Term Paper 01: SIRS Model

submitted by

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Contents

1 Introduction

1.1 Cellular Automata

A Cellular automaton is a discrete model of computation studied in automata theory. Cellular automata are also called cellular spaces, tessellation automata, homogeneous structures, cellular structures, tessellation structures, and iterative arrays.

Cellular Automata (CA) has shown to be a valuable approach in ecological modeling, in particular when dealing with local interactions between species and their environment. CA models have been proposed for a large number of biological applications. The advantage of CA lies in that it can reflect temporal dynamic and spatial dynamic simultaneously. Here I've tried to replicate (to some extent) the scene of an epidemic with the help of SIRS model.

1.2 SIRS Model

The SIRS model comprises of agents (i.e., people or other organisms) arranged on a two-dimensional lattice. These agents may contract some infection (e.g., the annual flu), and can be in one of three states:

- **Susceptible (State S)**: A condition where a population agent has not yet infected, but has certain probabilistic potential to be infected by the disease.
- **Infected (State I)**: A condition when an agent gets infected
- **Recovery (State R)**: a condition when the disease disappears from the agent; (be it recover or die) or the agent recovered from the infection (and hence immune to it)

The **SIRS** model is called like this because agents go through these states cyclically: **S** changes to **I** when a susceptible agent comes into contact with an infected one; recovery changes the agent from **I** to **R**; eventually, in the absence of contact with infected agents, the immune response wears off and **R** changes back to **S**.

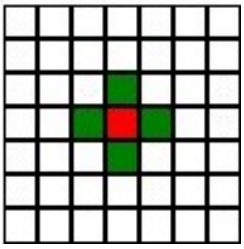
One way to simulate this model is with a fully parallel updating scheme. In one timestep, every lattice site is updated, and the state of site i at timestep t+1 is determined by the state of the lattice at time t (i.e., before any of the updates are made). [2]

This term paper shows spatial epidemiology using cellular automata tool. Cellular automata computational tool are giving assistance in understanding the disease spreading by noticing any elements related with the epidemic disease. This shows how important interdisciplinary approach in theoretical construction and constituting policy, in this case, epidemiology. Now, let us consider few types of neighbourhood spreading with regards to CA model.

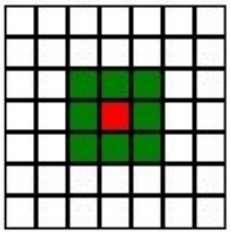
1.3 Types of Neighbourhood

In cellular automata, the Von-Neumann neighborhood (or 4-neighborhood) is classically defined on a two-dimensional square lattice and is composed of a central cell and its four adjacent cells. The Von-Neumann neighbourhood of a cell is the cell itself and the cells at a Manhattan distance of 1. It is one of the two most commonly used neighborhood types for two-dimensional cellular automata, the other one being the Moore neighborhood.

Moore neighborhood is defined on a two-dimensional square lattice and is composed of a central cell and the eight cells that surround it. The Moore neighbourhood of a cell is the cell itself and the cells at a Chebyshev distance of 1.



(a) Von-Neumann Neighbourhood



(b) Moore Neighbourhood

Figure 2: Types of Neighbourhood in Cellular automata

2 Changing parameters

2.1 Initial conditions

The initial condition is same for all the plots so that results can be analyzed carefully. Total 10 infectious individuals are put randomly in 75 $\times$ 75 population cells. I will use this to look through every time step to obtain our analysis. Here, I've shown only the variation in Moore neighbourhood, but we can do the same for Van-Neumann neighbourhood too.

Note: It might look deceptive, but in plots Whites are Susceptible individuals, Black ones are Refractory individuals, while Red ones are Infected individuals (ignore the numbers in colour bar)

