Dhirubhai Ambani Institute of Information and Communication Technology

CS 302

Modeling and Simulation

Dr. Mukesh Tiwari

Cellular Automata for SIR model

Authors:	*Student IDs:*
Divyesh Ransariya	201601460
Barot Kuldip	201601461

April 10, 2019

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1 Cellular Automata with SIR

1.1 Abstraction & Assumption

A stochastic cellular automata (CA) model is proposed to simulate susceptibleinfected-removed populations over space and time. Two initial grid configurations are used to compare and contrast the spatiotemporal dynamics of this system; random, and center. The simulations show that random configurations infect more of the population, but quickly dissipating through the space. The center case slowly propagates through space and infects less of the population, while the patchy configuration shows to be a middle case between random and center.

In this model we have some basic assumptions.

- Assume that after some time infected people will cure and immune to disease.
- Assume Birth rate and Death rates are Zero.
- Total population(N) remain constant.
- We also consider that latent period of person is zero.

where, Susceptible(S) have no immunity from the disease. Infected(I) have the disease and can spread it to others. Recovered (R) have recovered from the disease and are immune to further infection. β is infection rate which tell how infection spread through infected people to susceptible. α is recover rate which tell how people recover from infection. For better under- standing we take $s = \frac{S}{N}$, $i = \frac{I}{N}$ and $r = \frac{R}{N}$

1.2 Introduction

Landscape epidemiology studies the disease patterns across the landscape that arise from abiotic and/or biotic conditions. The objective of this project is to simulate the spatiotemporal dynamics of an infectious disease propagation on various landscapes using a stochastic cellular automata (CA) susceptible-infected-removed (SIR) model.

1.3 Background

CA applied to grid-based modeling is a means to model disease propagation over time and space. CA models provide rules that are biologically motivated and easily programmable. In this approach, a grid array of cells represents a landscape. Each cell contains an embedded mini-model composed of state variables describing its condition, a means of communicating with surrounding cells (neighborhood), and rules dictating the cell's response to its own state and communications from its neighbors through a series of time-steps. The imposition of relatively simple rules can generate complex emergent behaviors as the landscape evolves through time.

1.4 Dynamic System

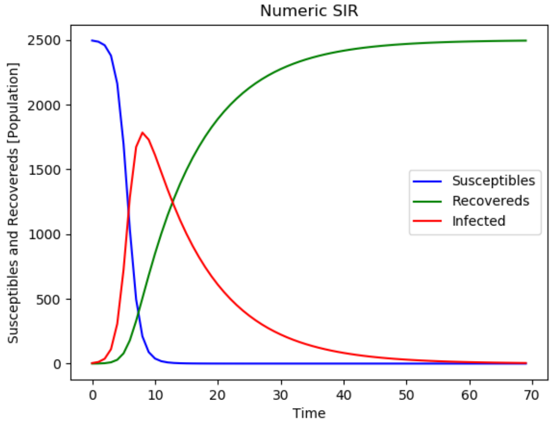
The CA rules can be extracted from the ideas behind the classical SIR models based on differential equations. The set of ordinary differential equations corresponding to the CA model is:

$$\frac{dS}{dt} = -\frac{\beta SI}{N}$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \alpha I$$

$$\frac{dR}{dt} = \alpha I$$

further more, $\frac{dI}{dt} = I\alpha(\frac{\beta S}{\alpha N} - 1)$ so here term R_0 is came in practice. $R_0 = \frac{\beta s}{\alpha}$. R_0 defines the shape of curve S and I.
where a is the infection rate, and b the recovering rate. The system is then divided into three groups, where each cell represents an individual that can be in one of three states: S, when the individual is susceptible to infection by neighbors; I, when the individual is infected and can transmit the disease for neighboring susceptible cells; and R, when the individual is recovered. Below Figure shows the ODE system plotted against time.
For simple simulation we choose $\beta = 1.2247$ and $\alpha = 0.1$ and $N = 2500$ and $S = 2499$ and $I = 1$. So $R_0 > 1$ so here Shape of I curve is first it will increase then attain certain maxima and then decrease.



