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Knowledge Aware and Culturally Sensitive SIR Models for Infectious Disease Spread

by

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Knowledge Aware and Culturally Sensitive SIR Models for Infectious Disease Spread

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Abstract

Mathematical models, such as the Susceptible-Infected-Removed (SIR) epidemiological model, have been proven successful in predicting the spread of disease. Studies show that knowledge held by people, coupled with cultural influences, play important roles in identifying preventive behavior of people during an epidemic spread. In this research, two complementary extensions to the basic SIR framework are proposed. The first extension includes building a knowledge aware SIR (KSIR) model, adding a knowledge factor, where knowledge represents preventive behavior during a disease spread. The second extension provides for a population learning model and thus introduces a culturally sensitive KSIR model. A basic agent based model incorporating SIR model has been built as an initial framework wherein cultural algorithms are employed to create a culturally evolving population during an epidemic spread. A case study based on a cross cultural survey was used to initialize the data and validate the framework. Experimental results show that during a disease spread cultural knowledge influences people's behavior and thus is a deciding factor in risk assessment.

Dedication

To God Almighty

Acknowledgments

I am greatly indebted to my supervisor Dr. Ziad Kobti for suggesting the area of study, leading me to the world of multi agents, giving me an opportunity to work in this research area and supporting me financially. His valuable guidance and inspiration was greatly needed and deeply appreciated.

My sincere thanks are due to thesis committee members Dr. Robert Kent and Dr. Kemal Tepe for their detailed review of my thesis and constructive criticism during the preparation of this thesis.

Last but not the least I would like to thank my family for being constant source of support whenever I stumbled.

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Chapter 1

Introduction

The increase in incidence of diseases, especially epidemics, necessitated the need for proper surveillance systems for risk assessment and formulating intervention policies. A model that could monitor disease dissemination in a crowded society and predict future trends can help health authorities to formulate public health policies. It can also evaluate the efficiency of the health policies discard wrong policies and come up with new ones. Time plays an important role in the case of an epidemic since for instance an outbreak in China can have far reaching consequences in distant places such as the US. An end to end model which could predict future trends by analyzing the disease patterns helps in taking timely decisions which may save many lives. The arrival of bio terrorism in developed countries and diseases in developing countries such as Typhoid and Cholera makes the whole world susceptible to infectious diseases. There has been many new emerging and re-emerging diseases in several nations in recent times, such as H1N1 flu, Spanish Flu, AIDS etc. which are taking millions of lives [Kramer et al.(2010)]. Surveillance systems also play an important role in epidemiological analysis.

1.1 Epidemic Modeling

Computational epidemiology attempts to combine both computer science and epidemiology. It facilitates what if analysis and risk assessment. Mathematical models have been used for a long time due to their simplicity in representing the susceptible, infected and recovered population. A set of mathematical equations represent the expected number of people in each set of population. A very evident disadvantage of mathematical models is its inability to access individual levels. Network models are also used extensively to simulate disease spread in a population where a network represents social interactions between people. Among the available epidemiological models, agent based systems have emerged as a state of the art model for simulating real life scenarios. They are proven successful in mimicking an epidemic and analyzing the dissemination pattern [Reynolds et al.(2004)].

1.2 Current Research Motivation

Understanding the dynamics of epidemic spread is of high significance since it assists in risk assessment and formulating intervention policies. The efficiency of a developed model depends upon how realistic the model is built. Studies show that people learn from their society and cultural knowledge about disease preventive behavior in turn influence people's behavior during an epidemic outbreak. In Cultural Algorithms (CA), the belief space represents cultural background [Reynolds et al.(2004)]. People contribute and accept new strategies from the belief space.

Mathematical models which define the population in the form of equations are simple and easy to build. However they does not take into account the knowledge factor where this knowledge factor represents the measure of reduction in the number of infected agents. In this research, we propose the idea that knowledge and cultural or social influence the preventive behavior of people during an epidemic outbreak. We believe that this kind of modeling helps health care practitioners to do risk assessment and in making more accurate predictions during an epidemic spread. The case study described in chapter 4 is an attempt to find out the significance of knowledge in modeling disease prevention.

1.3 Thesis Contribution

The Susceptible-Infected-Recovered or SIR mathematical model can be extended to enable the role of knowledge in the human population. This knowledge can be learned, exchanged and applied by individuals interacting in a social setting. In addition to individual evolution, population evolution can be enabled specifically to knowledge based SIR with the use of custom Cultural Algorithms. The objective is to create a model inspired by SIR that is sensitive to individual knowledge and cultural influence in a multi-agent simulation. Firstly, we make an extension to the existing basic Susceptible-Infected-Removed model that is KSIR model by adding a knowledge factor where knowledge comprises of self-acquired knowledge. Secondly, we build a KcSIR or cultural KSIR mathematical model in which we use the cultural algorithm to build a learning model.

Other than theoretical aspects, the research is also focused on the practical application of the additional functionality. The added functionality is applied in a multi-agent framework to test and analyze the result. The multi-agent model developed is built on the data obtained from a cross cultural survey done in the Singapore military.

1.4 Thesis Outline

An extension to the basic mathematical model has been made by adding a knowledge factor. A cultural framework is also added. A multi-agent system has been built and the agents are put under a cultural framework in which they learn from others and evolve. The learning model has been tested and documented.

Chapter 2 provides a literature survey on three epidemiological models: mathematical models, network models and agent based systems for simulating the disease spread during a epidemic and their advantages and disadvantages.

Chapter 3 describes the problem specification, knowledge aware SIR model and culturally evolving KcSIR model that has been proposed in this study. Chapter 4 describes the case study done with the values obtained from a cross cultural survey done in Singapore military. Chapter 5 presents the test results.

