Chapter 3
Methodology

In this chapter, we first describe a partial differential equation model for SIR-type epidemics and then the method of converting the partial differential equation model to cellular automata model is indicated. After that, we describe the method of creating SIS-type epidemics models based on cellular automata. In the last section the computer program to simulate the spread of epidemics using cellular automata model is described.

3.1 Creation of an SIR-type PDE Epidemics Model

In section 2.3, we described the SIR-type epidemics model (Eq. (2-26)) of Schneckenreither et al [12] based on a partial differential equation model originally suggested by Jones and Sleeman [11]. In this model it is assumed that people do not move and that infection is non-local in space, i.e., a susceptible individual at one position can be infected by an infected individual at a different point in space, with the probability of infection being a function of distance between the susceptible and infected individuals. As usual in an SIR model it is assumed that people who recover from an infection join a recovered (R) class and cannot be infected again because they become immune. The model was shown as:

$$\frac{\partial S}{\partial t} = -\alpha SI - \gamma S \nabla^2 I$$

$$\frac{\partial I}{\partial t} = \alpha SI + \gamma S \nabla^2 I - \beta I \qquad (3\text{-}1)$$

$$\frac{\partial R}{\partial t} = \beta I$$

where α is an infection rate between a susceptible individual and an infected individual in the same position

γ is an integrated infection rate between a susceptible individual and infected individuals in neighboring positions.

β is a recovery rate.

There are other possible PDE type models that can be developed for SIR-type epidemics, depending mainly on assumptions used for motion of people in space and time and for conditions under which infection can occur. In this chapter, we will develop a PDE model of reaction-diffusion type [10, 14] in which the movement of people in space can be modeled by a diffusion process and infection occurs only when a susceptible and an infected individual are at the same point in space at the same time. In this case, we consider movement of people in the three population classes, susceptible infected and recovered as occurring by a diffusion process with equal diffusion coefficients k. We also assume that infection occurs when susceptible people and infected people meet at the same point in space and time with an infection rate α. As in the model in section 2.3, the infected people are assumed to recover with a recovery rate β and to move to the R class. This reaction-diffusion model will be discussed in detail in section 4.1.

In this chapter, we show how the PDE model in Eq. (2-26) can be converted to a CA model and then develop methods and programs to compare the propagation of disease in the PDE and CA models.

3.2 Conversion of SIR-PDE Model to Cellular Automata Model

Schneckenreither et al [12] suggested in their work that an SIR-type epidemics model based on partial differential equations could be converted to a cellular automata model by a finite difference method. They described an approximate Laplacian of density of infected individuals' term but they did not show the step by step development or the CA model obtained after the conversion. In this chapter, we convert the SIR-PDE model of Schneckenreither et al to a cellular automata model by discretization. In chapter 4, we will show the conversion for the reaction-diffusion model.

A differential equation can be converted to a cellular automata model by a finite difference method [4]. The finite difference method gives a discretization of the model as a difference equation on a lattice. The difference equation can then be used to define the set of states, the transition function and the appropriate neighborhood for a cellular automata model.

For the discretization of the time variable, we use a time step Δt and a forward finite difference to approximate the first time derivative. For the Laplacian, we use a space discretization $\Delta x, \Delta y$ and a second-order finite difference approximation for the second space derivatives. From Eq. (3-1) and the finite-difference approximations in appendix A, the discretization can be written as

$$\frac{S_{i,j}^{n+1} - S_{i,j}^{n}}{\Delta t} = -\alpha S_{i,j}^{n} I_{i,j}^{n} - \gamma S_{i,j}^{n} \left(\frac{I_{i+1,j}^{n} - 2I_{i,j}^{n} + I_{i-1,j}^{n}}{(\Delta x)^2} + \frac{I_{i,j+1}^{n} - 2I_{i,j}^{n} + I_{i,j-1}^{n}}{(\Delta y)^2} \right)$$