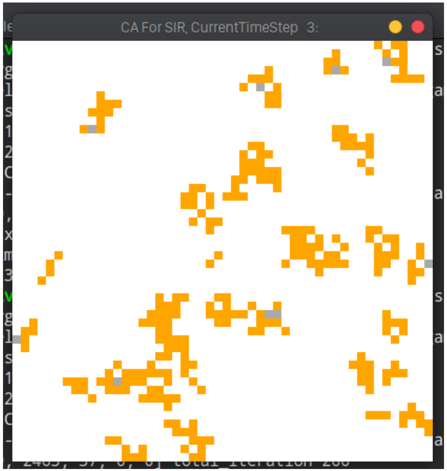
1.5 Method

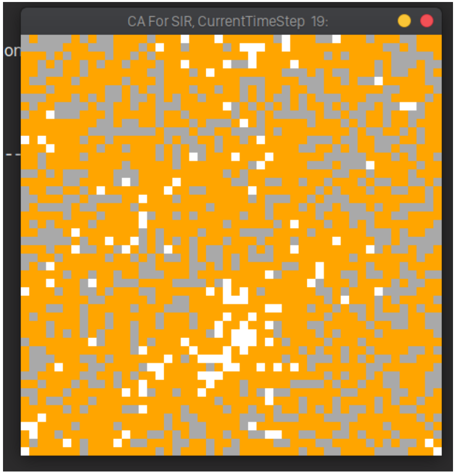
Scientific python was used to visualize the CA model depiction of the spatial disease propagation. The disease will propagate through the landscape based on a set of probabilities of state transitions. At each time step, there is a probability of a S cell becoming infected according to their set probabilities.Likewise, each I-cell can become recovered based on probability

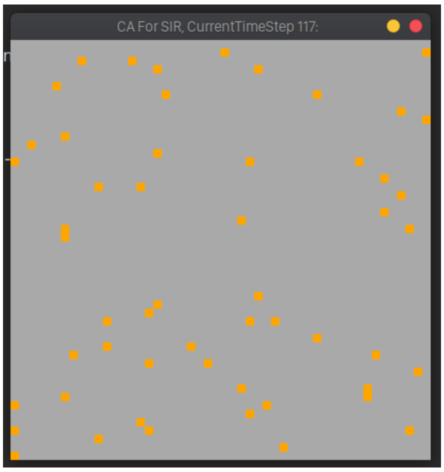
Pc or parameter α from the previous ODE model. The spatial and temporal dynamics were examined with simulations of various initial landscape population configurations, i.e., random, center, and patchy. The grid size used was 450x450 with ≈100% cell are susceptible and remaining one cell is infected. In first Center simulation we set probability to S become infected when its surrounded with infected is according to uniform random variable $\in (0, 1)$ if generated random sample is less than beta then we set S to I.

White pixel states susceptible, Orange pixel for Infected and Dark gray pixel for Recovered species.

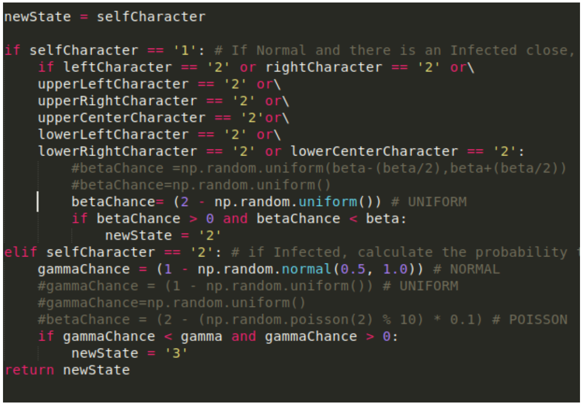
Below Three figures for infected spaced randomly, First snap is initial stage , second figure is when infected reached at maximum and last figure is when almost no infected remaining







For experiment purpose i choose below probability distribution (Here gamma is same as α).

