SIMULATION OF COMPLEX SYSTEMS

Report On Disease Spreading

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Exercise No:1

1. Initially the plot was plotted for a single agent. In the plot, a random walk was performed by the single agent, which was recorded for around 50 time steps. The figure 1 shows the various position of a single agent during different time steps.
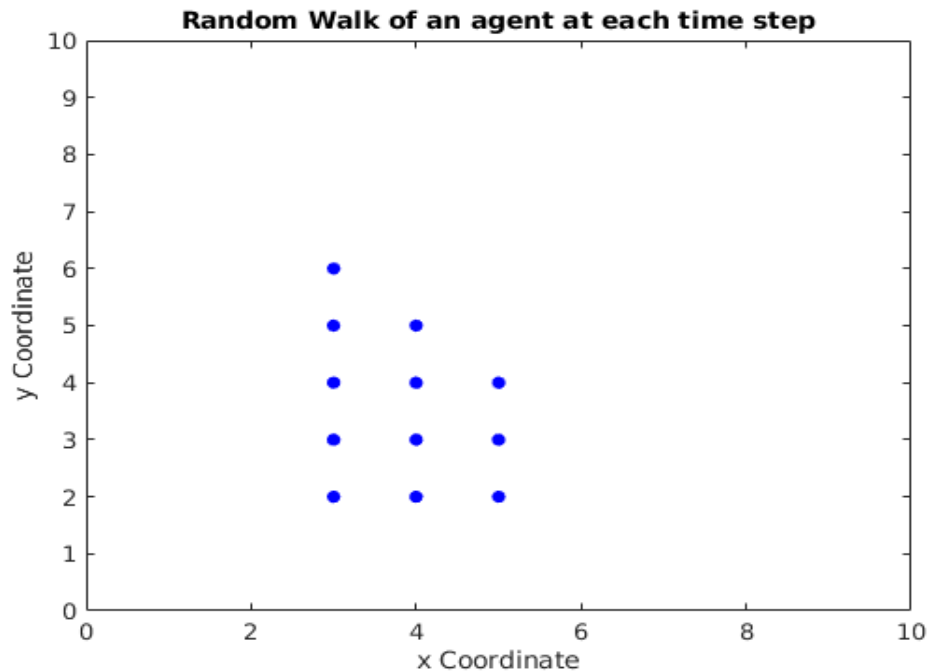

Figure 1: Random walk of an agent at each time step

2. The same plot was extended for multiple agents. The figure 2 shows the coordinate points of 20 agents at a time step. The number of time Steps is 50.
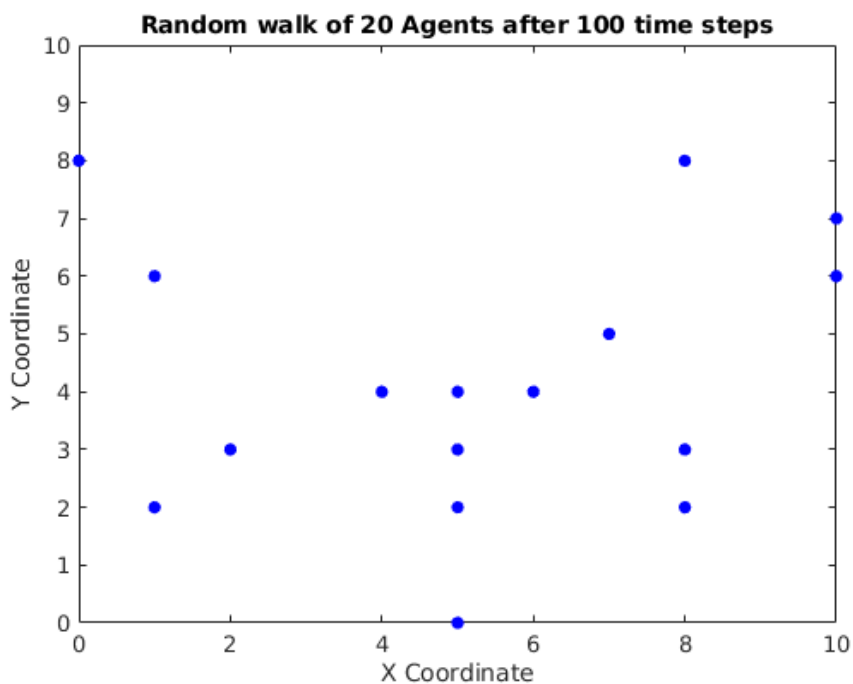