$$\frac{I_{i,j}^{n+1} - I_{i,j}^{n}}{\Delta t} = \alpha S_{i,j}^{n} I_{i,j}^{n} + \gamma S_{i,j}^{n} \left(\frac{I_{i+1,j}^{n} - 2I_{i,j}^{n} + I_{i-1,j}^{n}}{(\Delta x)^2} + \frac{I_{i,j+1}^{n} - 2I_{i,j}^{n} + I_{i,j-1}^{n}}{(\Delta y)^2} \right) - \beta I_{i,j}^{n} \quad (3\text{-}2)$$

$$\frac{R_{i,j}^{n+1} - R_{i,j}^{n}}{\Delta t} = \beta I_{i,j}^{n}$$

For the cellular automata, we use a square lattice with square cells of side 1 and therefore we assume $\Delta x = \Delta y = \varepsilon$. Then Eq. (3-2) will become

$$\frac{S_{i,j}^{n+1} - S_{i,j}^{n}}{\Delta t} = -\alpha S_{i,j}^{n} I_{i,j}^{n} - \frac{\gamma S_{i,j}^{n}}{\varepsilon^2} \left(I_{i+1,j}^{n} + I_{i-1,j}^{n} + I_{i,j+1}^{n} + I_{i,j-1}^{n} - 4I_{i,j}^{n} \right)$$

$$\frac{I_{i,j}^{n+1} - I_{i,j}^{n}}{\Delta t} = \alpha S_{i,j}^{n} I_{i,j}^{n} + \frac{\gamma S_{i,j}^{n}}{\varepsilon^2} \left(I_{i+1,j}^{n} + I_{i-1,j}^{n} + I_{i,j+1}^{n} + I_{i,j-1}^{n} - 4I_{i,j}^{n} \right) - \beta I_{i,j}^{n} \quad (3\text{-}3)$$

$$\frac{R_{i,j}^{n+1} - R_{i,j}^{n}}{\Delta t} = \beta I_{i,j}^{n}$$

For the special case of time step $\Delta t = 1$, we obtain

$$S_{i,j}^{n+1} = S_{i,j}^{n} - (\alpha - 4\gamma) S_{i,j}^{n} I_{i,j}^{n} - \gamma S_{i,j}^{n} \left(I_{i+1,j}^{n} + I_{i-1,j}^{n} + I_{i,j+1}^{n} + I_{i,j-1}^{n} \right)$$

$$I_{i,j}^{n+1} = (1 - \beta) I_{i,j}^{n} + (\alpha - 4\gamma) S_{i,j}^{n} I_{i,j}^{n} + \gamma S_{i,j}^{n} \left(I_{i+1,j}^{n} + I_{i-1,j}^{n} + I_{i,j+1}^{n} + I_{i,j-1}^{n} \right) \quad (3\text{-}4)$$

$$R_{i,j}^{n+1} = R_{i,j}^{n} + \beta I_{i,j}^{n}$$

Equation (3-4) can be written as

$$S_{i,j}^{t+1} = S_{i,j}^{t} - (\alpha - 4\gamma) S_{i,j}^{t} I_{i,j}^{t} - \gamma S_{i,j}^{t} \sum_{(k,l) \in V} I_{i+k,j+l}^{t}$$

$$I_{i,j}^{t+1} = (1 - \beta) I_{i,j}^{t} + (\alpha - 4\gamma) S_{i,j}^{t} I_{i,j}^{t} + \gamma S_{i,j}^{t} \sum_{(k,l) \in V} I_{i+k,j+l}^{t} \quad (3\text{-}5)$$

$$R_{i,j}^{t+1} = R_{i,j}^{t} + \beta I_{i,j}^{t}$$

where $V = \{(1,0),(-1,0),(0,1),(0,-1)\}$. Eq. (3-5) is similar to the SIR-CA model with von Neumann neighborhood that was created by White et al [1]. We will compare the result between the discretized SIR-PDE model and SIR-CA model in chapter 4.

We will use a similar method to convert the reaction-diffusion SIR-PDE model to a CA model and show the result in section 4.2.

