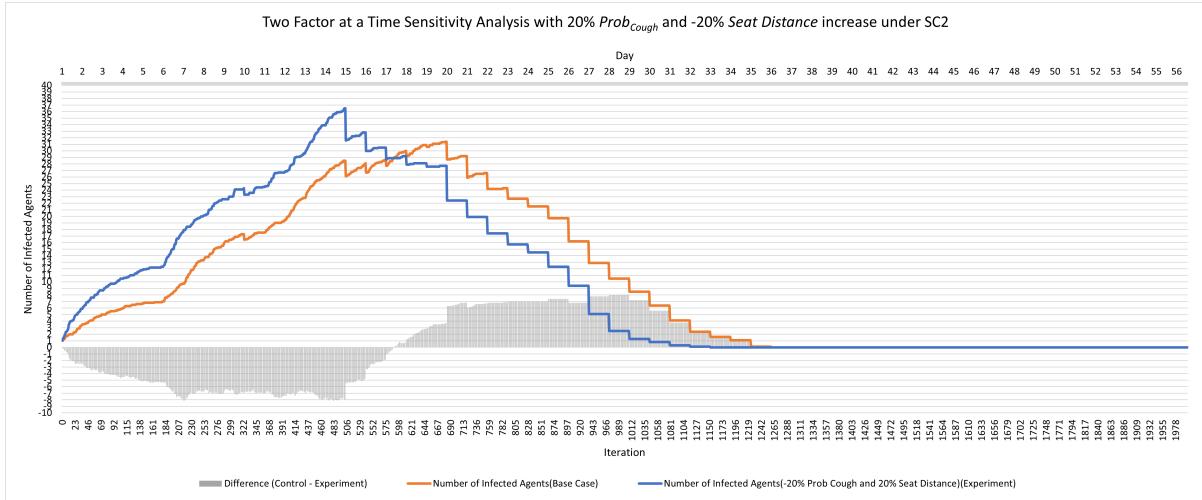
under this scenario. Figure 5.35 shows the time series of the best-case experiment and the Base Case(control) in this scenario. The best-case experiment was able to produce a 20.75% highest decrease and a 23% highest increase in the number of infections as shown in Table 5.11. Unlike the SC1, The best-case experiment was able to outperform the two positive OFAT configurations when compared individually as shown in Table 5.11. The best-case was able to reduce the peak number of infected agents by 8.5% to 9.5% less than the positive OFAT experimental cases. Moreover, the best-case experiment was able to delay the end of infection by up to 11 days when compared to the Base Case (control). This suggests that in this experiment the virus propagated over time in a much more dispersed manner, producing a more flat virus trend as shown in Figure 5.35.

On the other hand, increasing the  $Prob_{Cough}$  or  $Seat\ Distance$  by 20% and -20% generated the highest increase in number of infected agent in Section 5.2.1.2. Hence, we let the combination of the two as the configuration for the worst-case experiment in this scenario. Figure 5.36, shows the time series produced by the worst-case experiment and the Base Case. In this experiment, the worst-case experiment produced a much larger highest increase and decrease in the number of infected agents when compared to the 20% increased  $Prob_{Cough}$  OFAT experimental case as shown in Table 5.11. On the other hand, minimal change can be observed in the highest decrease and highest increase between the worst-case experiment and the -20% increased  $Seat\ Distance$  increased OFAT experimental case. This shows that a -20% increase in  $Seat\ Distance$  alone can substantially increase the risk of infection by generating higher increase in number of infected agents in this scenario. However, the worst-case experimental case reached a higher number

of infected during peak, infecting 4.25% to 9.5% more than the negative OFAT cases. Moreover, the end of infection was reached 3-4 days earlier than the two configurations, resulting in a worse case than the two negative OFAT cases.



**Figure 5.35:** Generated Time Series from the best-case experiment(-20%  $\text{Prob}_{\text{Cough}}$  and 20%  $\text{Seat Distance}$  increase) vs Base Case under SC2.



**Figure 5.36:** Generated Time Series from the worst-case experiment(20%  $\text{Prob}_{\text{Cough}}$  and -20%  $\text{Seat Distance}$  increase) vs Base Case under SC2.