Figure 2: Coordinate positions of multiple agents

3. The figure 3 is plotted for 1000 agents in a 100*100 lattice where each agent is initialized with a random position in which some agents are susceptible, some are infected and some are recovered agents. The number of time steps is 1000.
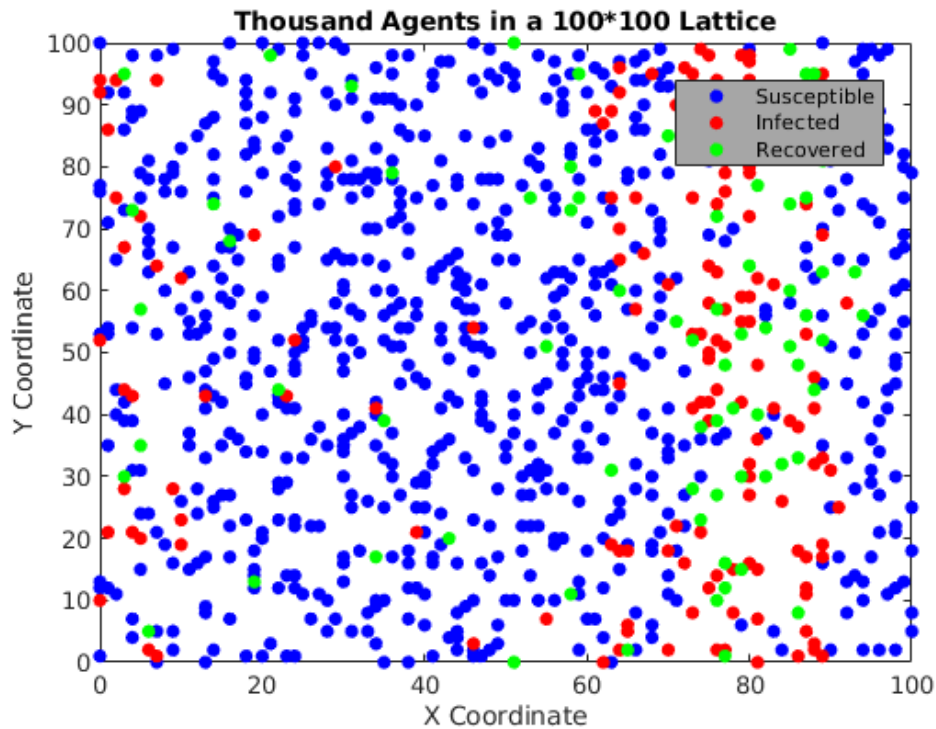

Figure 3: Thousand Agents in a 100*100 Lattice

Exercise No:2
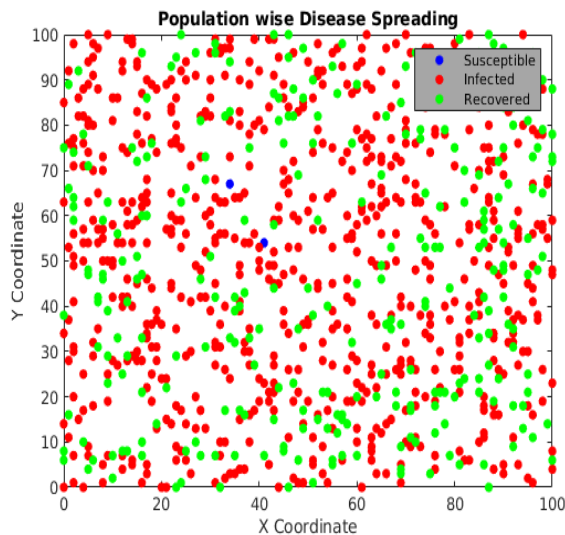
1. <u>Population wise Disease Spreading.</u>