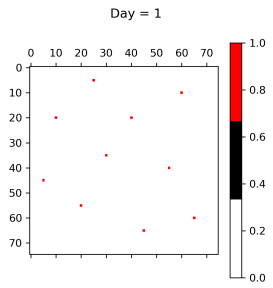


Figure 3: Initial condition

2.2 Changing I and R period

2.2.1 Deterministic Spreading

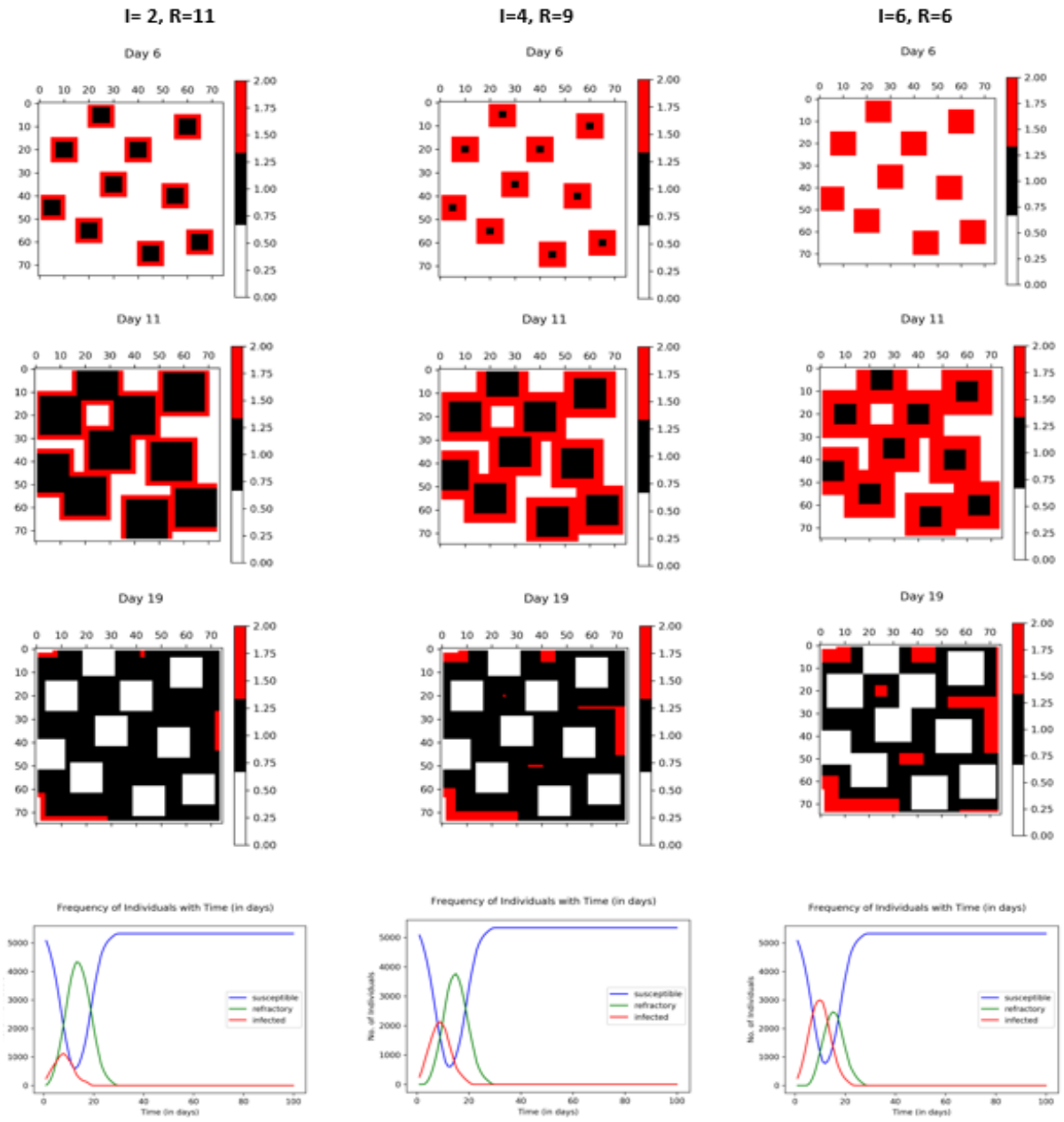


Figure 4: (a), (b) and (c) shows variation in I and R individuals with frequency plots at the bottom

2.2.2 Analysis

It can be clearly seen as we increase the persisting infection period in an individual, there is a rise in total no. of infected individuals over the complete period of the epidemic. This suggests that why controlling the infection rate is essential (drug resistance, vaccine etc) to gain immunity. This also tells how important is the refractory period is for the population.

