1. Goals

The objective of this study is to employ a computational framework for modeling the spread of the COVID-19 pandemic within a specific area, employing carefully determined parameters. By leveraging this modeling approach, we aim to simulate the progression of the disease and evaluate its impact under various scenarios. Through this process, we seek to gain valuable insights into the potential outcomes of different policy interventions. Initially, we have two main policies and to observe how the system behaves, we consider the five performance criteria which are the total number of infected people in the system, the total number of vaccinated people in the system, the total number of infected people who are vaccinated in the system, the total number of healed people in the system and the total number of dead people in the system.

2. Introduction of Simulation

This modeling basically consists of 7 files in total, including 1 main body, 1 test main and 5 functions named infection, isolation, movement, OneVaccination, TwoVaccination.

The movement function defines the movements of people, the isolation function defines the isolation policy, the infection function defines the spread and results of the disease, the OneVaccination function defines how people are affected in cases of 1 dose of vaccine, and the TwoVaccination function defines the effects on people when 2 doses of vaccine are applied.

The main body file contains the model parameters, the distribution of people on the grid, the simulationMatrix, and 200 iterated TEST PARTs where values are written into the SimulationMatrix. The simulationMatrix is a matrix of size N*14(where N represents the number of people) with N rows and 14 columns, containing 14 different data of people and simulation. The data represented by the 14 columns in simulationMatrix are as follows:

Column 1: Person's number

Column 2: x coordinate of person

Column 3: y coordinate of person

Column 4: sick or not? (1 if sick, 0 if not)

Column 5: How many iterations have passed since getting sick? (0 for initially infected)

Column 6: live or dead (1 if live, 0 if dead)

Column 7: isolation (0 if not isolated, 1 if isolated)

Column 8: infection probability

Column 9: 1st vaccination (1 if yes, 0 if not)

Column 10: 2nd vaccine received/not (1 if yes, 0 if not)

Column 11: number of days since vaccination

Column 12: in which iteration did he/she die?

Column 13 : in which iteration was the 1st vaccine given?

Column 14 : Number of healed people

By using those data in simulationMatrix, it is aimed to reach 5 data in the most accurate way at the end of the simulation. These are the data:

1. infectedCounts: total number of infected people in the system in each iteration,

2. healedCounts: total number of healed people in the system in each iteration,

3. deadCounts: total number of dead people in the system in each iteration,

4. vaccinatedCounts: total number of vaccinated people in the system in each iteration,

5. infectedVaccinatedCounts: total number of infected people who are vaccinated in the system in each iteration.

The data vaccinatedCounts and infectedVaccinatedCounts for Case1, Case2 and Case4 are not valid because there is no vaccine in these cases.

The main file actually contains the entire simulation itself. However, the data obtained from the main file contains many free variables such as the initial random location of the infected people, the random location of the infected people in the simulation, the number of random steps people take and the direction of these steps, the probability of getting the disease, and their desire to get the second vaccine. That's why we created the test file to process the data from the main file in order to get more accurate data to provide more accurate estimates to the government and to make our views more consistent. The test file repeats the simulation we designed 500 times and stores 5 data obtained from the simulation. Then it collects all of this data and divides it by 500, which is the number of repetitions. With this method, we aimed to ensure that the data obtained from our simulation were more consistent. The test file is also the file where the average data obtained is stored and graphed. Test file draws graphs showing how the 5 data obtained after a for loop repeated 500 times change in each iteration.