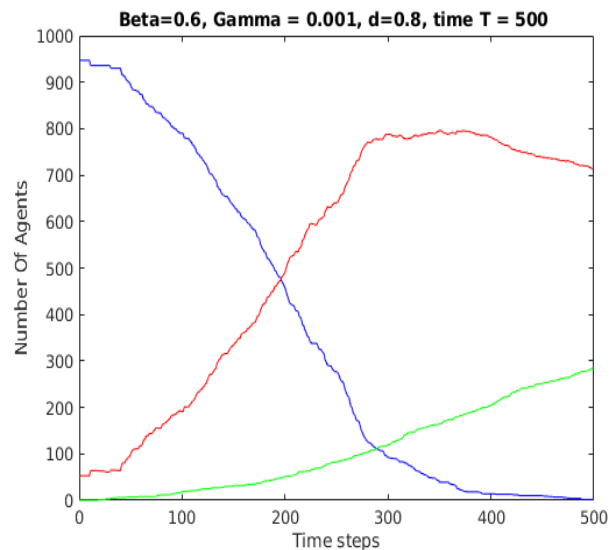Figure 4: Population Wise Disease Spreading

Figure 5: Plot of proportion of individuals

Figure 4 displays the population wise disease spread during the mentioned time period. The red dots mention the persons infected which are very huge in numbers,

the green dots denote the number of recovered persons. The number of susceptible persons are very low (only 2). This depicts that the disease is spread for the whole population.

Figure 5 shows that the proportion of susceptible agents (Blue line) decreases steadily as time passes by, the number of infected agents increases (Red Line) as time goes on, and the recovered persons also increase as time increases.
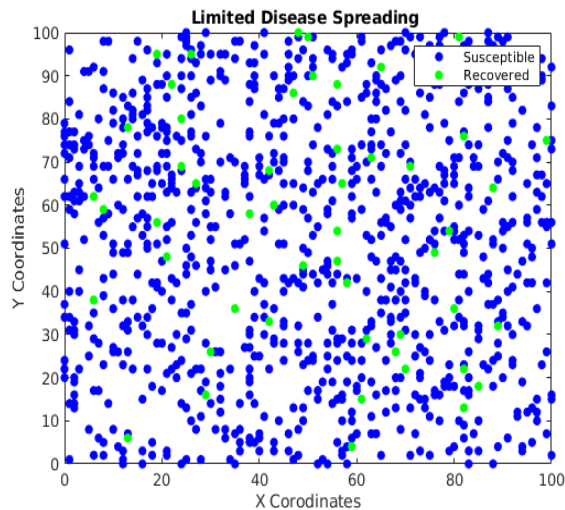
2. Limited Disease Spreading
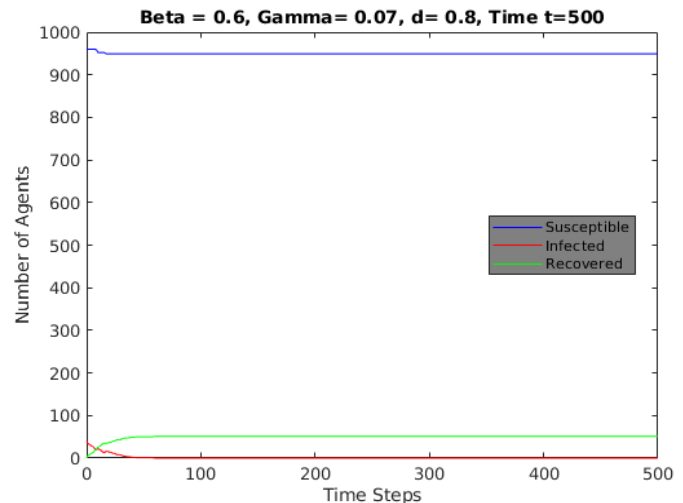

Figure 6: Limited Disease Spreading   Figure 7: Plot of Proportion of Individuals

Figure 6 can convey that the number of susceptible persons (Blue Dots) remain almost close to total population. This proves that the disease have not spread to the whole population at all. The number of infected agents (red dots) have already come to 0, and the number of recovered persons (green dots) are also very less. This shows the disease has spread only in limited quantity.

Figure 7 shows that the proportion of susceptible persons (blue line) is almost over 920, which shows that only a handful of people are infected. The number of infected persons (red line) has dropped to 0 after very less time itself.