2FAT Experiments				Positive OFAT Cases				Negative OFAT Cases			
2FAT Best-case Experiment (-20% $Prob_{Cough}$ and 20% $Seat\ Distance\ Increase$ )		2FAT Worst-case Experiment (20% $Prob_{Cough}$ and -20% $Seat\ Distance\ Increase$ )		-20% $Prob_{Cough}$ Increase		20% $Seat\ Distance\ Increase$		20% $Prob_{Cough}$ Increase		-20% $Seat\ Distance\ Increase$	
Highest Decrease (%)	Highest Increase (%)	Highest Decrease (%)	Highest Increase (%)	Highest Decrease (%)	Highest Increase (%)	Highest Decrease (%)	Highest Increase (%)	Highest Decrease (%)	Highest Increase (%)	Highest Decrease (%)	Highest Increase (%)
20.75% @ Day 14	23% @ Day 31 to 32	20% @ Day 28 to 29	20.5% @ Day 14	9.5% @ Day 17	8.25% @ Day 31 to 32	6.5% @ Day 13	6.75% @ Day 31 to 32	13.5% @ Day 26 to 27	13.75% @ Day 13	20.5% @ Day 25 to 26	21.5% @ Day 12

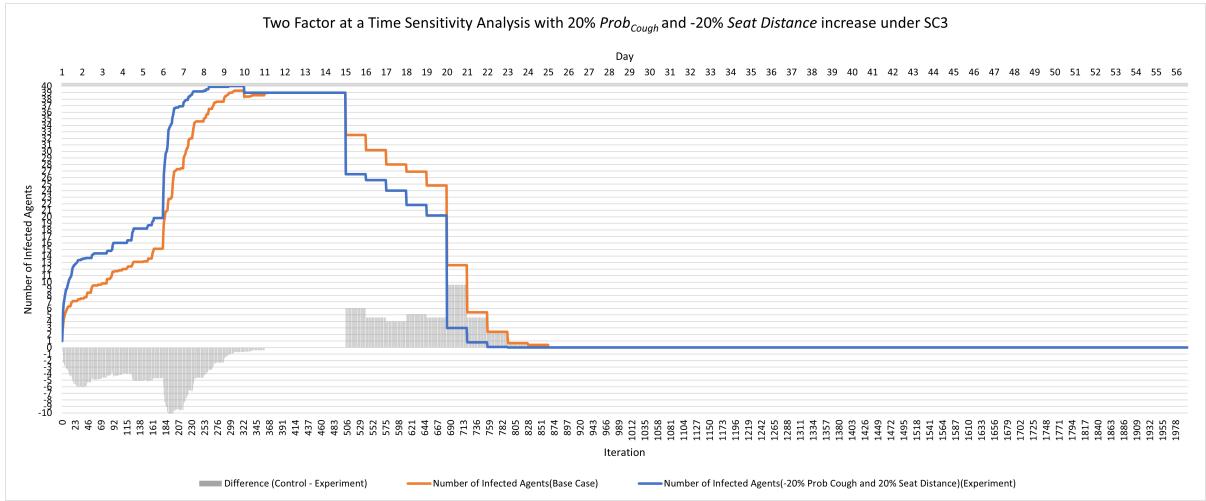
**Table 5.11:** Highest Decrease and Highest Increase in number of infected agents produced by the experimental case with sensitive parameters from OFAT Sensitivity Analysis together with the Best-Case experiment and Worst-Case Experiment under SC2.

### 5.2.2.3 2FAT SC3: Eating Healthy Scenario

In contrast to the other scenarios discussed above, the results from Section 5.2.1.3 only provided a list of sensitive parameters that contribute to the increase in the number of infected agent. Therefore, in this section, we skipped the best-case experiment and proceeded on simulating the worst-case one. Figure 5.37 shows the time series of the worst-case experiment and Base Case (control) under SC3. Similar to SC2, a combination of 20% increased  $Prob_{Cough}$  and -20% increased  $Seat\ Distance$  was set as the configuration for the worst-case experiment. The worst-case experiment produced a 24% highest decrease and a 28.25% highest increase in the number of infections, a relatively larger value when compared to the negative OFAT cases as shown in Table 5.12. Both the worst-case experiment and Base Case were able to infect all agent (40 agents) during peak. The results suggest that combining the two negative configurations can significantly increase the number of infected agent per iteration much worse than the negative OFAT cases alone.