3. Cases

Case 1

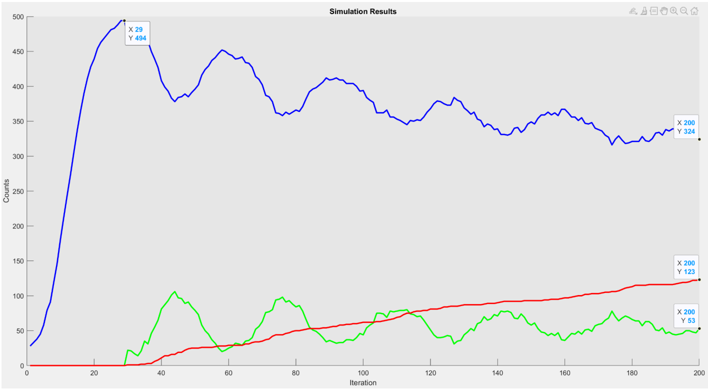


Figure 1: Results with the High Number of Population

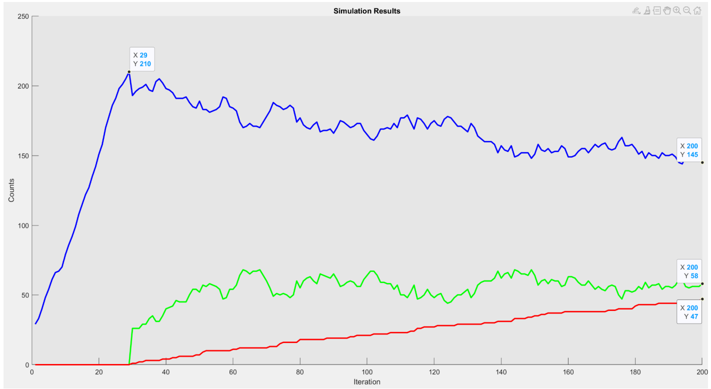


Figure 2: Results with the Low Number of Population

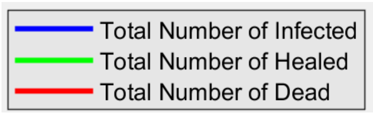


Figure 3: Legends of Colour

In this case, we analyze the impact of the initial number of infected people on the spread of pandemic. To observe how the simulation reacts to isolation; first we set parameters to average values to our model such that p=0.4 and M=30. Since, we know the initial number of infected people depends Δ1 and N. First we investigate the effect of Δ1 and N and keep Δ2 values constant such that equals to 50 . Our goal was to observe how the same initial number of infected people with different Δ1 and N values impact the spread of pandemic. Moreover, simulation results can be seen in Figure 1 for Δ1=5 and N=500 and Figure 2 for Δ1=10 and N=250. From these results we conclude even the same initial number of infected people with different Δ1 and N affects the spread of the pandemic. High number of population leads to more number of dead than low number of population and also affect the total infected people.

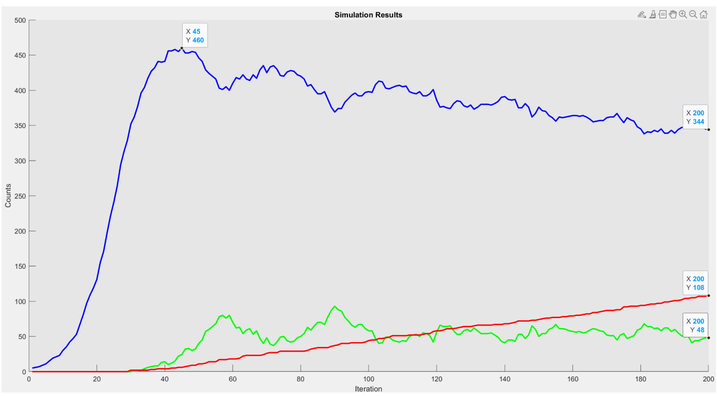


Figure 4: Results with the Low Number of Infected People with Low Application of Isolation Policy

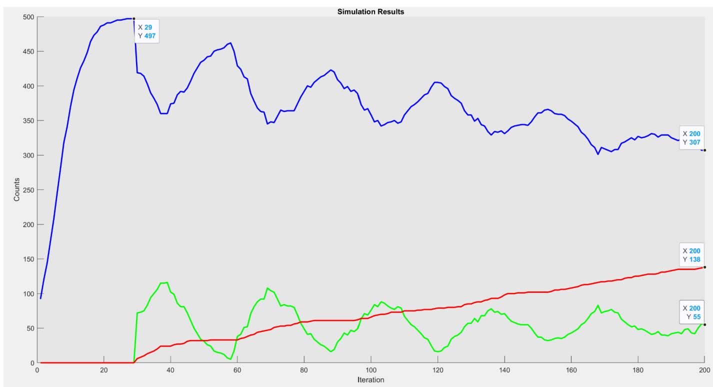


Figure 5: Results with the High Number of Infected People with Low Application of Isolation Policy