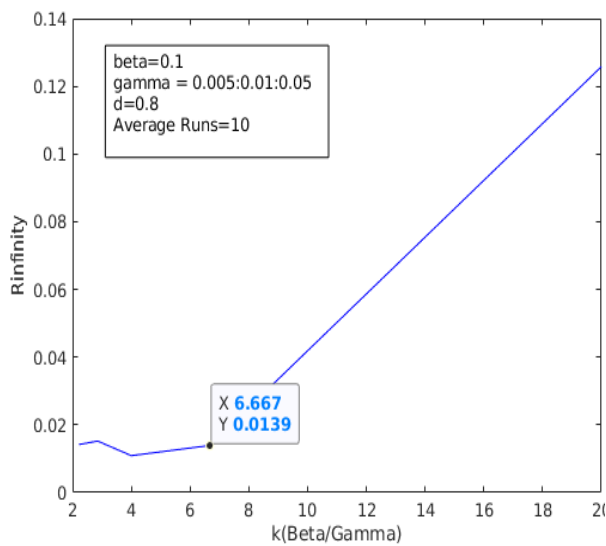|	Population Wise disease Spread parameters	Limited disease Spread parameters
Total Number Of Agents	1000	1000
Beta	0.6	0.6
Gamma	0.001	0.07
Time t	500	500
d	0.8	0.8
Initial Infected Agents	5 Percent	5 Percent

Exercise No:3

| Figure 8: Plot with Beta = 0.1 | Figure 9: Plot with Beta = 0.6 |
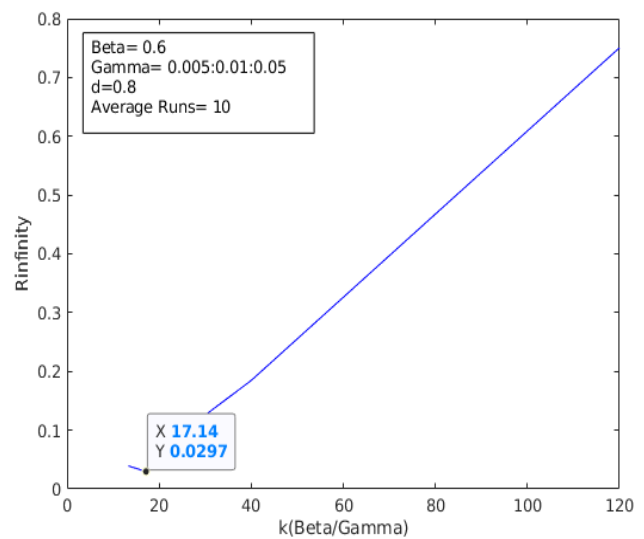
The figure 8 clearly indicates that when Gamma is very less (initial value of 0.005), the value of k will be very high, since k and Gamma are inversely proportional. Since the infection parameter (Beta) is small, the extent to which the disease can spread among the individuals is less only.

This is the reason the proportion of Rinfinity (Number of Recovered Agents/Total Agents) is relatively small around the values of 0.1 in the figure 8. The threshold point is marked in figure 8 which indicates that the disease spreads without any control after the mentioned point.

The figure 9 shows that since the beta is large here (0.6), the disease can spread rapidly among the population, and the number of recovered agents will be significantly higher. From this, we can clearly understand why the y axis limits of graph in figure 9 extends till 0.9. This shows that almost 80 percent of total population is affected y the disease when the Beta value is set in a higher rate.

Also the threshold point is mentioned in the figure 9, after which the disease cannot be controlled.

	Beta = 0.6	Beta = 0.1
Total Number Of Agents	1000	1000
Threshold Point	6.67,0.0139	17.14,0.0297
Gamma	0.005:0.01:0.05	0.005:0.01:0.05
Average runs	10	10
d	0.8	0.8

