Lab - 9: Cellular Automata based model of epidemic spread (SIR)

Kashyap Halavadia (202003040)* and Jay Patel (202003019)†
Dhirubhai Ambani Institute of Information & Communication Technology,
Gandhinagar, Gujarat 382007, India
MC312, Modeling and Simulation

In this lab we modelled SIR model of pandemic using a 2-D grid, a space-based model which does rule-based simulations. That's why it is called cellular-automata based simulation. Our main focus in this report will be to highlight the comparison between automata-based model and differential equation based model of SIR that we did in Lab-5.

I. INTRODUCTION

Cellular automata finds huge applications in modelling various different problems coming from various different domains. Here we are using automata for modelling SIR.

II. MODEL

If our population size is some number N then we have to take a 2-D grid in which each cell represents a person in the population.Each cell can take the states of integer values from 0 to 7, where 0 represents susceptible, 1 and 2 means infected and 3,4,5,6,7 represents different stages of immunity.

We took the following steps in preparing the code for the simulation:-

1. Initialize the 2-D grid using the probSusceptible , which is the probability that a cell will be susceptible during initialization.

2. Then do the rule-based simulations.

We have taken into consideration 4 type of rules :-

1. If any neighbour of a cell is infected it will become infected

2. If any neighbour of a cell is infected then the cell will get infected with a probability of probCatch.

3. Probability of a cell being infected depends on percent on infected neighbours.

4. Probability of a cell being infected depends on level of infection of neighbours.

III. RESULTS

For comparison between the two models we see that:-

1. The differential equation based model works in continuous time whereas in automata based model we have values of infected, susceptible and recovered at discrete time steps.We can see this following plot:-

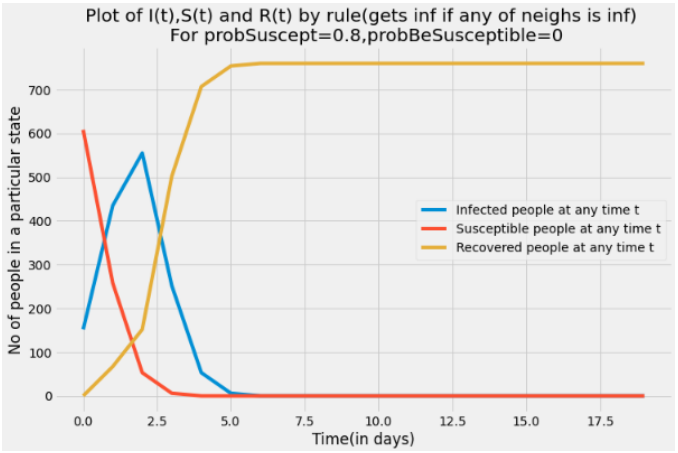

FIG. 1: Plot for Infected, susceptible and Recovered at any time t

In above figure, no of infected people at initialisation is a fair number i.e. it is comparable to the no of susceptible initially and because of which change in no of infected people will vary by a large amount when compared to the change in time(i.e 1 day), that's the reason the infected people curve is not smooth. The curve would have looked smooth(**??**) if the change in the no of infected people which are infected is small and in that case it would have been comparable to change in time which is by 1 unit.

*Electronic address: 202003040@daiict.ac.in
†Electronic address: 202003019@daiict.ac.in

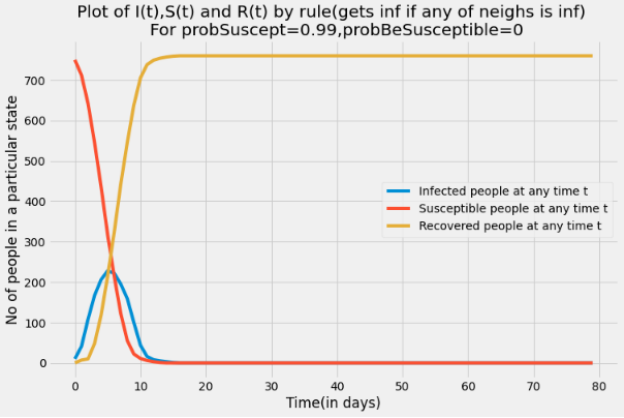

FIG. 2: Plot for Infected, susceptible and Recovered at any time t

Above plot is of the same initial parameters as 2 had.But it leads to a different path.
Because we are using probability for initialising the matrix so for different initialisations it will definitely lead to some different paths. But In RULE 2 another term of probability will make it further random and RULE 3, RULE 4 will lead to different simulations as probability of person getting infected depends on the state of its neighbours.
So for analysing such cases, we have done Monte Carlo simulations for all these 4 rules.Below are there plots:-

2. In this model to prevent recovered persons from going back to susceptible compartment we make probBeSuceptible=0 to make it similar to differential equation based model. However it is to note that we can tweak this parameter to be able to model effect of partial vaccination as it was in Lab-5.