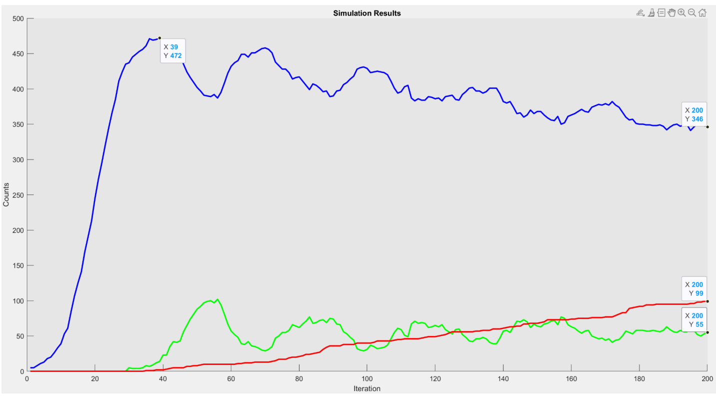


Figure 6: Results with the Low Number of Infected People with High Application of Isolation Policy

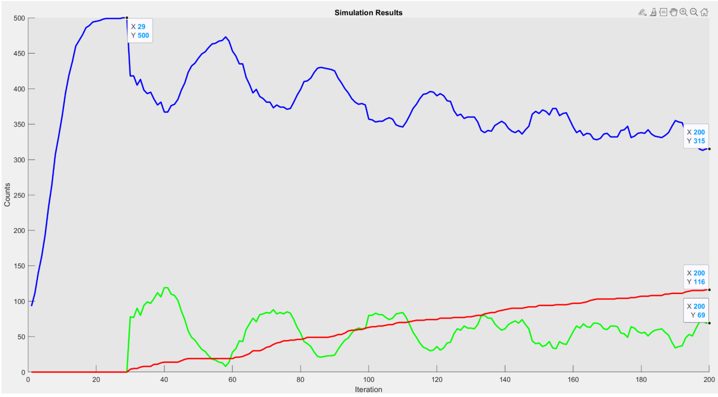


Figure 7: Results with the High Number of Infected People with High Application of Isolation Policy

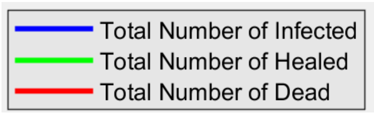
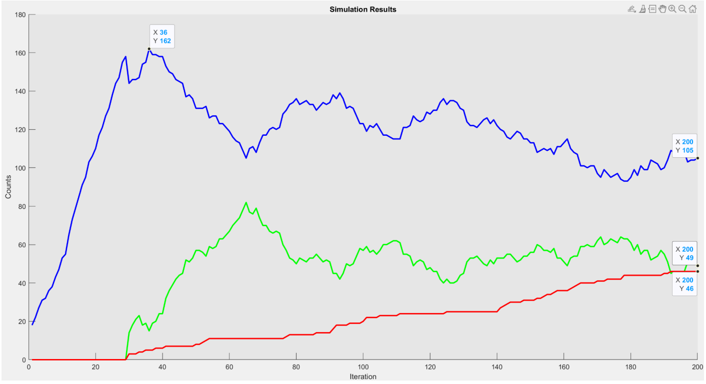


Figure 8: Legends of Colour

Now, we investigate the impact of the initial number of infected people on the spread of the pandemic using different isolation policies. To observe how the simulation reacts we applied different $\Delta 2$ values. Moreover, for $\Delta 2$ =20 simulation results can be seen in Figure 4 for $\Delta 1$=1 and N=500 and Figure 5 for $\Delta 1$=15 and N=500. From these results we conclude, initially high numbers of infected people with low application of Isolation Policy lead to increased spread of pandemic and infected people reached a peak dramatically with a higher number of infected people. Moreover, this result increased the total number of dead people.

