Chapter 1
Introduction

1.1 Background and General Statement of the Problem

Epidemics refer to a disease that spreads extensively and rapidly and infects many individuals in an area or a population at the same time [1]. There are many mathematical models in epidemiology [1, 2], for example, susceptible-infectious (SI) model, susceptible-infectious-recovered (SIR) model, susceptible-infectious-susceptible (SIS) model, susceptible-exposed-infectious-recovered (SEIR) model, susceptible-vaccinated-infectious-recovered (SVIR) model. These models can be continuous-time differential-equation models or discrete-time difference-equation models. In this work, we look at models of spread of disease in space and time. The spatial spread can be modeled either as a continuous process through partial differential equations or as a discrete process through cellular automata [1, 3].

Most of the epidemic models are based on ordinary or partial differential equations [4]. However, the solution of a differential equation usually cannot be obtained analytically and numerical methods must be used. The numerical methods involve the discretization of the time and space variables in the model. This discretization can be regarded as creating a cellular automata model. If we want to create an epidemic model based on cellular automata, we should know the relations between the cellular automata and the differential equation model. In general, a differential equation can be approximated by a finite difference equation and a finite difference equation can be considered as a cellular automaton. Then a cellular automaton obtained from a PDE can be considered as a system of discretized differential equations.

Cellular automata (CA) in two dimensions are discrete dynamical systems formed by a finite number of $a \times b$ identical objects called cells which are arranged uniformly in a two dimensional lattice [1]. Each cell has a state (from a state set Q). The states of the cells are assumed to change at a discrete set of times by a local transition rule. In this sense, the state of a cell at time t depends on the state of a set

of cells, called its neighborhood, at the time $t-1$. So that, a CA in two dimensions is defined by the 4-tuple (L,Q,W,f). L is the lattice. The state of a cell (i,j) at time t is denoted by s_{ij}^t, where $s_{ij}^t \in Q$. W is a finite set of indices defining the neighborhood of each cell (i,j). In this work, we use two neighborhoods [1], Von Neumann neighborhood and Moore neighborhood. The von Neumann neighborhood of cell (i,j) consists of the cell itself and the cells that are up, down, left and right of cell (i,j). The Moore neighborhood of cell (i,j) consists of the cell itself and all cells around the cell. The function f is the local transition function which gives the new state s_{ij}^t of cell (i,j) at time $t+1$ given the state of the neighborhood of (i,j) at time t.

A cellular automata model is based on a discrete-time system. We now introduce a discrete-time model of epidemics for two examples, an SIR-type and an SIS-type [5, 6]. In an SIR-type epidemic model, the population is divided into three classes: susceptible (S), infectious (I) and recovered (R). One version of a discrete-time SIR model is as follows:

$$\begin{aligned} S(t+1) &= S(t) - \alpha \frac{\Delta t}{N} S(t)I(t) \\ I(t+1) &= I(t) + \alpha \frac{\Delta t}{N} S(t)I(t) - \beta \frac{\Delta t}{N} I(t) \\ R(t+1) &= R(t) + \beta \frac{\Delta t}{N} I(t) \end{aligned} \qquad (1\text{-}1)$$

where $t = 0,1,2,3,...$ is a time index, $S(t)$ are the people in the population who are susceptible at time t, $I(t)$ are the people in the population who are infectious at time t, and $R(t)$ are the people in the population who have recovered at time t. We assume that the population is constant, i.e., $S(t)+I(t)+R(t)=N$. Two positive parameters α and β describe a contact rate between a susceptible individual and an infected individual, and a recovery rate of an infected individual [1, 3]. In the SIR model an individual who has recovered from the disease is immune and cannot become infected again.

In an SIS epidemic model, the population is divided into two classes: susceptible (S) and infectious (I). A discrete-time SIS model is as follows:

$$
\begin{aligned}
S(t+1) &= S(t) - \alpha \frac{\Delta t}{N} S(t) I(t) + \beta \Delta t I(t) \\
I(t+1) &= (1 - \beta \Delta t) I(t) + \alpha \frac{\Delta t}{N} S(t) I
\end{aligned}
\tag{1-2}
$$

where all parameters have the same meaning as in the SIR model. We assume that the population is constant, i.e., $S(t) + I(t) = N$. In this SIS model, an individual who has recovered is not immune and can become infected again.

We now briefly summarize a CA model of the SIR epidemic model given by White et al [1]. It is supposed that the ground where the epidemic is spreading is divided into a two dimensional lattice of equal squares which represent the lattice of cells of a cellular automata. In each cell, the population is divided into three classes: susceptible (S), infectious (I) and recovered (R).