3 Moore vs Von-Neumann Neighbourhood

We compare the spreading of Moore and van-Neumann types in our SIRS model. Different patterns could be seen below.

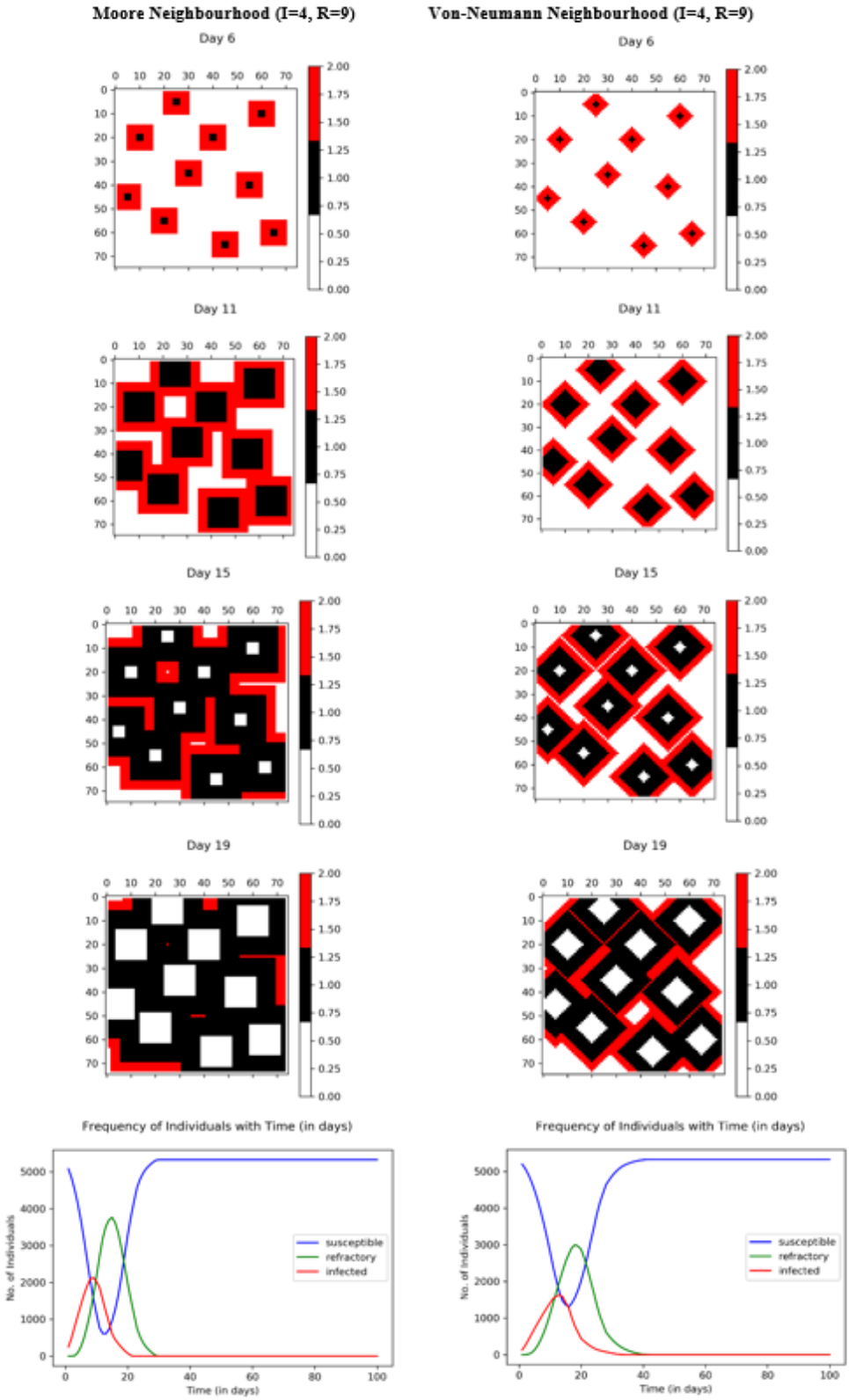
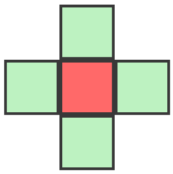


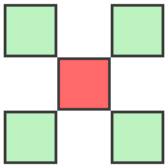
Figure 5: Deterministic Moore vs Von-Neumann Comparison (down) Frequency Plots

4 Equal Neighbourhood Comparisons

In this section, we look at some of the commonly used neighbourhoods in Cellular Automata. For four neighbourhood, we have Von-Neumann and Rotated Von-Neumann neighbourhood. I will show how their deterministic and probabilistic spreading pattern and we'll analyse them.