Furthermore, for $\Delta 2$ =80 simulation results can be seen in Figure 6 for $\Delta 1$=1 and N=500 and Figure 7 for $\Delta 1$=15 and N=500. From these results we can observe similar results to the Low Application of Isolation Policy with different initial numbers of infected people. From these results, we could say that Isolation Policy decreases the spread of the pandemic and number of dead people. However, the impact of the initial number of infected people is much more important than Isolation Policy. Thus, our recommendation to the government is that despite the initial number of infected people, the government should implement higher Isolation Policies to take control of the pandemic.

Case 2



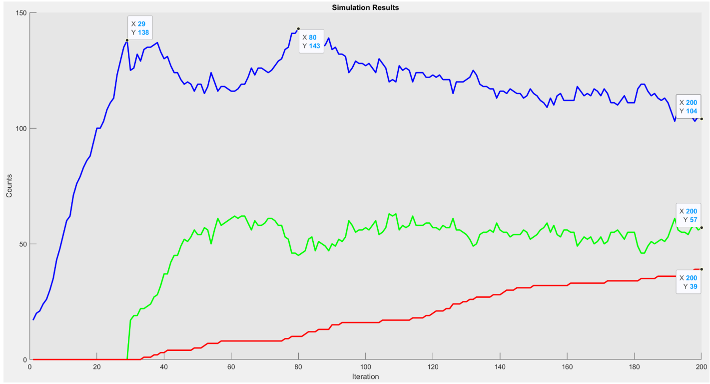


Figure 9: Results with the Low Application of Isolation *Figure 10: Results with the High Application of Isolation*

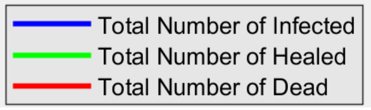
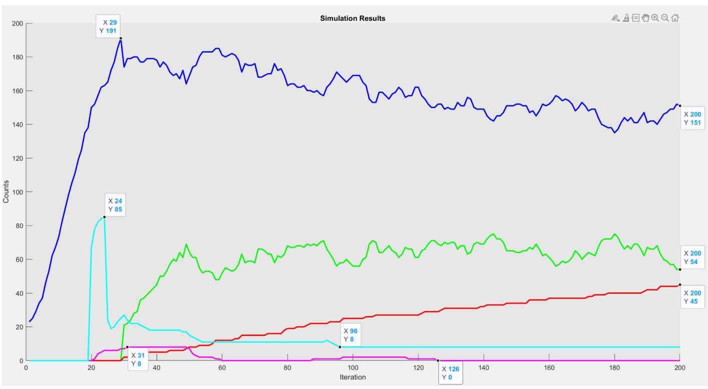


Figure 11: Legends of Colour

In this case, we analyze the impact of the isolation on the spread of the pandemic. To observe how the simulation reacts to isolation; first we set parameters to average values to our model such that N=200, Δ1= 8%, p=0.4 and M=30. To analyze, impact of implementation of isolation on the spread of the pandemic first we set Δ2= 0% and $q_s = 0$ and simulation results can be seen in Figure 7. Then, we set Δ2= 100% and $q_s = 100$ and simulation results can be seen in Figure 8. From these results we can conclude that strict isolation policy prevents the high number of infected people and also decreases the number of dead people. Thus, our recommendation to the government is to apply a strict Isolation Policy to take control of the spread of pandemic.

Note: In this case, we considered it as the absence of isolation and the isolation of every infected individual without exception.

Case 3



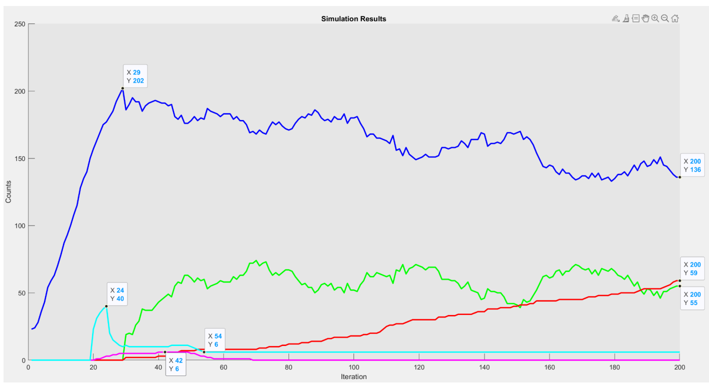


Figure 12: Results with the High Vaccination Rate *Figure 13: Results with the Low Vaccination Rate*