2FAT Experiments				Positive OFAT Cases				Negative OFAT Cases			
		2FAT Worst-case Experiment (20% $Prob_{Cough}$ and -20% Seat Distance Increase)		-20% $Prob_{Cough}$ Increase		20% Seat Distance Increase		20% $Prob_{Cough}$ Increase		-20% Seat Distance Increase	
Highest Decrease (%)	Highest Increase (%)	Highest Decrease (%)	Highest Increase (%)	Highest Decrease (%)	Highest Increase (%)	Highest Decrease (%)	Highest Increase (%)	Highest Decrease (%)	Highest Increase (%)	Highest Decrease (%)	Highest Increase (%)
-	-	24% @ Day 20 to 21	28.25% @ Day 6	4.75% @ Day 20 to 21	8.75% @ Day 6	9.25% @ Day 20 to 21	9.25% @ Day 7	12.25% @ Day 20 to 21	14.75% @ Day 6	15.75% @ Day 20 to 21	17.75% @ Day 6

**Table 5.12:** Highest Decrease and Highest Increase in number of infected agents produced by the experimental case with sensitive parameters from OFAT Sensitivity Analysis together with the Best-Case experiment, and Worst-Case Experiment under SC3.

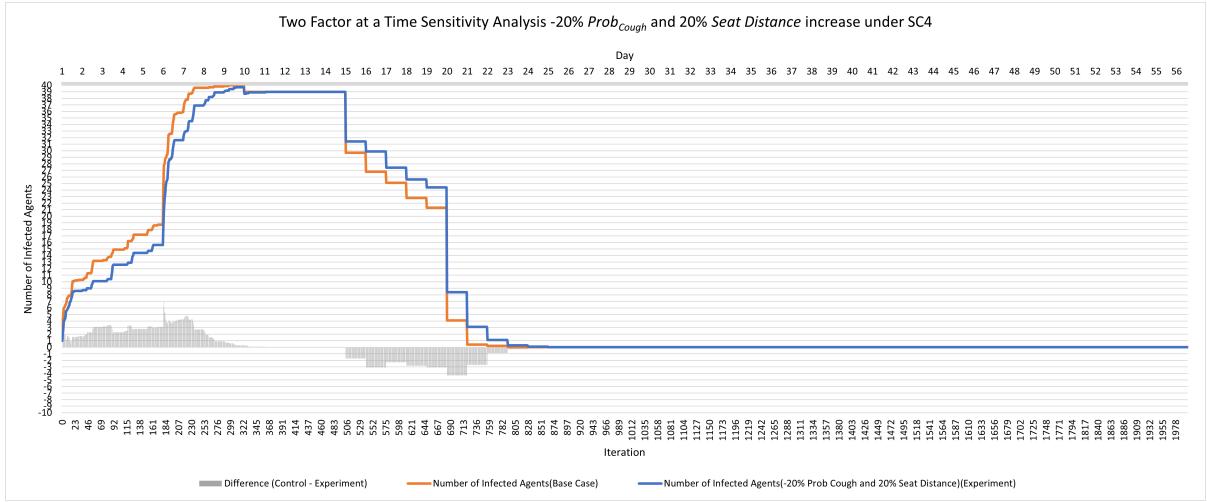


**Figure 5.37:** Generated Time Series from the worst-case experiment(20%  $Prob_{Cough}$  and -20%  $Seat Distance$  increase) vs Base Case under SC3.