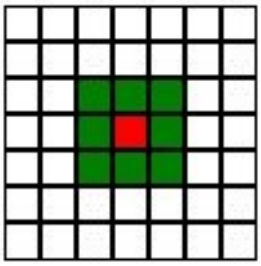
(a) Von-Neumann Neighbourhood



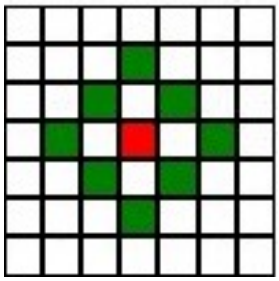
(b) Rotated Von-Neumann Neighbourhood

Figure 6: Types of Four Neighbourhood

For eight neighbourhood, I'll compare Moore neighbourhood spreading and the 2nd order Von-Neumann neighbourhood as shown in the figure below. I will use both deterministic and probabilistic cases to look into more details and make tings as real as possible.



(a) Moore Neighbourhood



(b) 2nd order Von-Neumann Neighbourhood

Figure 7: Types of Eight Neighbourhood

The initial condition is same for all the plots so that results can be analyzed carefully. Total 10 infectious individuals are put randomly in 75 $\times$ 75 population cells. I will use this to look through every time step to obtain our analysis.

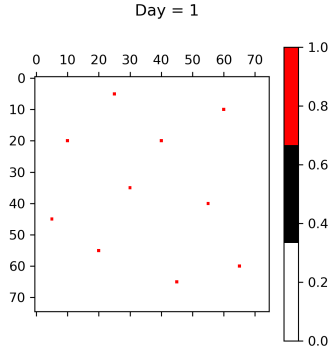


Figure 8: Initial condition

4.1 Four Neighbourhood Comparison

4.1.1 Deterministic Spreading Comparison

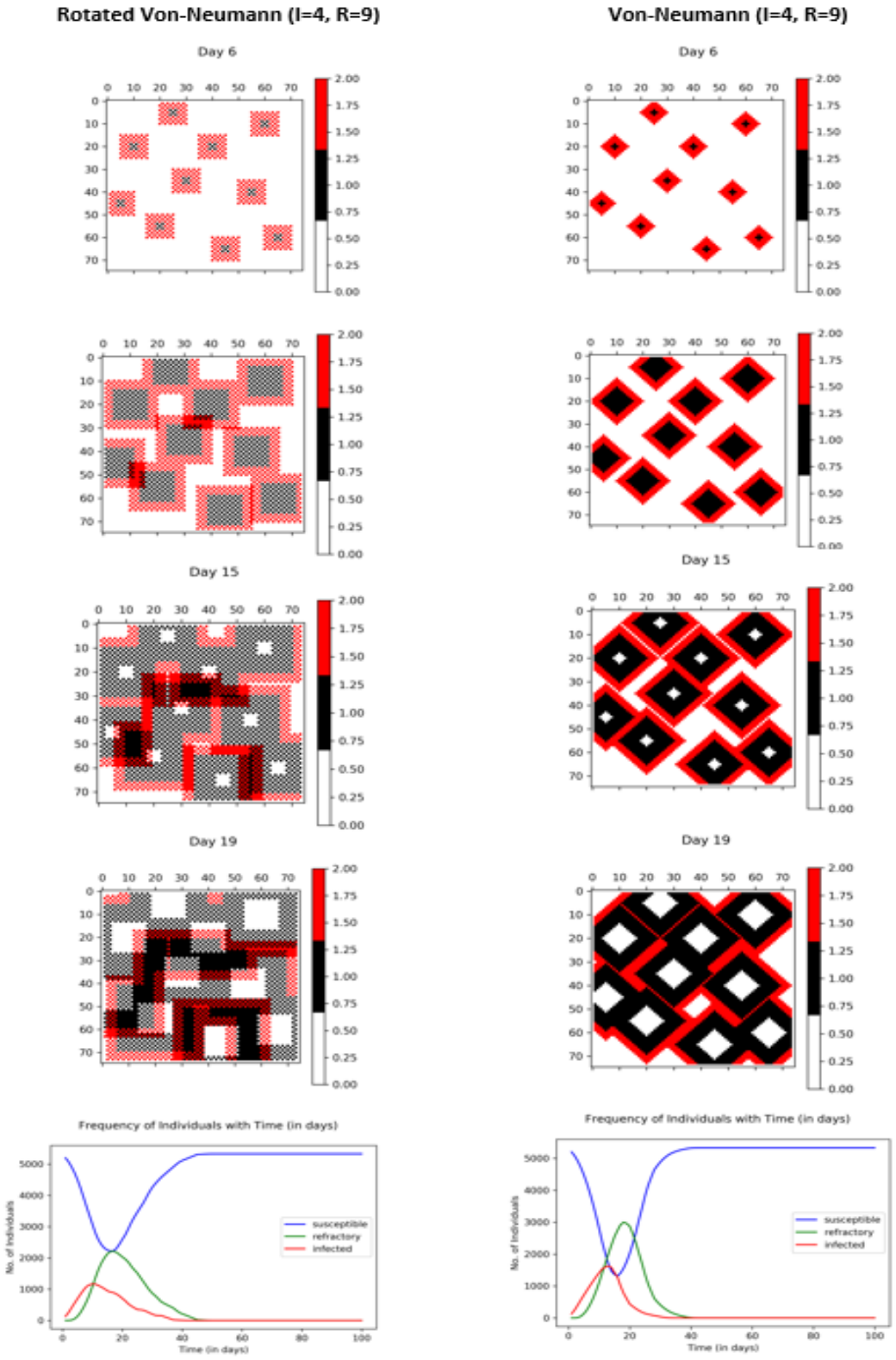


Figure 9: Rotated vs Normal Von-Neumann Comparison (down) Frequency Plots

4.1.2 Probabilistic Spreading Comparison

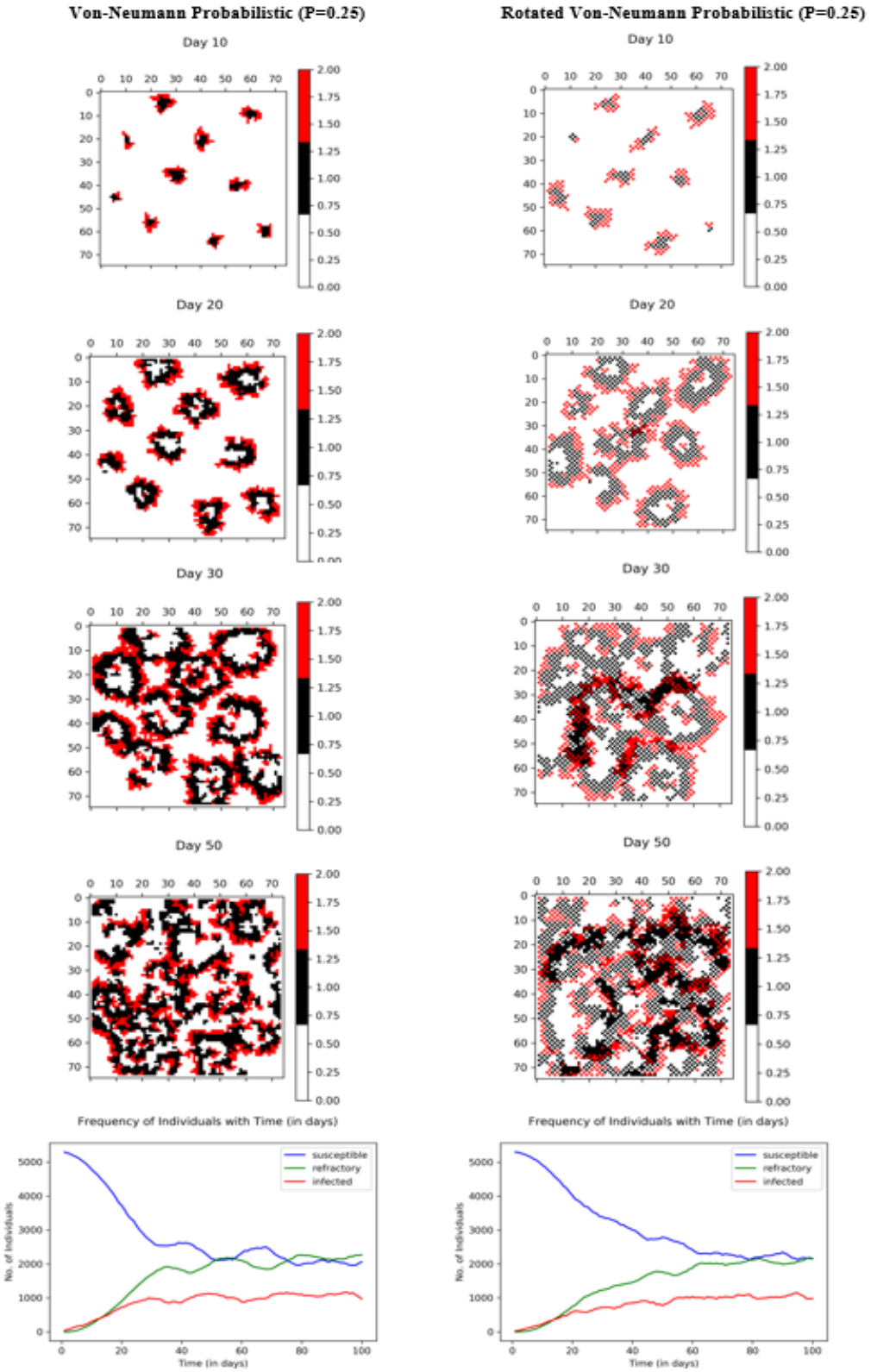


Figure 10: Probabilistic Normal vs Rotated Von-Neumann Comparison (down) Frequency Plots