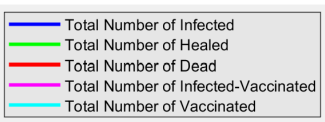


Figure 14: Legends of Colour

In this case, we analyze the impact of the vaccination rate on the spread of the pandemic. To observe how the simulation reacts to isolation; first we set parameters to average values to our model such that N=200, p=0.4 and M=30. To analyze, impact of implementation of isolation on the spread of the pandemic, first we set k= 1.5 and simulation results can be seen in Figure 12. Then, we set k= 4 simulation results can be seen in Figure 13. From these results we can conclude that higher Vaccination rates decreased the total number of dead people. However, we also observe that in the higher vaccination rates, the total number of infected people is higher than the lower vaccination rate. Thus, our recommendation to the government is to apply higher vaccination rates to decrease the total number of dead people.

Case 4

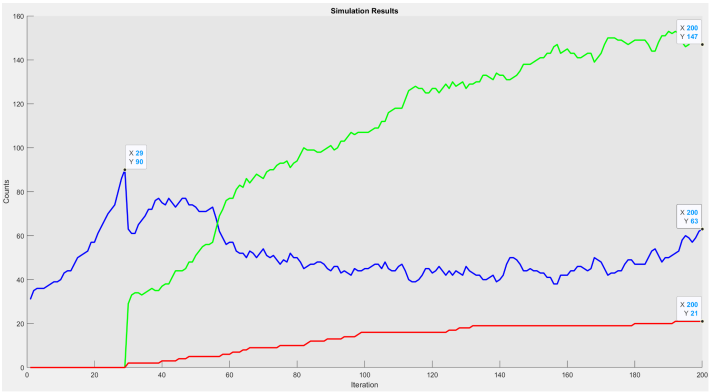


Figure 15: Results with the Low Contagiousness of Disease

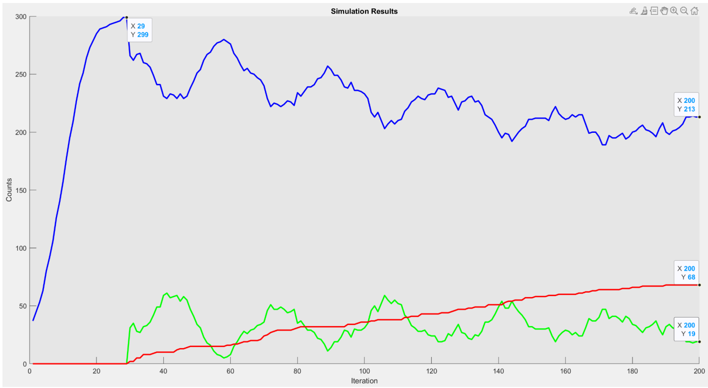


Figure 16: Results with the High Contagiousness of Disease

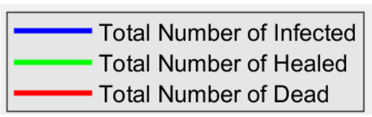


Figure 17: Legends of Colour

In this case, we analyze the impact of the contagiousness rate of disease on the spread of pandemic. To observe how the simulation reacts to isolation; first we set parameters to average values to our model such that N=300, Δ1= 8 % and M=30. To analyze, impact of the contagiousness rate of disease on the spread of the pandemic, first we set p= 0.1 and simulation results can be seen in Figure 15. Then, we set p=0.7 and simulation results can be seen in Figure 16. From these results we can conclude that higher contagiousness levels of disease increased the total number of infected people and total number of dead people. Because of the high contagiousness level of disease people got sick more frequently and this led to the pandemic not ending. Since, the contagiousness level is out of control of the government we can not recommend anything to this situation.