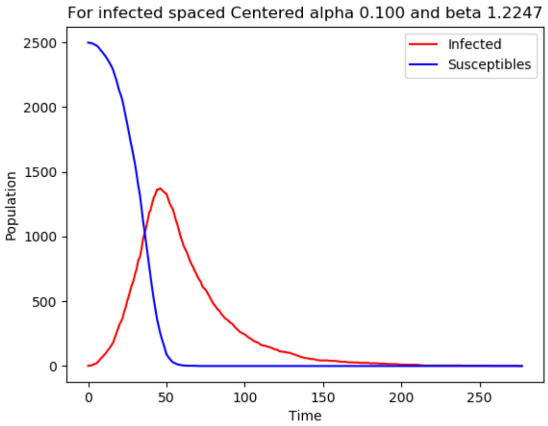


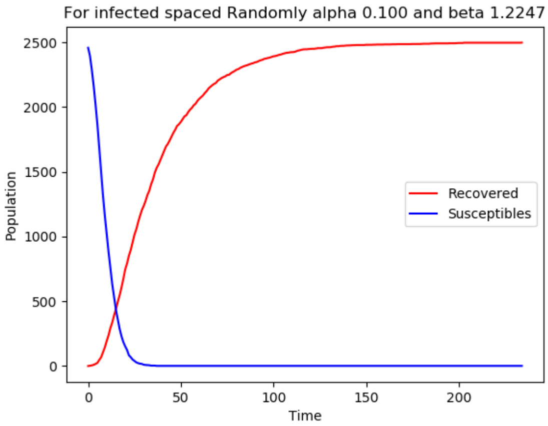
```
newState = selfCharacter

if selfCharacter == '1': # If Normal and there is an Infected close,
    if leftCharacter == '2' or rightCharacter == '2' or\
    upperLeftCharacter == '2' or\
    upperRightCharacter == '2' or\
    upperCenterCharacter == '2'or\
    lowerLeftCharacter == '2' or\
    lowerRightCharacter == '2' or lowerCenterCharacter == '2':
        #betaChance =np.random.uniform(beta-(beta/2),beta+(beta/2))
        #betaChance=np.random.uniform()
        betaChance= (2 - np.random.uniform()) # UNIFORM
        if betaChance > 0 and betaChance < beta:
            newState = '2'
elif selfCharacter == '2': # if Infected, calculate the probability t
    gammaChance = (1 - np.random.normal(0.5, 1.0)) # NORMAL
    #gammaChance = (1 - np.random.uniform()) # UNIFORM
    #gammaChance=np.random.uniform()
    #betaChance = (2 - (np.random.poisson(2) % 10) * 0.1) # POISSON
    if gammaChance < gamma and gammaChance > 0:
        newState = '3'
return newState
```

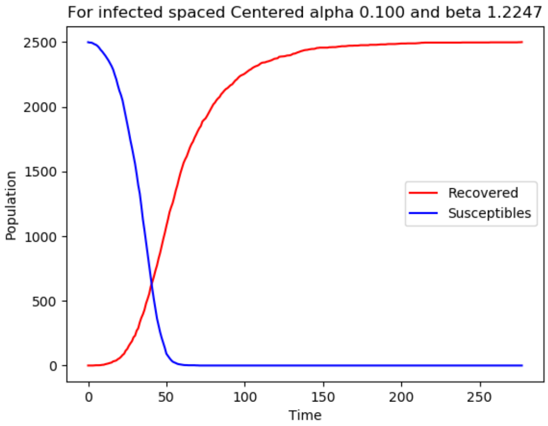
1.6 Results

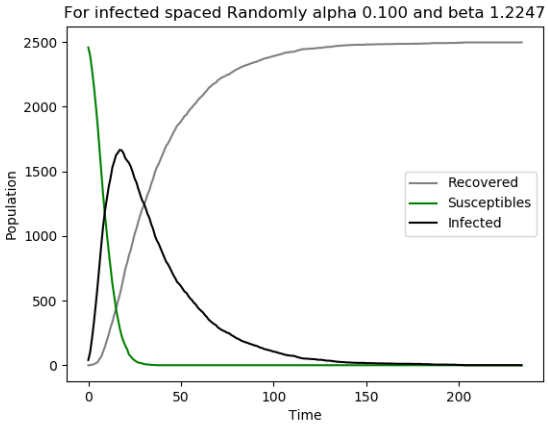
Each initial case (random, center, and patchy) were initiated and simulated over 300 time steps and averaged over 10 runs. Below Figures show an example snapshot of each case after 10 time steps. Here, it is clear that the random case infects the population more quickly than the center or patchy cases. Table shows the averaged maximum infected populations and time steps with their corresponding standard deviations. In combination with below figures, which show the example runs S, I, and R populations plotted against time, we see that the center case takes the longest time to propagate through the population while infecting the least amount of individuals. The random case infects the most individuals, but relatively quickly. And finally, the patchy case fits somewhere in between the random and center cases.