4.2 Eight Neighbourhood Comparison

4.2.1 Deterministic Spreading Comparison

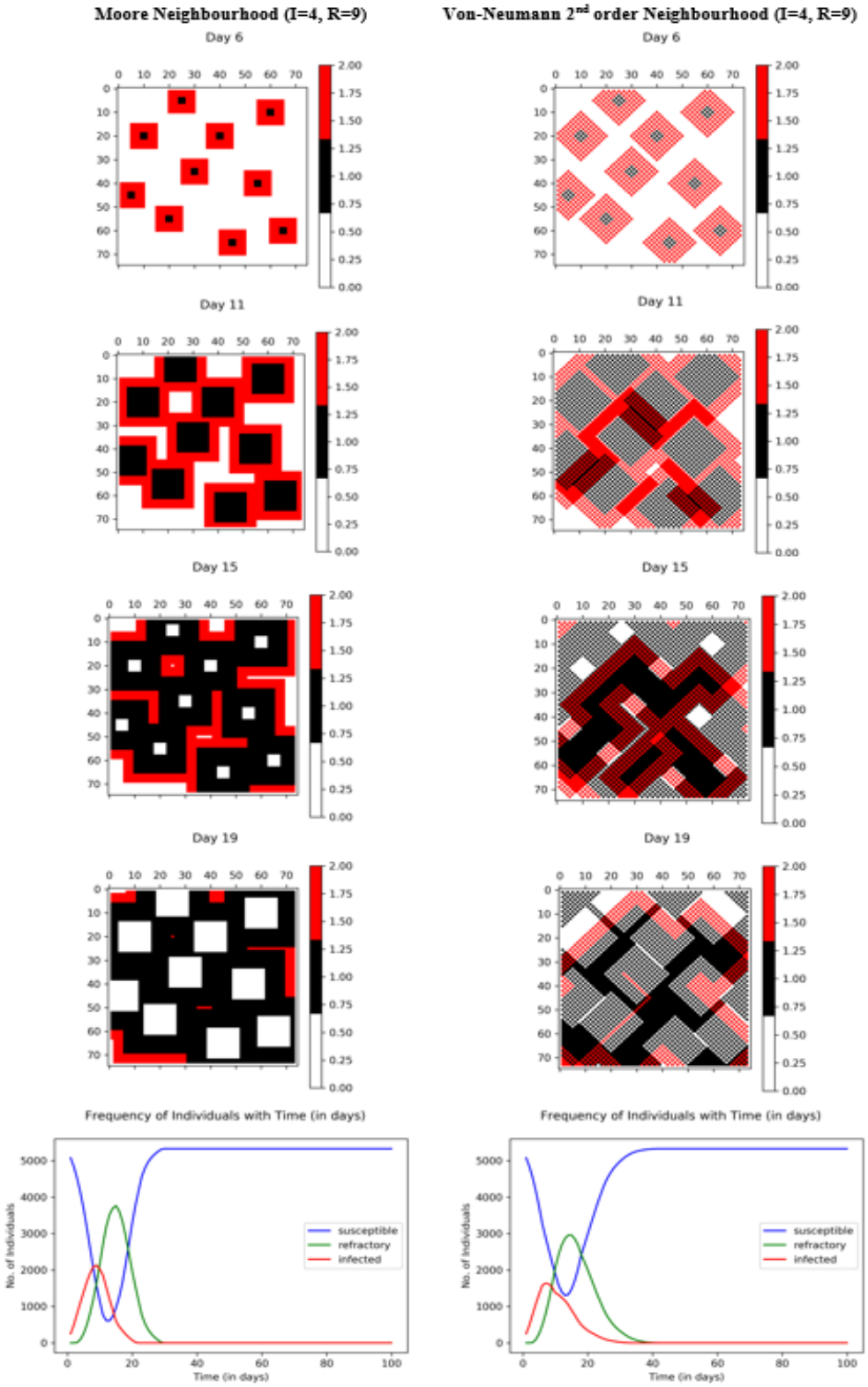


Figure 11: Deterministic Moore vs Von-Neumann 2nd Order Neighbourhood Comparison (down) Frequency Plots