Beta=0.1:0.1:1, Gamma=0.005:0.005:0.05
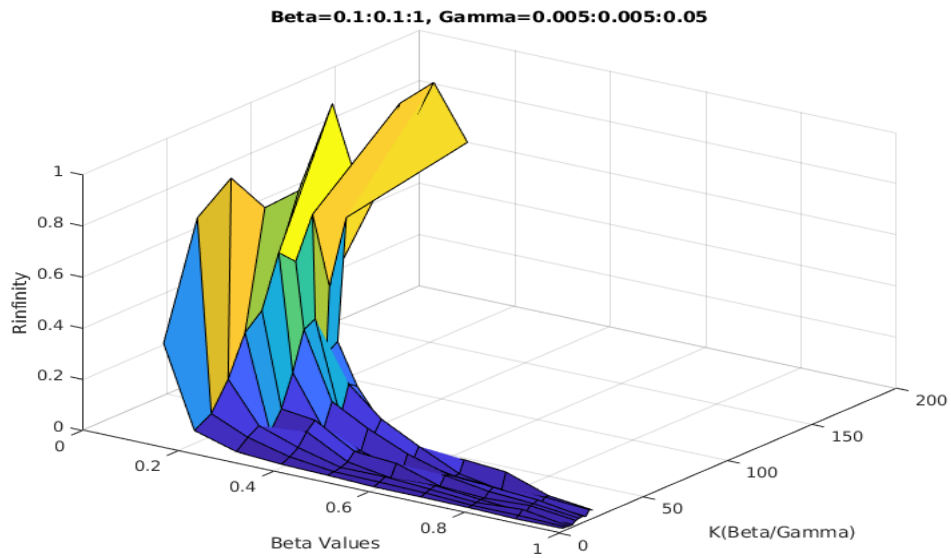
Figure 10: 3D surface phase diagram View 1

Beta=0.1:0.1:1, Gamma=0.005:0.005:0.05
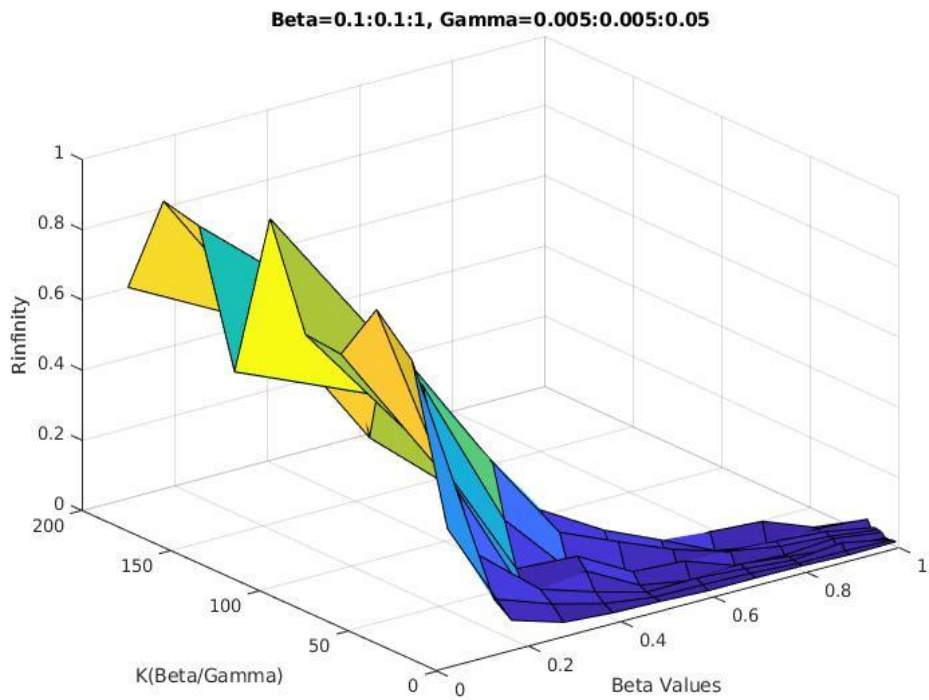
Figure 11: 3D surface phase diagram View 2

The parameters used for describing the 3D phase diagram are
Beta= 0.1:0.1:1
Gamma = 0.005:0.005:0.05
d= 0.8, Average Runs= 10

Here in figure 10 and figure 11, the Beta values are measured from 0.1 to 1 in which during 0.1, the agents' probability to get infected is very less and in 1, agent will get infected for sure.

The Gamma values are measured from 0.005 to 0.05, if the gamma values are 0.005, the infected person will take very long time to recover. Because of this he also have the chance of spreading the disease to others. This is the reason why the R infinity value reaches nearly 0.50 (that is 50 percent population is infected) when k = 200 (Beta=0.1, Gamma = 0.005). These cases will change for each beta and gamma.