Case 5

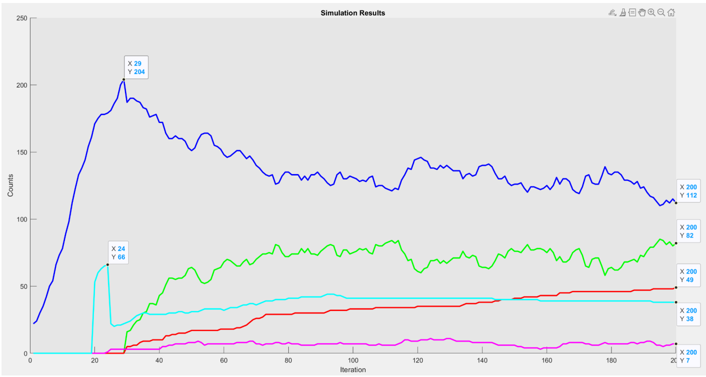


Figure 18: Results with the Low Numbers of Iterations between Double Vaccination

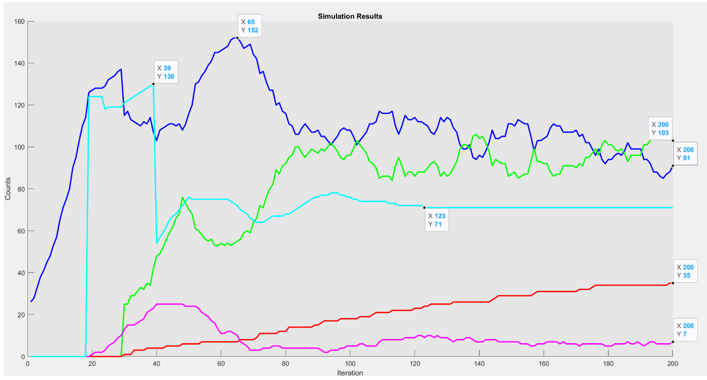


Figure 19: Results with the Mid Numbers of Iterations between Double Vaccination

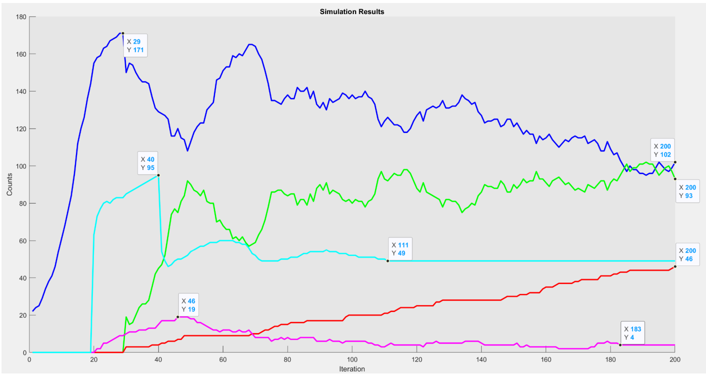


Figure 20: Results with the Low Numbers of Iterations between Double Vaccination

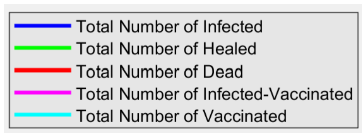


Figure 21: Legends of Colour

In this case, we analyze the impact of the prevention of vaccination on the spread of the pandemic under a double vaccination policy for different numbers of iterations between two vaccinations. To observe how the simulation reacts to different t_{sec} values; first we set parameters to average values to our model such that N=250, Δ1=8,M=30, k=3. To analyze the impact of different numbers of iterations between two vaccinations, first we set t_{sec} = 4 and simulation results can be seen in Figure 18. Then, we set t_{sec} = 10 and simulation results can be seen in Figure 19. Finally, we set t_{sec} = 20 and simulation results can be seen in Figure 20. Based on these data, it can be observed that increasing the t_{sec} period up to a certain value reduces the number of deaths, decreases the number of infected and increases the number of people followed up. However, when the t_{sec} value is increased too much, it is observed that this positive effect gradually loses its effect.