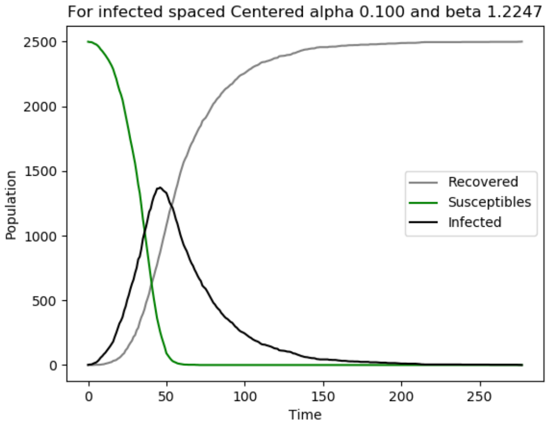
Below Figures are for infected spaced centered,





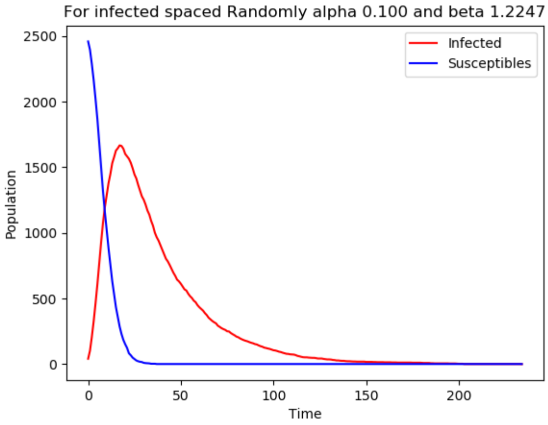






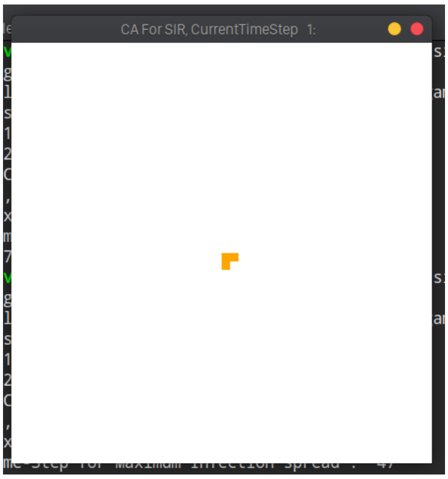
From figures we can show that in random case infection spreads more quickly compare to centered case this is because of R_0. In random case our $R_0 = \frac{\beta S_0}{\alpha}$ changed. In random case initial average $32-35$ people infected initial stage where in spaced centered case 1 people infected. So R_0 is less compare to second case since we know lesser the R_0 more the epidemic spread (More no of people infected/infection spread rapidly).

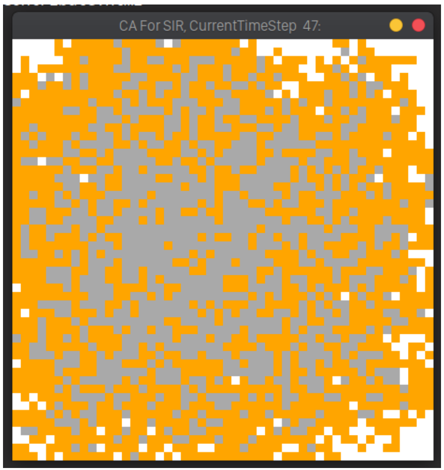
Below Figures are for infected spaced random,

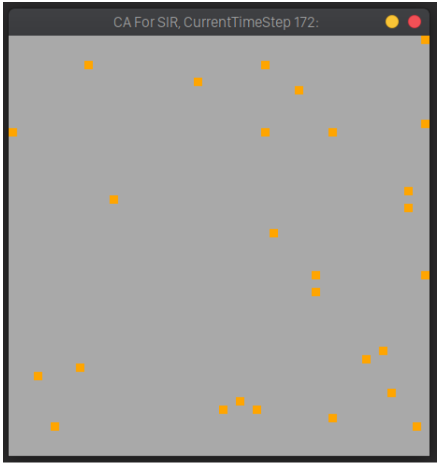


White pixel states susceptible, Orange pixel for Infected and Dark gray pixel for Recovered species.