3. In automata model that we simulated , we have considered a fixed no of days(i.e. 2 days) for a person to recover from a disease whereas in differential model we have a recovery rate i.e. α ,so $1/alpha$ denotes the average no of days for a person to recover from a disease.Note that in automata model also, we can introduce this by considering probability that a sick will recover or not on a particular day and that probability can be taken from distribution whose mean is α.

4. Also we see that in case of these automata based simulations it is stochastic because probability is involved in some of the parameters of the model, so we will see different plots for the same value of parameters , for eg the below plot:-

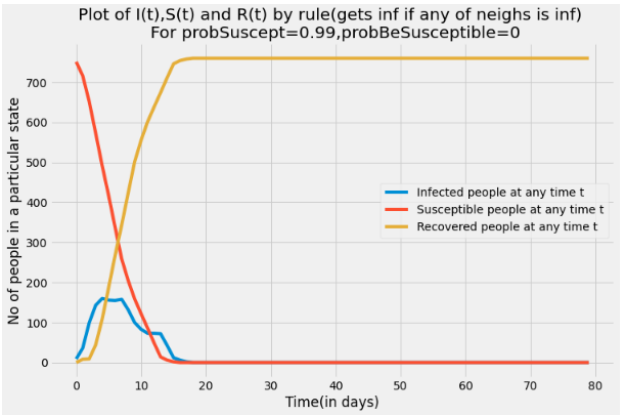

FIG. 3: Plot for Infected, susceptible and Recovered at any time t (second sample)