#### 5.2.2.4 2FAT SC4: With Comorbidity Scenario

Similar to the SC2 and SC3, increasing parameters  $Prob_{Cough}$  and  $Seat Distance$  by -20% and 20% produced the highest decrease in number of infection in SC4 as discussed in Section 5.2.1.4. We set the combination of the two as a configuration for the best-case experiment in this Scenario. Figure 5.38 shows the time series of the best-case experiment and the Base Case(control) in this scenario. The best-case experiment produced a 17.25% highest decrease and 10.75% highest increase in the number of infections, outperforming

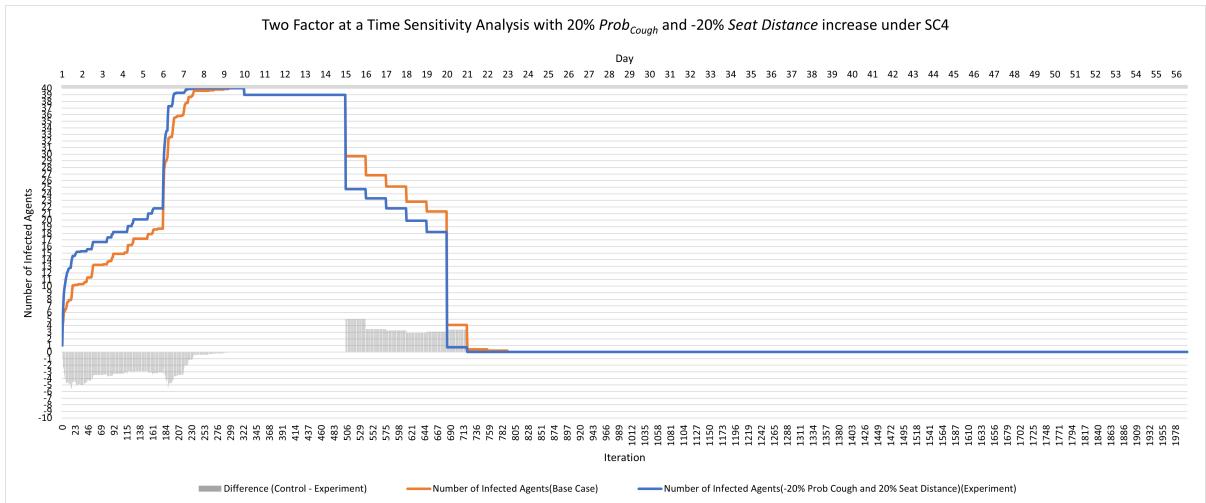
the two positive OFAT cases by a large value as shown in Table 5.13. This indicates that combining the two sensitive parameter can effectively reduce the spread of the virus when compared to single ones. For the worst-case experiment, we combined 20% increased  $Prob_{Cough}$  with the -20% increased  $Seat\ Distance$ . Figure 5.39, shows the time series produced by the worst-case experiment and the Base Case. The worst-case experiment produced a 12.5% highest decrease and 13.75% highest increase in the number of infection, outperforming the 20% increased  $Prob_{Cough}$  experimental case by a large value. However, the -20% increased  $Seat\ Distance$  produced a larger highest decrease and increase when compared to the worst-case experiment, indicating that decreasing  $Seat\ Distance$  alone has the capability to increase the rate of infection more than the worst-case experiment as shown in Table 5.13.



**Figure 5.38:** Generated Time Series from the best-case experiment (-20%  $Prob_{Cough}$  and 20%  $Seat\ Distance$  increase) vs Base Case under SC4.

2FAT Experiments				Positive OFAT Cases				Negative OFAT Cases			
2FAT Best-case Experiment (-20% $Prob_{Cough}$ and 20% Seat Distance Increase)		2FAT Worst-case Experiment (20% $Prob_{Cough}$ and -20% Seat Distance Increase)		-20% $Prob_{Cough}$ Increase		20% Seat Distance Increase		20% $Prob_{Cough}$ Increase		-20% Seat Distance Increase	
Highest Decrease (%)	Highest Increase (%)	Highest Decrease (%)	Highest Increase (%)	Highest Decrease (%)	Highest Increase (%)	Highest Decrease (%)	Highest Increase (%)	Highest Decrease (%)	Highest Increase (%)	Highest Decrease (%)	Highest Increase (%)
17.25% @ Day 6	10.75% @ Day 20 to 21	12.50% @ Day 15 to 16	13.75% @ Day 1	13.25% @ Day 6	8.25% @ Day 20 to 21	9.5% @ Day 6	4.5% @ Day 20 to 21	8% @ Day 18 to 19	9.5% @ Day 6	14% @ Day 15 to 16	15.5% @ Day 1

**Table 5.13:** Highest Decrease and Highest Increase in number of infected agents produced by the experimental case with sensitive parameters from OFAT Sensitivity Analysis together with the Best-Case experiment, and Worst-Case Experiment under SC4.



