In this chapter, we define an epidemiological model that is spatially explicit using stochastic cellular automaton on a square lattice with SIR structure. It is considered that COVID-19 has divided the society into 3 distinct subpopulations. S ,I ,R are the susceptible, infected and recovered as traditional compartmental SIR epidemic model. Another phase is also included in this model where in susceptible could go to recovered category after getting vaccination. The number of vaccinated only recorded in the case to get the demography of the stated changes of the population during the epidemic simulation. Consider the case of an SIR outbreak in a two-dimensional lattice of size LxL. Each 'cell' in this lattice is assumed as inhabited by a person.

Here are the consideration made default for the simulation

* No births or immigration are taken into account, i.e. the total population is always constant.
* Death due to infection is not considered. Every infected person will be considered to get recovered.
* Simulation runs until all the cells is recovered.

With these characteristics assumed, the structure for SCA is developed with a mix of the discrete event model and transition probability model , where the virus transmission is set to happen through a number of subevents or transition rules. The different states of cell in the matrix are finite values s {belong to} A ,where A ={ S,I ,R} where each letter denotes the same as the typical SIR model.

Following are the rules of the SCA for this particular simulation.

* Getting Infected- There are 2 ways of getting infected. Global infection or Local infection. Local infection occurs among the neighbors as mentioned above. And Global includes the whole Susceptible. Infection probability is Beta. That is there is beta time probability of a Infected person infecting another susceptible.
* Getting Recovered- This is the number of day it would take for the infected person to change into Recovered Person. The Poisson value is denoted as gamma. It is 1/number of days needed to recover.
* Getting vaccinated- Here is in this SCA due to less number of parameters considered , it was decided to vaccinate both Susceptible and Infected. Once getting an effective Vaccination the cell is changed to Recovered. 2 parameters are considered during vaccination. It is the number of people to be vaccinated in a day and the effectiveness of the vaccination. Vaccination are said to be not effective for all the doses. Efficacy is the value that determines how good the vaccination is in making the person immune to the virus.

The adjacent cell in the horizontal and vertical direction are considered as the neighbors. This is in focus as objective is to analyze how the local and community spread effects the spread of the virus.

Chart

Description automatically generated

Figure 1 Neighbors of the Infected Cell to be considered for local transmission

In the fig 1, the Shaded susceptible are the cells which will be considered to be infected as the local transmission. The common neighboring cells are made sure to be avoided during the simulation by using a tuple variable. And as far as the global transmission is considered , all the susceptible is taken to consideration during infection. Simply to represent that all the susceptible are likely to meet during the community spread including the neighbors and rest of the cells.

One discrete time step is considered as day in the simulation. On each day either global and local transmission occurs. The proportion of the local and global transmission is a predefined ratio called transmission ratio ( TR) in this simulation. The value of TR ranges from 0 to 1. 0 being the value for complete global transmission and 1 being the transmission solely local transmission. Stochasticity is applied to the decide how the transmission occurs on the particular time step. A random number is generated between the 0 and 1. If the value is less than the TR that particular time step undergoes global transmission and vice versa. The stochasticity was verified by running number of trials and having average ratio between the local and global transmission at the desired value. Also during the particular time step vaccination and recovery happens with their respective Poisson ratio. After each time step the count of each compartmental category is stored to a Pandas data frame. A particular Simulation is run for 100 times and have their value stored , of which average is taken to make the plots.

To do the simulation Jupyter Notebook was chosen as platform as the data is much more easier to handle in this platform. To represent the susceptible 0 is assigned as each value to the matrix. That is to initialize the population a null matrix of dimension L will be declared. When an infection is triggered the value is changed to 1 and it represent that the person is infected. And to represent recovery of the person the value is changed to 2. For now the recovery of person happens with a probability. This probability will be able to achieve the concept of recovery time for the infected person. One could change the algorithm to make sure that the particular infected person actually undergoes the recovery time. In case of vaccination the value directly moves to 2 to show that the either infected or the susceptible is vaccinated.

Graphical user interface, application

Description automatically generated

The infection Poisson ratio is called beta this is probability of the infected person infecting the susceptible after having a contact. Beta varies with respect to the viruses. The covid variants have had different beta values with each mutation. This paper have tried to iterate the beta values to find how the value change the dynamics of the spread. Other value are recovery rate and vaccination rate which are 1/7 and 1/10 respectively. Each of the actions happens in each time step with respect to its own probability.

Susceptible

Infected

Recovered

Vaccinated