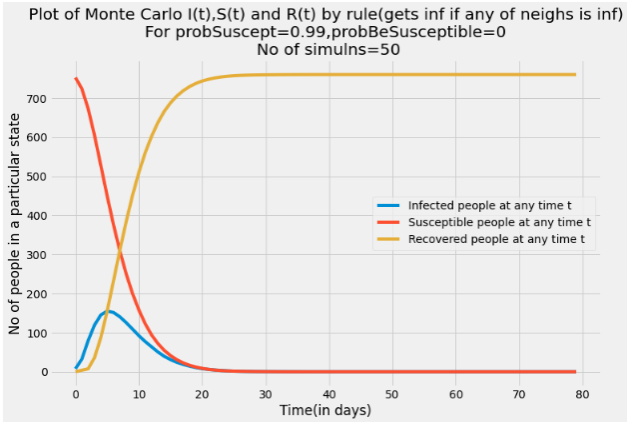

FIG. 4: Monte Carlo simuln plot for Rule1

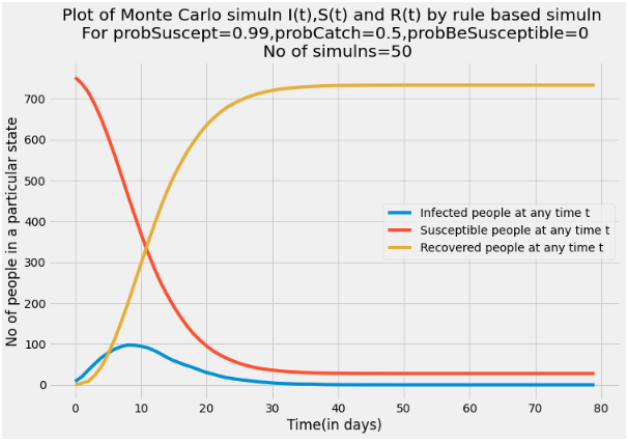

FIG. 5: Monte Carlo simuln plot for Rule2

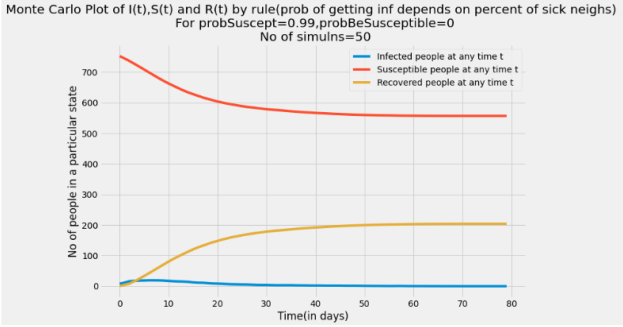

FIG. 6: Monte Carlo simuln plot for Rule3

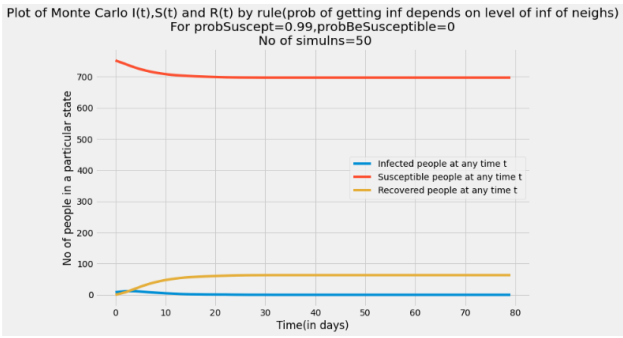

FIG. 7: Monte Carlo simuln plot for Rule4

We see that the Monte Carlo plots are very much similar to the plots that we obtained using differential eqn based model. We see that in RULE 2 , we can control how fast or easily the infection can spread to a susceptible person by setting the value of parameters(probCatch). Also in my opinion Rule 4 better models the situatiom than Rule 3, and Rule 3 models better than Rule2.Beacuse in Rule 3 , a person getting infected on percent of sick neighbours and in Rule4 , the probability of getting infection depends on level of infection of neighbours.

5. Controlling this speed of spread(in RULE 3) is like controlling *beta*(transmission coeff) in differential eqn based model which in turn determines Basic Reproduction no.

6. ALso we see that RULE 4 gives lower size of epidemic and lower intensity than compared to RULE4, a possible reason we can see is that because of assumptions of RULE 4 the probability of getting infection will be generally low.

7. So for getting plots similar to those of automata model in differential model we need to set beta accordingly.Below are some similar plots in differential model:-

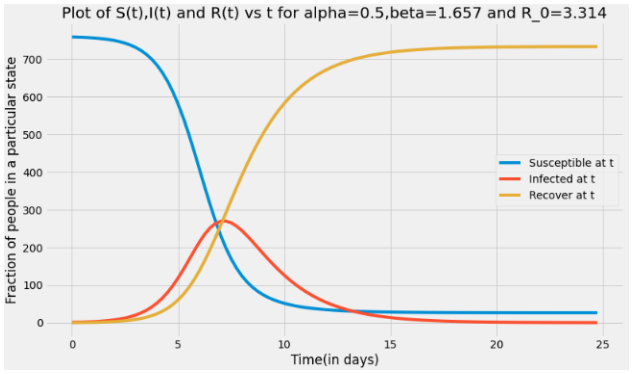

FIG. 8: Diff eqn based plot for *beta* =

We can see that above plot gives similar results as the plot of Monte Carlo simulation of RULE1 or RULE2. **??** and **??**

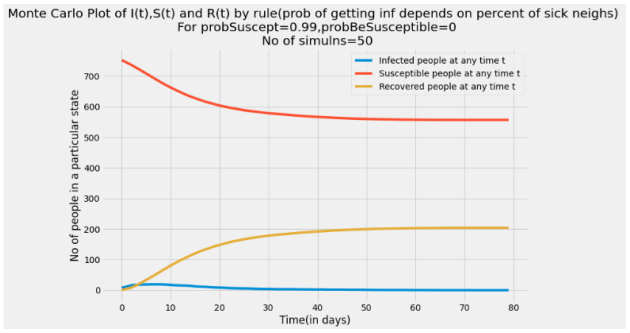

FIG. 9: Diff eqn based plot for *beta* =

We can see that above plot gives similar results as the plot of Monte Carlo simulation of RULE3.**??**

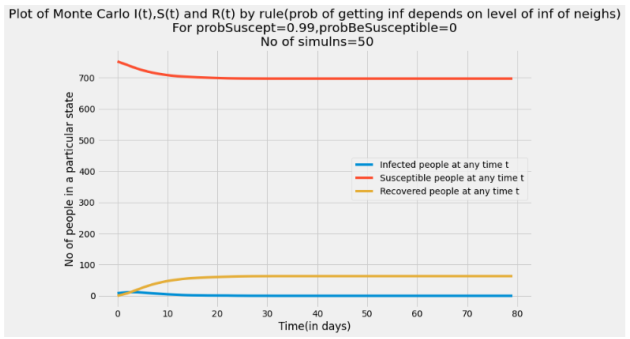

FIG. 10: Diff eqn based plot for *beta* =

We can see that above plot gives similar results as the plot of Monte Carlo simulation of RULE4.**??**

8. Also we can say that automata based model considers contact of person with its neighbours only for entire duration of time, this can be seen as resonable assumption as a person can get a infection

from its neighbours only , but we know that people are not stationary objects and they will visit different public places so a person might be in contact with a very large no of persons at a partiuclar point in time , so for a longer duration of time we have to consider contacts with other people as well at a particular time instant. This is captured in differential eqn based model where we use $beta = c.p$ where c is average no of contacts a person has per unit time and p is the probability of transmission of infection. So in this regard differential based model seems to be good choice.

---

[1] A. Shiflet and G. Shiflet, *Introduction to Computational Science: Modeling an Simulation for the Sciences*, Princeton University Press.3, 276 (2006).