**Figure 5.39:** Generated Time Series from the worst-case experiment(20%  $Prob_{Cough}$  and -20%  $Seat Distance$  increase) vs Base Case under SC4.

# Chapter 6

## Conclusion and Recommendation

In this paper, we proposed an ABM to simulate COVID-19 transmission among students in a public high-school classroom under particular scenarios namely SC1: Base Model, SC2: Vaccinated Scenario, SC3: Eating Healthy Scenario, and SC4: With Comorbidity Scenario. Common specifications of a public high school classroom were adapted as parameters for the environment in the model particularly the classroom size, seating arrangement, and number of students in a single classroom. For the agents' behavior, we have implemented the basic movement of students in a classroom during a 9-hour class to imitate their Movement Behavior. Moreover, to simulate the virus transmission, we have constructed a 2 layer threshold for the Infection Behavior using the parameters  $Prob_{Cough}$  (Probability of Coughing) and  $Prob_{Infect}$  (Probability of Infection from Cough) to represent the nature of cough which is the primary mode of transmission used in the model.

In the experiments, we subjected each of the 4 scenarios on 10 simulation runs to determine their differences in the transmission of the COVID-19 virus. Among the list, SC2 comes first in the ranking by showing the slowest COVID-19 spread with an average of 1.40 newly infected agents per day from Day 1 to peak day. SC3 comes second with an average of 4.36 newly infected agents per day, followed by SC1 which had an average of 4.38 newly infected agents per day, and lastly, SC4 which had an average of 4.44 newly infected agents per day.

One Factor at a Time (OFAT) Sensitivity Analysis was conducted for each scenario to determine the most sensitive parameters among  $Prob_{Cough}$ ,  $Prob_{Infect}$ , and  $Seat\ Distance$ . For SC1,  $Prob_{Infect}$  and  $Seat\ Distance$  produced the highest deviation in the number of infected agents producing a 14.75% decrease and a 9.75% decrease, respectively. In the case of SC2,  $Seat\ Distance$  and  $Prob_{Cough}$  produced the highest deviation in the number of infected agents recording 20.5% decrease and 16.5% increase, respectively. Similar

to SC2, *Seat Distance* and *Prob<sub>Cough</sub>* remained as the sensitive parameters for SC3 by producing 15.25% and 13.25% decrease in the number of infected agents. Lastly, for SC4, *Seat Distance* and *Prob<sub>Cough</sub>* produced the highest deviation producing 15.5% increase and 9.5% increase in the number of infected agents.

We also conducted a Two Factor at a Time (2FAT) Sensitivity Analysis to determine the best and worst case for each scenario using the sensitive parameters determined from OFAT. For SC1, increasing *Prob<sub>Infect</sub>* and *Seat Distance* by -20% and 20% was determined as the best-case scenario. However, results show that -20% increased *Prob<sub>Infect</sub>* experimental case outperformed the best-case of SC1, indicating that decreasing *Prob<sub>Infect</sub>* alone can significantly reduce the transmission of the virus better than the best case. For the worst case of SC1, it was shown that increasing *Prob<sub>Infect</sub>* by 20% produced the highest increase in the number of infected agents among the experimental cases. This experiment suggests that under SC1, controlling the probability of infection (i.e. wearing masks, covering coughs, drinking multivitamins, and ventilated room to disperse droplets/air) and conducting distancing on seats are important as these can pose a substantial decrease or increase in the number of infected agents.

Scenarios SC2, SC3, and SC4 used the same configurations for the best and worst-case experiments. The three used the combination of -20% increased *Prob<sub>Cough</sub>* and 20% increased *Seat Distance* for the best-case. For the worst-case, each scenario used the combination of 20% increased *Prob<sub>Cough</sub>* and -20% increased *Seat Distance*.