3.3 Creation of SIS-type Epidemics Models based on Cellular Automata

As stated in chapter 2 and the previous sections of this chapter, an epidemics model can be created by various methods, such as, partial differential equation [12] or cellular automata [1]. For an SIS-type epidemics model, the behavior of the spreading out of an SIS disease can be very complicated as we will show in chapter 4. In this section, we will develop a cellular automata model directly, as the direct development of a CA model is actually much easier to understand than the development of a PDE model. The development of the SIS-CA model is based on the development of an SIR-type CA by White et al [1].

We first suppose that the ground where an epidemic is spreading is divided into a two dimensional lattice of equal squares which represent the lattice of cells of a CA. In each cell, the population is divided into two classes: susceptible (S) and infected (I). We assume that the population of each cell is constant and all cells have equal populations. Although these assumptions are not theoretically necessary, the results of numerical simulations become much more difficult to understand if these assumptions are not made.

Let $S_{i,j}^t$ be the proportion of the population in cell (i, j) at time t that is susceptible, and let $I_{i,j}^t$ be the proportion of the population in cell (i, j) at time t that is infected. Since an individual in the population will be either susceptible or infected and S and I are defined to be fractions, we have

$$S_{i,j}^t + I_{i,j}^t = 1. \tag{3-6}$$

The assumptions about the lattice and the interactions between cells are as follows:

- The total population of each cell and the total population in the lattice are the same for all time.

- A susceptible individual can get a disease when they come in contact with an infected individual in their own cell, and after infection, they can move to a neighboring cell and therefore individuals in neighboring cells can infect each other in one time step.

- An infected individual will recover, but they will not be immune and therefore can get the disease again. Therefore an infected individual who recovers becomes a susceptible individual again.

- People can move from one cell to a neighboring cell by way of transportation. However, in one time step if one individual moves between two cells then another individual must move in the reverse direction to maintain equal numbers of individuals in each cell at each time step.

- It is supposed that when an infectious individual arrives at a cell, the number of susceptible individuals contacted by him/her is the same independent of the population of the cell.

- The set of states is $Q = K \times K$ where

$$K \in [0.00, 0.01, 0.02, 0.03, ..., 0.99, 1.00], \tag{3-7}$$

and the state of cell (i, j) at time t is shown in Eq. (3-8)

$$s_{i,j}^t = \left(S_{i,j}^t, I_{i,j}^t\right). \tag{3-8}$$

where $\left(S_{i,j}^t, I_{i,j}^t\right) \in Q$

The local transition function used is the following:

$$S_{i,j}^{t+1} = S_{i,j}^t - \alpha S_{i,j}^t I_{i,j}^t + \beta I_{i,j}^t - \alpha S_{i,j}^t \sum_{(k,l) \in W^*} c_{k,l}^{(i,j)} m_{k,l}^{(i,j)} I_{i+k,j+l}^t, \tag{3-9}$$

$$I_{i,j}^{t+1} = (1 - \beta) I_{i,j}^t + \alpha S_{i,j}^t I_{i,j}^t + \alpha S_{i,j}^t \sum_{(k,l) \in W^*} c_{k,l}^{(i,j)} m_{k,l}^{(i,j)} I_{i+k,j+l}^t, \tag{3-10}$$

where W^* is an index set of the neighborhood.

For von Neumann neighborhood:

$$W^* = \{(0,1), (0,-1), (1,0), (-1,0)\}, \tag{3-11}$$

and for Moore neighborhood:

$$W^* = \{(0,1), (0,-1), (1,0), (-1,0), (-1,-1), (-1,1), (1,-1), (1,1)\}. \tag{3-12}$$

$c_{k,l}^{(i,j)}$ are the connection factors. In this work, we use the same three ways of transportation between the cells as in White et al [1]: namely, by airplane, by train and by car or bus. This connection is given by the coefficients $c_{k,l}^{(i,j)}$ such that:

$$
c_{k,l}^{(i,j)} = \begin{cases} 1, & \text{if there exist the three ways of transport between the cells,} \\ 0.6, & \text{if there are two ways of transport between the cells,} \\ 0.3, & \text{if there is only one way of transport between the cells,} \\ 0, & \text{if there is not any way of transport between the cells} \end{cases}
$$

$m_{k,l}^{(i,j)}$ are the movement factors between the main cell (i,j) and its neighbor

cells $(i+k, j+l)$,

α is an infection rate.