Assume the population of each cell is constant and normalized to 1, i.e., $S(t) + I(t) + R(t) = 1$. Let $S_{i,j}^t \in [0,1]$ be the proportion of susceptible individuals of cell (i, j) at time t, $I_{i,j}^t \in [0,1]$ be the proportion of infected individuals of cell (i, j) at time t and $R_{i,j}^t \in [0,1]$ be the proportion of recovered individuals of cell (i, j) at time t. The total population of each cell and the total population in the lattice are assumed to be constant, i.e., no births or deaths, and no net immigration or emigration between cells. It is assumed that people can move from their home cell to another cell during a time step $t-1$ to t, but will return to their home cell before time t. The set of states is $Q = K \times K \times K$ where $K \in [0,1]$ and the state of cell (i, j) at time t is $s_{ij}^t = (S_{i,j}^t, I_{i,j}^t, R_{i,j}^t)$. The main goal of the model is to compute the factors S_{ij}^t, I_{ij}^t and R_{ij}^t. The model is as follows:

$$
\begin{aligned}
S_{i,j}^{t+1} &= S_{i,j}^t - \alpha \cdot S_{i,j}^t \cdot I_{i,j}^t - S_{i,j}^t \cdot \sum_{(k,l) \in W^*} \frac{N_{i+k,j+l}}{N_{i,j}} \cdot \mu_{k,l}^{(i,j)} \cdot I_{i+k,j+l}^t \\
I_{i,j}^{t+1} &= (1 - \beta) I_{i,j}^t + \alpha \cdot S_{i,j}^t \cdot I_{i,j}^t + S_{i,j}^t \cdot \sum_{(k,l) \in W^*} \frac{N_{i+k,j+l}}{N_{i,j}} \cdot \mu_{k,l}^{(i,j)} \cdot I_{i+k,j+l}^t \\
R_{i,j}^{t+1} &= R_{i,j}^t - \beta \cdot I_{i,j}^t
\end{aligned}
\tag{1-3}
$$

where $W^* = \{(0,1), (0,-1), (1,0), (-1,0)\}$ if we use the neighborhood of Von Neumann and $W^* = \{(0,1), (0,-1), (1,0), (-1,0), (-1,-1), (-1,1), (1,-1), (1,1)\}$ if we use the

neighborhood of Moore. The meaning of the two parameters α and β are the same as in the SIR discrete-time model. $\mu_{k,l}^{(i,j)}$ is defined as the product of three factors : $\mu_{k,l}^{(i,j)} = c_{k,l}^{(i,j)} \cdot m_{k,l}^{(i,j)} \cdot \alpha$, where $c_{k,l}^{(i,j)}$ are the connection factor and $m_{k,l}^{(i,j)}$ are the movement factor between the main cell (i,j) and its neighborhood cell $(i+k, j+l)$.

The form of an SIS model is simpler than the form of an SIR model, but the solutions of an SIS model are considerably more complicated as the solutions can show the bifurcation path to chaos of the solutions of the discrete logistic equation [7].

In this thesis, we plan to start from a detailed study of the SIR-type epidemics model in partial differential equation and cellular automata models. We will then extend this work to develop cellular automata models for SIS-type epidemics model and compare between the cellular automata and differential equation models.

1.2 Purpose of the Study

The purpose of this study can be defined as follows:

1.2.1 To develop a partial differential equation for SIR-type epidemics.

1.2.2 To convert differential equation models to cellular automata for SIR-type by a finite difference method.

1.2.3 To develop cellular automata for an SIS model.

1.2.4 To develop computer programs for simulating the spread of epidemics in space and time for the SIR and SIS models.

1.2.5 To compare the solutions of the discretization SIR-PDE model with the solutions of the SIR-CA models.

1.3 Scope of the Study

The review and development of mathematical models using differential equations, difference equations and cellular automata for epidemics of the SIR and SIS types.

1.4 Method of the Study

1.4.1 Study SIR-type and SIS-type epidemics models based on continuous-time differential equation models and discrete-time difference equation models.

1.4.2 Study cellular automata.

1.4.3 Study the SIR cellular automata model and develop computer programs for simulating the spread of epidemics in space and time for both differential equation and cellular automata models.

1.4.4 Develop an SIS cellular automata model and computer programs for simulating the spread of epidemics in space and time.

1.4.5 Compare selected CA models with differential equation models.

1.5 Utilization of the Study

1.5.1 Obtain an SIS cellular automata model and computer programs for simulating the spread of epidemics in space and time.

1.5.2 Obtain the results of comparison between cellular automata and differential equation epidemics model.