4.2.2 Probabilistic Spreading Comparison

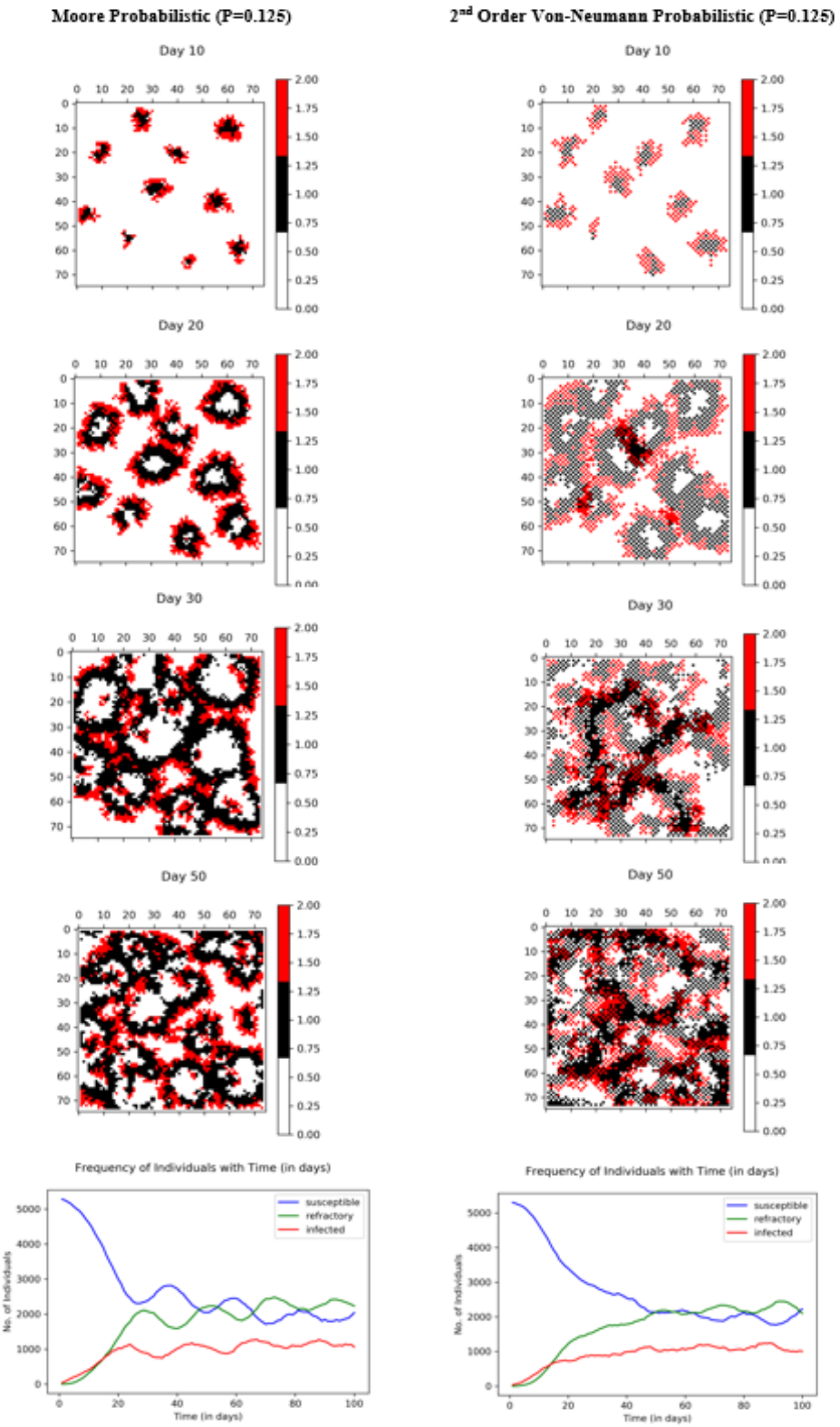


Figure 12: Probabilistic Moore vs Von-Neumann 2nd Order Neighbourhood Comparison (down) Frequency Plots

5 Analysis

From all the plots we infer the following:

The SIRS model works well for incomplete immunization (people become susceptible again if the come in contact with the infected individual). Some examples are small pox, tetanus, uenza, typhoid fever and cholera. In general, epidemics will also lead to death, and so taking all these into account we may give us some suggestions for epidemic control in Human Beings, conservation of wild populations, etc. We can create more complicated models to to understand and control the epidemic. [1]

In section 2, we changed the parameters to see how things might change when infection period is increased or decreased. This is also related to the development of health sector; the refractory period is increased if the population gets proper medication to resist the infection, so that an individual can remain immune for most of the period. Let's assume that the government have done a good job early on when there was fewer infections whether it was mandatory masks or travel restrictions, such that the R period increases, and we can see this by increasing the refractory period model (be it deterministic or probabilistic). [3]

In section 3, we see that since Von-Neumann neighbours are half than the Moore neighbours, it is clear from the plots that at some point in time in Moore neighbourhood spreading, the infected people are way more than the Von-Neumann one. This is a good plot to observe in Moore, the infected individual affects all its neighbours (8 out of 8 i.e. 100%) whereas in Von-Neumann only 4 out of 8 (50%) individuals are affected.