β is a recovery rate.

We develop a computer program to simulate a spreading out behavior for a CA model in the next section. The results obtained from this program are shown in chapter 4.

3.4 The Computer Program to Simulate Cellular Automata Epidemics Model

We have developed two main computer programs based on the cellular method to simulate spatial spreading of a SIR-type and SIS-type epidemics. The source codes of these two models are shown in appendices B, C and D.

In this section, we give two flow charts for simulating cellular automata epidemics models. A flow chart for SIR-type models is shown in FIGURE 3-1 and for an SIS-type model in FIGURE 3-2.
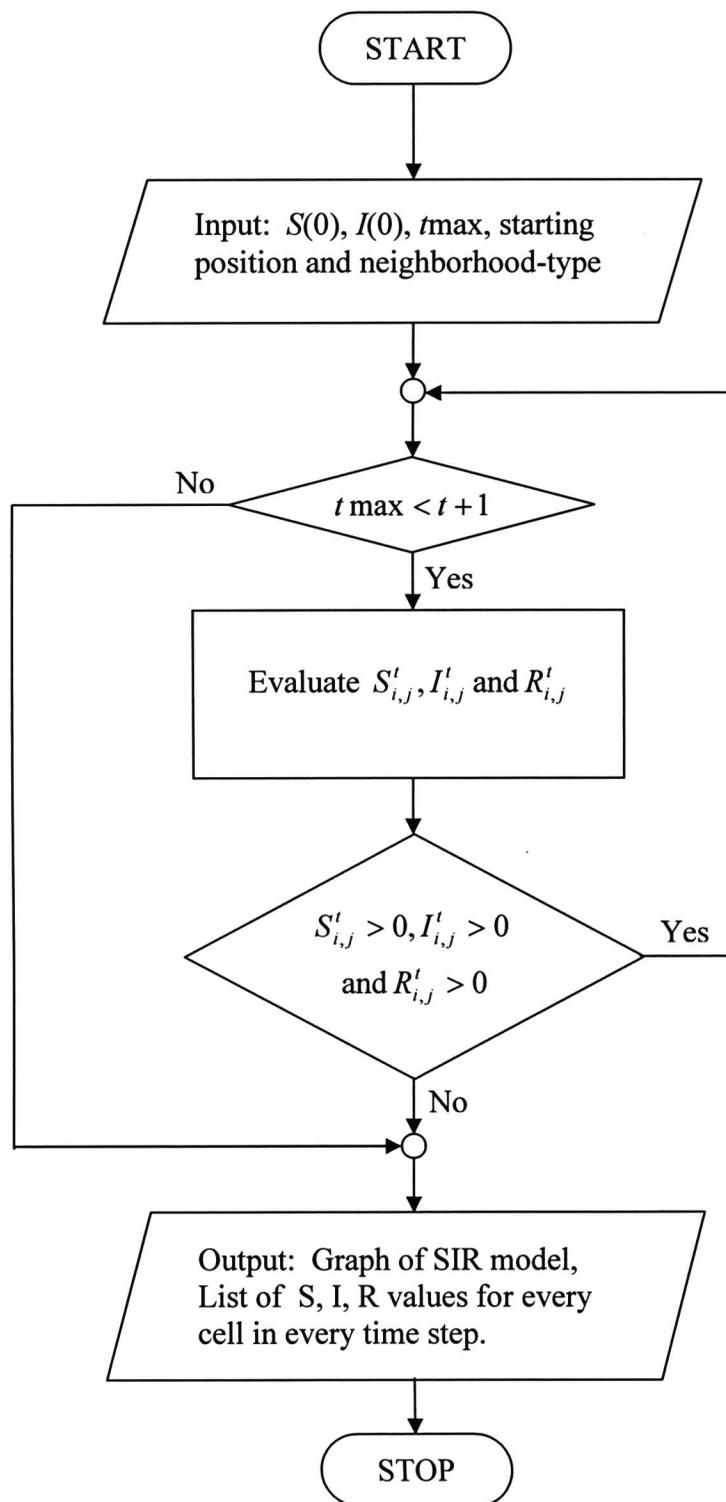
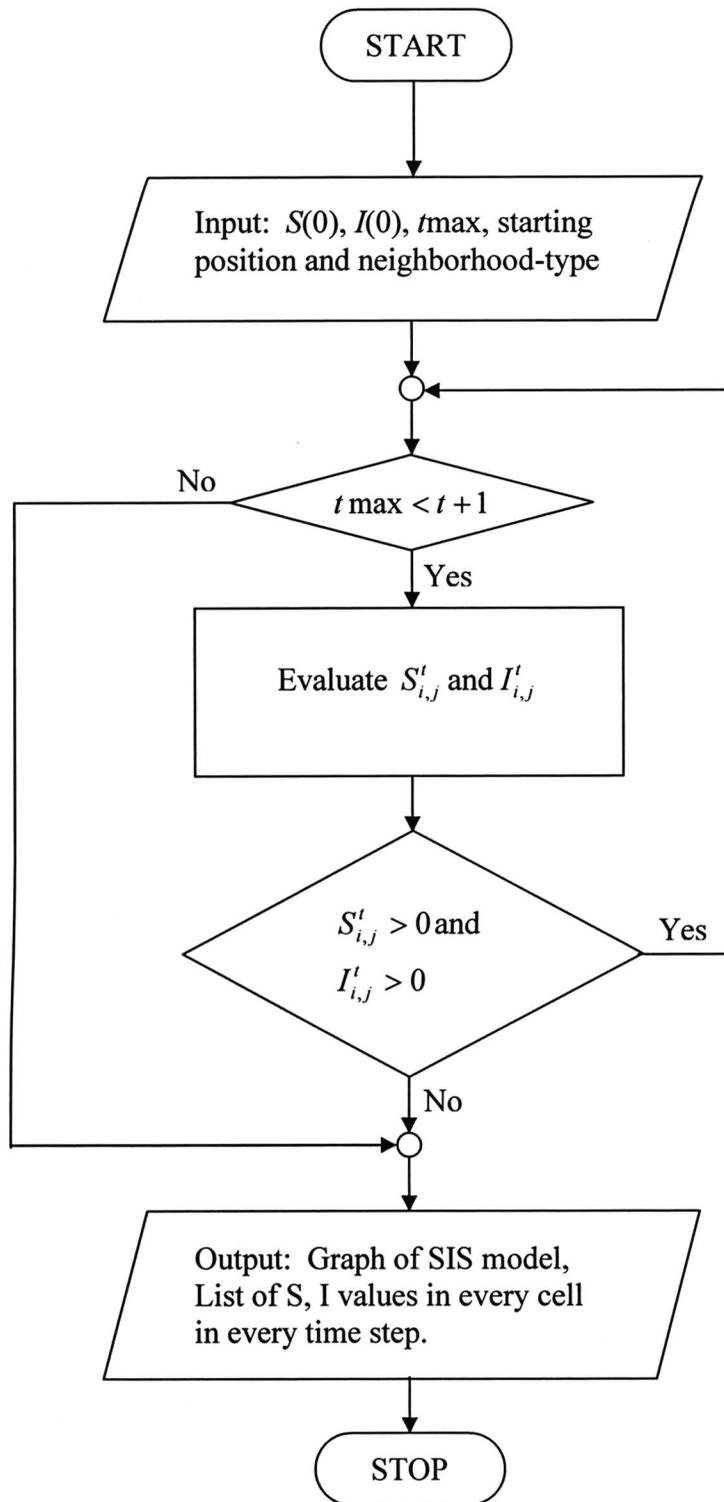**FIGURE 3-1** Flow chart for simulating the SIR-CA model

FIGURE 3-2 Flow chart for simulating the SIS-CA model

We show the results of these models and the results of the simulation in the next chapter.