Same as ODE model, here the number of Infected Individuals increases when susceptible come in contact with infected persons with an infection rate of Beta. In the same time the number of susceptible decreases. But the infected persons also recover with the rate of Gamma which tends to increase the number of Recovered Agents.

This proves that the graph is also similar to the ODE model of SIR.

CODE:
Here the basic code for spread of disease is attached.

```matlab
%% initialization
clear all
clc
population= randi([0,100],1000,2);
beta = 0.6;
lambda = 0.07;
d=0.8;
%%
index = ones(1000,1);
infected = [];
susceptible = [];
susceptibleSize=[];
infectedSize=[];
recoveredSize=[];
for i=1:1000
    if rand<0.05
        index(i) = 2;
        infected = [infected;i];
    else
        susceptible = [susceptible;i];
    end
end
susceptibleSize1=size(susceptible,1);
infectedSize1=size(infected,1);
%%
for iteration=1:500

    for j=1:1000
        temp = population(j,:);
        if rand<d
            condition=0;
            while condition==0
                a=randi([1,4],1,1);
                switch a
                    case 1 % left
                        if population(j,1) == 0
                            break;
                        else
                            population(j,:) = population(j,:) - [1 0];
                        end
                        break;
                    case 2 % right
                        if population(j,1) == 100
                            break;
                        else
                            population(j,:) = population(j,:) + [1 0];
                        end
                        break;
                    case 3 % Up
                        if population(j,2) == 100
                                break;
                        else
```

```matlab
                            population(j,:) = population(j,:) + [0 1];
                        end
                        break;
                    case 4 % Down
                        if population(j,2) == 0
                            break;
                        else
                            population(j,:) = population(j,:) - [0 1];
                        end
                        break;
                end
                if temp ~= population(j,:)
                    condition=1;

                end
            end
        end
    end
end

% check for same position of susceptible and infected persons
for k=1:size(infected,1)
    for l=1:size(susceptible,1)
        if population(infected(k),:) == population(susceptible(l),1)
            if rand < beta
                index(susceptible(l)) = 2;
            end
        end
    end
end

% recover the infected persons
infected = [];
susceptible = [];
for i=1:1000
    if index(i) == 2
        infected = [infected;i];
    end
    if index(i) == 1
        susceptible = [susceptible;i];
    end
end
for j=1:size(infected,1)
    if rand<lambda
        index(infected(j)) = 3;
    end
end

infected = [];
susceptible = [];
recovered=[];
for i=1:1000
    if index(i) == 2
        infected = [infected;i];
    end
    if index(i) == 1
        susceptible = [susceptible;i];
```

```matlab
            end
            if index(i) == 3
                recovered = [recovered;i];
            end
        end
    end

    % graph Plotting
    x1=[];y1=[];x2=[];y2=[];x3=[];y3=[];
    for i= 1:size(susceptible,1)
        x1 = [x1;population(susceptible(i),1)];
        y1 = [y1;population(susceptible(i),2)];
    end

    for i= 1:size(infected,1)
        x2 = [x2;population(infected(i),1)];
        y2 = [y2;population(infected(i),2)];
    end

    for i= 1:size(recovered,1)
        x3 = [x3;population(recovered(i),1)];
        y3 = [y3;population(recovered(i),2)];
    end
    figure(1)
    plot(x1,y1,'.b','Markersize',20);
    hold on
    plot(x2,y2,'.r','Markersize',20);
    hold on
    plot(x3,y3,'.g','Markersize',20);
    hold off
    pause(0.001);

    % number of people in 3 different colours
    susceptibleSize=[susceptibleSize;size(susceptible,1)];
    infectedSize=[infectedSize;size(infected,1)];
    recoveredSize=[recoveredSize;size(recovered,1)];
end

susceptibleSize=[susceptibleSize1;susceptibleSize];
infectedSize=[infectedSize1;infectedSize];
recoveredSize=[0;recoveredSize];
figure(2)
time=0:1:500;
plot(time,susceptibleSize,'b',time,infectedSize,'r',time,recoveredSize,'g
');
```