In section 4, we see how different spreading patterns lead to different distributions. In probabilistic case, we see that the pattern is repeating (kind of damped harmonic oscillations) if we look at the frequency plots. This is very different form deterministic case, where at some point in time the infection dies out and the system goes back to its initial state. This can be seen in both 4 and 8 neighbourhood cases.

6 Conclusions

The SIRS model is very useful to study the spread of epidemic and its control mechanisms. The vaccine can have a decisive influence on the course of the epidemic such that the vaccinated individual cannot become infected or contagious. By vaccinating to achieve herd immunity, the government can successfully lower the percentage of the population that are susceptible, or susceptible/population. I didn't introduce it in this term paper. Some people staying in part R are transferred to S and may become infected again. We can still lessen the rate of infection period. Let's say the government have locked down large parts of society, the daily encounters constant will go considerably down. By making masks mandatory, the government can lower the infectivity period. It is possible to simulate a situation where the treated people infect others to a lesser extent.

References

[1] Herbert W. Hethcote. Qualitative analyses of communicable disease models. *Mathematical Biosciences*, 28, 1976.

[2] DANIEL SHIFFMAN. *Chapter 7. Cellular Automata.* Addison-Wesley, Reading, Massachusetts, 1993.

[3] Xiaodong Lin; Joseph W.-H. So. Some results on a sirs epidemic model with subpopulations. *Mathematical and Computer Modelling*, 14, 1990.