Unlike SC1, SC2's best case outperformed the two positive OFAT experimental cases separately. On the other hand, SC2's worst-case was outperformed by the -20% increased *Seat Distance* experimental case, indicating that reducing *Seat Distance* alone can effectively increase the transmission similar to the worst case. For this reason, it is highly advised to avoid reducing the distance of seats, instead maintain a large distance between seats ( $\leq 0.6$  meters), and find ways to lower the chance of coughing when experiencing COVID-19 symptoms (i.e. Taking Cough Drops, Drinking more water, gargling salt water, avoiding dusty and dirty rooms, limiting exhaustion/tiredness).

For the case of SC3, the worst-case scenario produced the highest decrease and increase in the number of infections among all the experimental cases. The results provides similar suggestion, students should avoid close seat distance in the classroom. Moreover,

symptomatic students should perform precautions to minimize the chance of coughing (i.e. Taking Cough Drops, Drinking more water, gargling salt water, avoiding dusty and dirty rooms, limiting exhaustion/tiredness), or better yet, perform self-isolation.

For the case of SC4, the best-case experiment was able to outperform the two positive OFAT cases by a large value. Similar to SC2, -20% increased *Seat Distance* outperformed the worst-case of SC4, implying that decreasing *Seat Distance* alone can significantly increase the rate of infection similar to the worst-case. The results suggest similar recommendations to SC2, students in this scenario should perform precautions to minimize the chance of cough (i.e. Taking Cough Drops, Drinking more water, gargling salt water, avoiding dusty and dirty rooms, limiting exhaustion/tiredness) and maintaining seat distance of at least 0.6 meters to achieve a slower spread of the virus. Moreover, decreasing the seat distance should be avoided as it can also produce a significant increase in infection similar to the worst-case.

In future research, we suggest considering multiple modes of transmission (i.e. Sneeze, Physical Contact, Fomites) for the Infection Behavior. Also, we suggest incorporating social contact behavior similar to [14] for a more complex movement and contact behavior of agents.

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# Appendix A

## Source Code

```
model TwoBlockLayout
global{
    float width_size <- 7.0;      //  Size of Classroom
    float length_size <- 9.0;
    float grid_cell_length <- 0.25;
    geometry shape <- rectangle(width_size#m,length_size#m);
    int nb_susceptible_init <- 39; //  Initial number of Susceptible agents
    int nb_infected_init <- 1;   //  Initial number of Infected agents
    int nb_recovered_people_init <- 0; //  Initial number of Recovered agents
    int population <- nb_susceptible_init + nb_infected_init; //  Total Population
    // Updating number of agents per compartment
    int nb_infected_people <- nb_infected_init update: people count (each.agent_color = #red or
    each.agent_color = #orange);
    int nb_susceptible_people <- nb_susceptible_init update: people count (each.agent_color = #blue);
    int nb_recovered_people <- nb_recovered_people_init update: people count (each.agent_color = #green);
    float num_newly_infect <- 0.0;
    float prev_num_newly_infect <- 0;
    float prob_cough <- 0.61; //  Probability of Coughing parameter
    float rad_infect <- 1; //  Radius of Infection parameter
    float prob_infect <- 0; //  Probability of Infection from Cough parameter
    float increase <- 0; //  Percentage increase for prob_infect
    float increase_prob_cough <- 0; //  Percentage increase for prob_cough
    int maxiter <- 2000; //  Maximum Number of Iteration
    float multiplier <- 0; //  prob_infect multiplier for scenarios
    bool vaccinated <- false; //  Scenarios Booleans
    bool eat_healthy <- false;
    bool comorb <- false;
    bool micro_nut_deficiency <- false;
    date my_date <- date("2023-02-01-08-00-00"); //  Global Clock and Timestep
    float step <- 15 #mn;
    int nb_day <- 1;
    init{
        if(vaccinated){ //  Multiplier values for each scenario
            multiplier <- -0.91;
        }
        if (eat_healthy){
            multiplier <- -0.1;
        }
        if(comorb){
```

```

        multiplier <- 0.5;
    }

    create people from:csv_file( "../includes/twoblock.csv",true) with: // Other files for
    Seat Distance Sensitivity Analysis: twoblock_min_20 | twoblock_min_10 | twoblock_min_5
    | twoblock | twoblock_plus_5 | twoblock_plus_10 | twoblock_plus_20
        [grid_x::float(get("gridx")), // Initialization of Susceptible, Infected, and Recovered Agents
         grid_y::float(get("gridy")),
         state::string(get("state"))
    ];
}

ask nb_infected_people among people{
    state <- "Infected Contagious";
    num_day_infected <- 5;
    is_infected <- true;
    agent_color <- #red;
}
}

reflex print_iteration{ // Iteration number printer
    write("");
    write("Iteration: " + cycle);
}

reflex update_time{
    my_date <- my_date plus_minutes 15; // Increment real time per iteration
}

bool check <- false;
reflex cal_day { // Increment current day every 36 iteration
    if (((my_date.hour != 0) and (my_date.hour mod 9 = 0)) and !check) {
        nb_day <- nb_day + 1;
        check <- true;
        my_date <- my_date plus_hours 15;
        loop i over: people{ // Update number of days infected for all infected agents
            if(i.is_infected){
                i.num_day_infected <- i.num_day_infected + 1;
            }
        }
        prev_num_newly_infect <- num_newly_infect;
        num_newly_infect <- 0;
        loop i over: people{
            if(i.num_day_infected = 1){ // Update number of newly infected individuals per day
                num_newly_infect <- num_newly_infect + 1;
            }
        }
    }
    if (current_date.hour mod 9 = 1) {
        check <- false;
    }
}
}