Below is snap shot of CA simulation for both cases, first snap is initial stage second snap is when infected is reached maximum and last snap is when infected is 10% of total population.


CA For SIR, CurrentTimeStep 1:
me-Step for Maximum Infection spread : 47

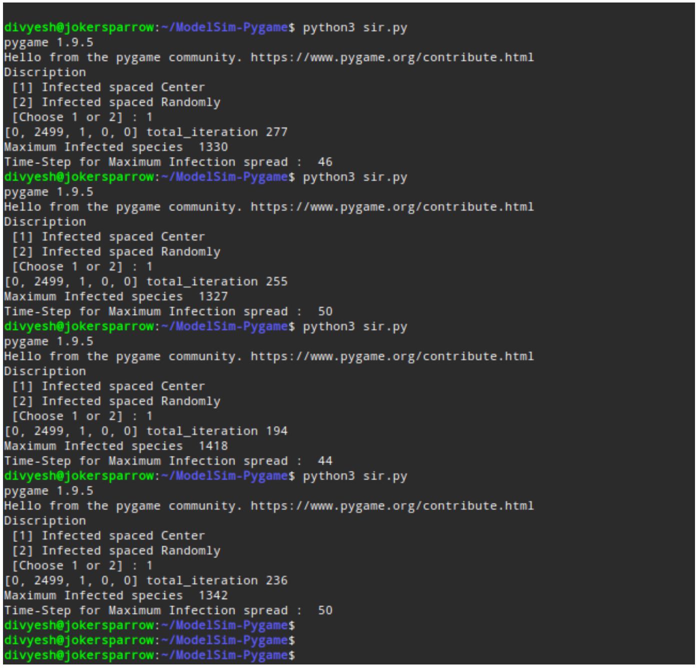




This model can be extended by including environmental layers, thus incorporating actual landscape barriers into the rules. It can also be improved to consider long-range interactions between CA cells that would incorporate metapopulation dynamics.

Observation over 30 simulations ± standard deviations		
Initial case	Maximum Infected cell(out-of 2500)	Time Step Maximum Infected(Out-of 300 ± 25)
Spaced center	1354 ± 50	48 ± 4
Spaced Random	1586± 100	17 ± 3

Various Simulations of spaced centered Infected



```
divyesh@jokersparrow:~/ModelSim-Pygame$ python3 sir.py
pygame 1.9.5
Hello from the pygame community. https://www.pygame.org/contribute.html
Discription
 [1] Infected spaced Center
 [2] Infected spaced Randomly
 [Choose 1 or 2] : 1
[0, 2499, 1, 0, 0] total_iteration 277
Maximum Infected species  1330
Time-Step for Maximum Infection spread :  46
divyesh@jokersparrow:~/ModelSim-Pygame$ python3 sir.py
pygame 1.9.5
Hello from the pygame community. https://www.pygame.org/contribute.html
Discription
 [1] Infected spaced Center
 [2] Infected spaced Randomly
 [Choose 1 or 2] : 1
[0, 2499, 1, 0, 0] total_iteration 255
Maximum Infected species  1327
Time-Step for Maximum Infection spread :  50
divyesh@jokersparrow:~/ModelSim-Pygame$ python3 sir.py
pygame 1.9.5
Hello from the pygame community. https://www.pygame.org/contribute.html
Discription
 [1] Infected spaced Center
 [2] Infected spaced Randomly
 [Choose 1 or 2] : 1
[0, 2499, 1, 0, 0] total_iteration 194
Maximum Infected species  1418
Time-Step for Maximum Infection spread :  44
divyesh@jokersparrow:~/ModelSim-Pygame$ python3 sir.py
pygame 1.9.5
Hello from the pygame community. https://www.pygame.org/contribute.html
Discription
 [1] Infected spaced Center
 [2] Infected spaced Randomly
 [Choose 1 or 2] : 1
[0, 2499, 1, 0, 0] total_iteration 236
Maximum Infected species  1342
Time-Step for Maximum Infection spread :  50
divyesh@jokersparrow:~/ModelSim-Pygame$
divyesh@jokersparrow:~/ModelSim-Pygame$
divyesh@jokersparrow:~/ModelSim-Pygame$
```