Case 6

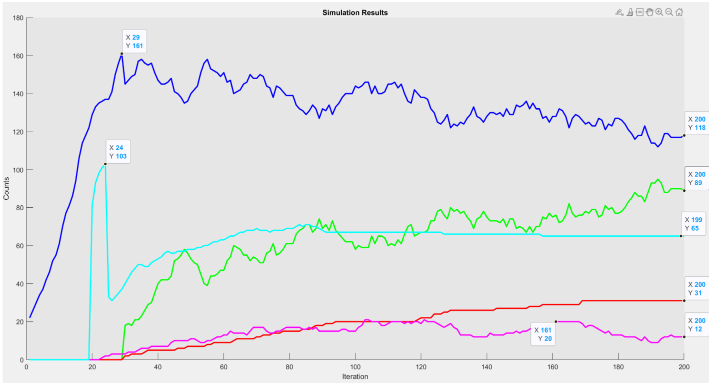


Figure 22: Results with the Low Probability of Healthy People

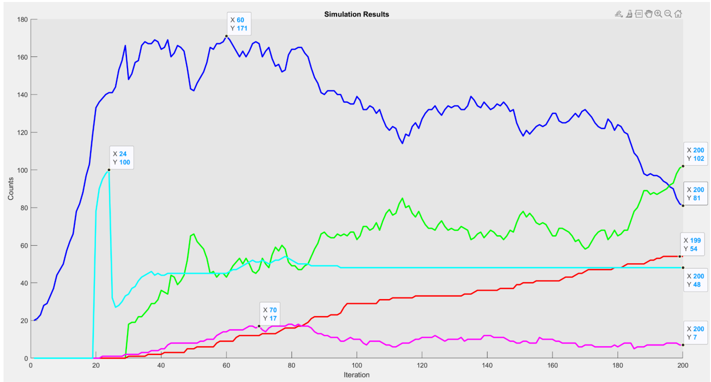


Figure 23: Results with the High Probability of Healthy People

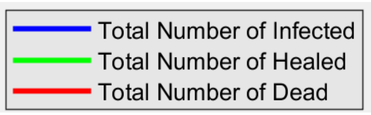


Figure 24: Legends of Colour

In this case, we analyze the impact of the willingness of people for the second vaccination on the spread of the pandemic. To observe how the simulation reacts to different w values; first we set parameters to average values to our model such that N=250, Δ1=8,M=0, k=1.5 and p =0.4. To analyze the impact of the willingness of people for the second vaccination on the spread of the pandemic, first we set w=0.4 and simulation results can be seen in Figure 22. Then, we set w=0.8 and simulation results can be seen in Figure 23. Based on these data, it can be observed that increasing the w value reduces the number of deaths, decreases the number of infected and increases the number of people followed up.