```

```

reflex end_simulation when: cycle = maxiter { // Simulation ends at iteration 2000
    do pause;
}

reflex extract_output_data{ // Record current number of SIR for each iteration in a csv file
    save [increase_prob_cough ,increase, nb_day,cycle, nb_susceptible_people, nb_infected_people,
    nb_recovered_people, num_newly_infect, vaccinated, eat_healthy, comorb, micro_nut_deficiency]
    to: name + "_Experiment_1.csv" type: csv rewrite: (cycle = 0) ? true : false;
}

bool move <- false;

reflex move_agents{ // Moving Behavior for all agents
    loop i over: people{
        if(((my_date.hour = 2) and (my_date.minute = 15)) or ((my_date.hour = 4) and (my_date.minute = 15))){
            move <- true;
        }
        if(((my_date.hour = 2) and (my_date.minute = 45)) or ((my_date.hour = 5) and (my_date.minute = 15)) ){
            move <- false;
            i.location <- {i.grid_x, i.grid_y};
        }
        if(move){
            i.location <- any_location_in(shape);
        }
    }
}

species people skills:[moving]{ // Defining agents' attributes and actions
    float grid_x; // Coordinates of the initial positions of an agent
    float grid_y;
    string state;
    rgb agent_color <- #blue; // Agents' color based on infection status
    bool is_infected <- false; // Infection status
    int num_day_infected <- 0; // Agents' number of day infected
    date date_got_infected; // Date when an agent got infected
    init{
        location <- {grid_x,grid_y}; // Initialize agents' locations
    }
    reflex update_state when: is_infected{ // Update infection status: noncontagious -> contagious -> recovered
        if(num_day_infected >= 5 and num_day_infected < 14){
            state <- "Infected Contagious";
            agent_color <- #red;
        }
        if(num_day_infected >= 14){
            state <- "Recovered";
            is_infected <- false;
            agent_color <- #green;
        }
    }
    reflex cough when: is_infected and (state = "Infected Contagious"){ // 2-layer threshold
}

