Conclusion

In this master thesis, the aim was to generate the covid numbers with the simulation of the traditional SIR model of the disease. A basic model of stochastic simulation is developed by incorporating Gillespie algorithm. Unlike the traditional compartmental SIR model the spread of the virus was also regulated by restricting the movement of the infected person. Both the TR and Beta value plays an important role in deciding the dynamics of the disease. We have made considered case with making one feature constant and iterating the other value. Introducing the vaccination has also given a insight how it would affect the disease spread. The results have shown a considerable results with the real situation. The dynamics of the disease were able to be explained with real reasoning.

This simulation can be further extended by adding more details in the dynamics with recovery. By removing the stochasticity in the recovery and implementing the counting days for the particular infected cell. Another way the simulation can be extended is adding more stages of the virus. Adding more compartments to the simulation. Also the cellular automaton can be more dynamic with the local infection of the virus. That is infection can be much more realistic rather than considering only horizontal and vertical cells.