Case 7

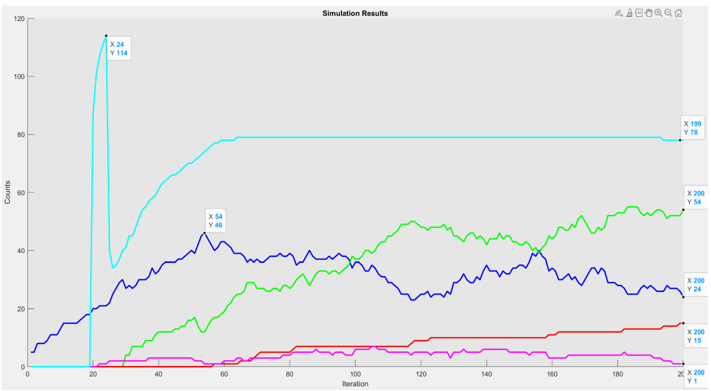


Figure 25: Scenario 1

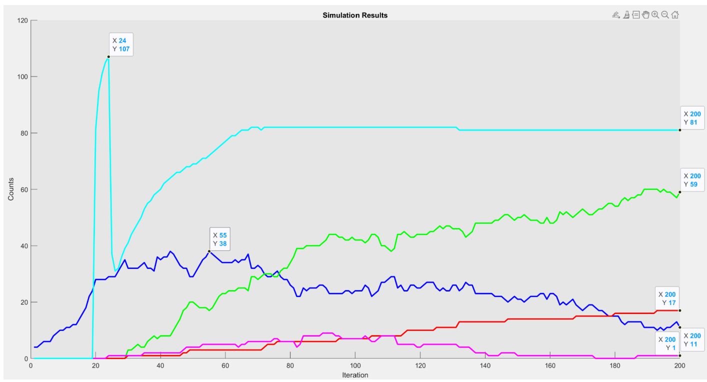


Figure 26: Scenario 2

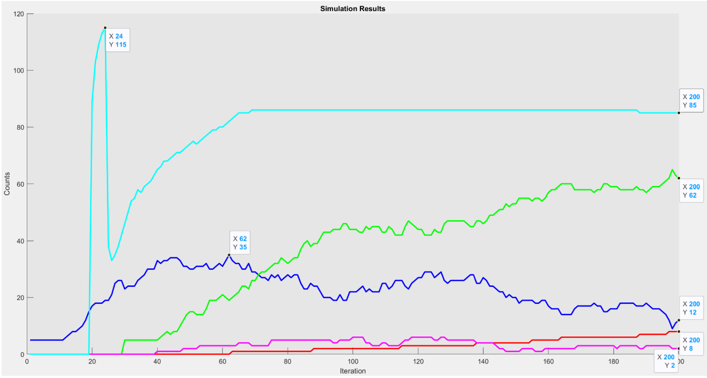


Figure 27: Scenario 3

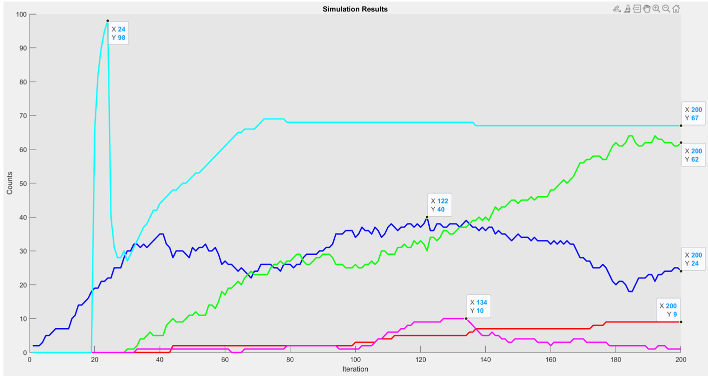


Figure 28: Scenario 4

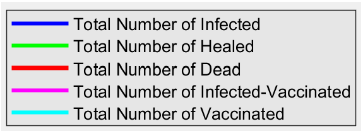


Figure 29: Legends of Colour

In this case, the government aims to control the spread such that at most 30% of the population is infected. For such a case, N = 150, p = 0.5, Δ2 = 5%, M = 30. To observe how the simulation reacts to different Δ1, w and k values, we design four scenarios. Scenarios 1 Δ1 = 3, w= 0.8, k=1.5 and simulation results can be seen in Figure 25. Scenarios 2 Δ1 = 2, w= 0.4, k=1.5 and simulation results can be seen in Figure 26. Scenarios 3 Δ1= 3, w= 0.6, k=1.5 and simulation results can be seen in Figure 27. Scenarios 4 Δ1 = 1, w= 0.4, k=2 and simulation results can be seen in Figure 28. As seen in the figures, in these scenarios we designed, the number of infected does not exceed 30%. However, the prerequisite for this is the Δ1 value. If the Δ1 value is more than 4, the ratio of the highest number of patients seen in the simulation to the population will be more than 30%, no matter what policy the government unfortunately implements. The k value should be 1.5 in any scenario where the population is not initially Δ1. Otherwise, the desired amount of the vaccine will not be used and the number of patients will exceed 30% of the population. If the Δ1 value is less than 3, the w value may be less than 0.6. However, if Δ1 = 3, the w value must be greater than 0.6.

Based on these observations, if the ratio of the number of patients at the beginning of the population to the population is more than 3%, our government will unfortunately not be able to achieve the desired target. However, incentive campaigns for 2nd dose vaccination, high vaccination numbers, etc. With these applications, the number of deaths can be reduced, the number of patients can be reduced and the number of recovered patients can be increased. If the ratio of the initial number of patients to the population is 3% or less, our government can achieve its desired target with high vaccination and public awareness-raising campaigns for the second dose of vaccine.