```

```

Infection Behavior using prob_cough and prob_infect
float r <- rnd(0.00,1.00, 0.01);
if(r <= ((prob_cough*increase_prob_cough) + prob_cough)){ // Increasing prob_cough for
the Sensitivity Analysis
  write("Cough Performed by: " + self);
  if(state = "Infected Contagious"){
    ask people at_distance rad_infect#m { // Loop over all susceptible agents within
    1 meter radius of infected agent
      if(!self.is_infected and self.agent_color = #blue){
        float distance_between <- self distance_to myself; // Calculate distance
        between actor(infected agent) and susceptible agent
        write("");
        write("Infected " + myself);
        write ("Susceptible " + self);
        write("Distance: " + distance_between);
        if((distance_between >= 0) and (distance_between <= 0.25)){ // prob_infect values
        depending on the distance of the two agents
          prob_infect <- 0.61;
        }
        if((distance_between > 0.25) and (distance_between <= 0.50)){
          prob_infect <- 0.55;
        }
        if((distance_between > 0.50) and (distance_between <= 0.75)){
          prob_infect <- 0.38;
        }
        if((distance_between > 0.75) and (distance_between < 1.00)){
          prob_infect <- 0.15;
        }
        if(distance_between >= 1){
          prob_infect <- 0.03;
        }
        prob_infect <- (prob_infect * multiplier) + prob_infect; // Different Prob_infect
        values for each scenario
        prob_infect <- (prob_infect * increase) + prob_infect; // For Sensitivity Analysis
        | Experimental cases (i.e 20%\ increase)
        float r <- rnd(0.00,1.00, 0.01);
        write("Prob_infect value: " + prob_infect);
        write("Random Number Generated: " + r);
        if(r <= prob_infect){ // Checker if an agent got infected from the cough
          self.is_infected <- true;
          self.state <- "Infected Non-Contagious";
          self.agent_color <- #red; // Can use color orange to make noncontagious distinct
          self.date_got_infected <- my_date;
          write("Agent "+myself+ " infects agent "+self);
        }
        else{ // No infection happened
          write("No infection happened");
        }
      }
    }
  }
}

```

```

        }
    }
}
}

aspect circle { // Agents representation in the model: 0.125 meter radius
    draw circle(0.125#m) color: agent_color;
}

aspect name { // Displays name of an agent in the simulation
    draw name size: 3 color: #black ;
}

aspect num_day_infect {
    draw string(num_day_infected) size: 2 color: #white; // Displays number of days an agent got infected
}

grid grid_cell cell_width: 0.25#m cell_height: 0.25#m neighbors: 8 { // Initialize grid
    list<grid_cell> neighbors1 <- (self neighbors_at 1);
}

experiment explore_increase_prob_cough type: batch repeat: 10 until: cycle = 2000{ // OFAT Sensitivity
    Analysis values for prob_cough, Experimental cases values (-20\%, -10\%, -5\%, 0\%, 5\%, 10\%, 20\%)
    parameter "increase_prob_cough" var: increase_prob_cough among: [-0.20,-0.10,-0.05, 0, 0.05, 0.10, 0.20];
    output {
    }
}

experiment explore_increase_prob_infect type: batch repeat: 10 until: cycle = 2000{ // OFAT Sensitivity
    Analysis values for prob_infect, Experimental cases values (-20\%, -10\%, -5\%, 0\%, 5\%, 10\%, 20\%)
    parameter "increase" var: increase among: [-0.20,-0.10,-0.05, 0, 0.05, 0.10, 0.20];
    output {
    }
}

experiment TwoBlockLayout type: batch repeat: 10 until: (cycle=2000){ // Main experiment of ABM
    output { // Monitor updated values for each iteration
        monitor "Current Hour" value: my_date.hour;
        monitor "Date" value: my_date;
        monitor "Day Counter" value: nb_day;
        monitor "Total Population" value: population;
        monitor "Initial Number of Susceptible" value: nb_susceptible_init;
        monitor "Initial Number of Infected" value: nb_infected_init;
        monitor "# of NEWLY INFECTED Individuals" value: num_newly_infect;
        monitor "# of INFECTED Individuals" value: nb_infected_people;
        monitor "# of SUSCEPTIBLE Individuals" value: nb_susceptible_people;
        monitor "# of RECOVERED Individuals" value: nb_recovered_people;
        monitor "# of HEALTHY Individuals" value: nb_susceptible_people + nb_recovered_people;
    }

    display main_display {
        grid grid_cell lines: #black;
    }
}
}
```

```
    species people aspect:circle;  
}  
}  
}
```