CHAPTER 5
CONCLUSION

In this thesis, we have discussed partial differential equation and cellular automata models for two types of epidemics: SIR-type and SIS-type. For SIR-type epidemics, we have considered two different PDE models and obtained CA models corresponding to them for both von Neumann and Moore neighborhoods. We have also considered a CA model created directly by White et al [1] for an SIR-type epidemic. We have adapted the CA model of White et al for SIR-type epidemics to obtain a CA model for SIS-type epidemics. We have created Matlab programs to simulate the solutions for all models and used these programs to study the behavior of the solutions for selected parameter values.

5.1 Discussion and Conclusions

We have considered two PDE models for an SIR-type epidemic. In the first model proposed by Schneckenreither et al [12], it is assumed that the people do not move and that the spread of the infection is through a non-local interaction in which a susceptible person can be infected by an infected person with a probability depending on distance between them. Schneckenreither et al approximate the non-local interaction by expanding in a Taylor series to obtain a second-order PDE approximation for the interaction. The second PDE model we have considered is of reaction-diffusion type. It is assumed that people move through a diffusion process and that infection occurs when an infected and a susceptible individual are at the same position. We then convert both PDE models to corresponding CA models using finite difference approximations for the derivatives. CA models are developed for both von Neumann and Moore neighborhoods.

We also considered the CA model of White et al [1] for SIR-type models. In this model it is assumed that people move between neighboring cells and that infection occurs only between infected and susceptible individuals in the same cell.

Finally, we adapted the CA model of White et al to study the spread of infection in SIS-type models for both von Neumann and Moore neighborhoods.

We have created Matlab programs to obtain solutions for all models and carried out simulations for selected parameter values.

For the SIR-type models we found that the qualitative behavior of the solutions was similar for all models. For the CA models derived from the PDE's, the qualitative behavior will be similar only for small time steps and cell sizes, since it is only under these conditions that the CA approximations give nonnegative solutions that are a good approximation to the PDE. However, even when the qualitative behavior of the solutions was similar, there were differences in detail between the models. In general, epidemics spread more rapidly in CA models with Moore neighborhoods than in CA models with von Neumann models. This is due to the fact that in a Moore neighborhood a cell has 8 neighbors and in a von Neumann neighborhood a cell has 4 neighbors. In general, CA models are much easier to solve than PDE models especially when, as in the disease models considered in this thesis, the PDE models are non-linear parabolic equations.

For the SIS-type model, we found that the qualitative behavior of the solutions in individual cells of the lattice was very sensitive to parameter values and could be very different for Moore and von Neumann neighborhoods. We found that for smaller values of the infection rate, the CA models with both Moore and von Neumann neighborhoods converged to steady state solutions in both individual cells and in the whole lattice. For an intermediate value of the infection rate, the CA with von Neumann neighborhood converged to steady state solutions in both individual cells and in the whole lattice. However, for the Moore neighborhood, the populations in individual cells showed a 2-point limit cycle behavior but the populations in the whole lattice converged to steady state solutions. For a high value of the infection rate, the CA's with both von Neumann and Moore neighborhoods showed 2-point limit cycle behavior in individual cells but converged to steady state solutions for the whole lattice. The sensitivity in the CA models corresponds to the sensitivity of discrete-time SIS models which show a bifurcation path to chaos [6, 7, 15, 16] as either the infection rate or the time step is increased.

5.2 Suggestions for Further Research

In this thesis, we have studied CA models for SIR and SIS-type epidemics models. The methods used can easily be adapted to other epidemic models, e.g., susceptible(S)-exposed(E)-infected (I) and recovered (R), S-vaccinated(V)IR, SEIRS, SE-quarantined(Q)I-isolated(J)R-type models.

In the CA models we have only considered von Neumann and Moore neighborhoods. These neighborhoods are suitable if the disease is spreading through local contact. If infected individuals can travel longer distances, then a non-local model is required. Suitable models in this case are CA with arbitrary neighborhoods or network models (see, e.g., Awachai et al [9]).

A basic assumption in all of the models considered is that the population is uniform in space and does not change with time, i.e., no births, deaths or migration. CA models can be developed for changing populations, but the results are likely to be considerably more complicated.