Chapter 6 discusses the experiments in different settings and their results. Finally the last chapter discusses the conclusion and the future work to be done in this direction.

Chapter 2

Literature Review

This chapter includes a short survey on basic epidemiology, epidemiological models - mathematical models, network based models, multi-agent based systems, and cultural algorithm. The survey also includes the terminologies related to computational epidemiology, epidemiological models and cultural algorithms. It also includes the practical applications of the disease spread models.

2.1 Basic Epidemiology

A widely accepted definition of Epidemiology is:

> “the study of the distribution and determinants of health-related states or events in specified populations, and the application of this study to control of health problems " [Feinleib(2001)].

Epidemiology is defined by Kramer *et al.*[Kramer et al.(2010)] as

> "It is a scientific method which can be applied to a broad range of health and medical problems, from infectious diseases to health care."

The word Epidemiology is derived from a Greek word meaning study among populations (epi-upon, demos-people, logos-study). The high incidence of diseases necessitates epidemiology significant for disease control and prevention. The problem is increasing exponentially and an efficient method for epidemic management must be adopted. The newly emerging and re emerging infectious diseases are supposed to increase in future. These diseases include Acquired Immuno Deficiency Syndrome (AIDS), Cholera and Tuberculosis. AIDS which is supposed to emerge in the 1980s is affecting an approximate population of 1 million and more. These diseases cannot be eradicated but can be kept under control.

When referring to disease spread various terminologies are used.

1. Disease Outbreak: A disease outbreak occurs when there is a sudden increase in the expected number of affected people.
2. Epidemic: During a disease outbreak, when the incidence rate increases above the previous occurrences of the outbreak it is known as epidemic.
3. Pandemic: Epidemic affecting a large population is known as pandemic
4. Endemic: If the epidemic remains within a particular community, it is called endemic [Claude et al.(2009)].

2.1.1 Brief History

The epidemics have been recorded in history as early as 430 B.C. in Athens [Nelson(2006)]. Mortality rate of 33% due to the influenza epidemic in Athens shows how devastating the results can be. The reasons behind the epidemic were thought to be climate, soil, water and nutrition. Ancient records show the effect of epidemic on Europeans as well. Plague, also known as Black Death was prominent in Europe that killed approximately 24 million people during an epidemic.

Another epidemic that had profound effect on the history of epidemic is smallpox first recorded in 1350 B.C. Records show that it was present in Europe and is supposed to have killed 10% of deaths in the eighteenth century. Syphilis is another epidemic that existed in Spain, Italy and France.

2.1.2 Means of Transmission

The infectious organisms such as HIV, Hepatitis B and C virus are spread by humans whereas Rabies, Brucella non typhoid Salmonella are spread through animals. Soil and water is another reservoir of infectious organisms [Nelson(2006)]. There are four main infection causing organisms : viruses, fungi, bacteria and parasites [Murray(2002)]. Epidemiologists classify infectious diseases based upon two characteristics: means of transmission of disease and reservoir of disease. The means of transmission of infectious diseases can be classified to as follows:

1. Contact diseases which require direct or indirect contact
2. Food or waterborne diseases which are spread by having contaminated food or water
3. Airborne diseases, which are spread by inhaling contaminated air
4. Vector borne diseases which depends upon the infectivity of the vector organism
5. Perinatal diseases that may get be transferred through uterus during the time of pregnancy or child birth.

In [Page(1995)], the authors have described the six elements needed for the infection. Figure 2.1 shows the chain of the infection cycle. The portal of entry is the way through which the infectious agent enters the host. Examples of portals of exit are skin, respiratory tract, mucous membrane and blood. The portal of exit is the way through which the infectious agent leaves the host.

2.1.3 Study of Epidemiology for Public Health

Epidemiological studies aim to identify the key actors in infection and disease spread to assist health professionals in strategic decision making. According to Kramer *et al.* [Kramer et al.(2010)], some of the important tasks of epidemiology for public health are:

- To describe the spectrum of disease (the symptoms of the disease and frequency of occurrence).
- To describe the evolution of disease (the stages of disease a person goes through).
- To identify the risk factors of the disease and also the prevention factors (how to prevent the disease and what factors accelerate disease).

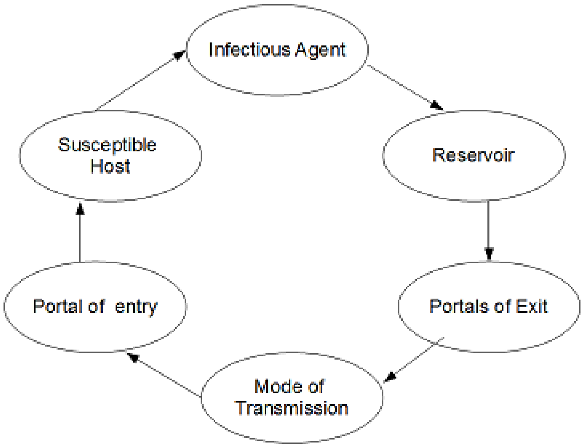


Figure 2.1: Chain of infection[Kramer et al.(2010)]

- To estimate the health care needs of the public.
- To evaluate a strategic plan's effectiveness for an intervention introduced to the population.

2.1.4 Stages of Infection

The infection has different stages in a person and the duration and strength vary according to a person's immunity, age, health, previous exposure to the infection etc. A person who is not infected and has a chance of getting infected is said to be in susceptible stage. A person's immunity system may destroy the infectious organism. It may continue to stay inside a person's body depending upon his characteristics. Different stages of infection are as follows:

- Latent Period

The latent period is the period between the start of infection to the infectious period.

- Incubation Period

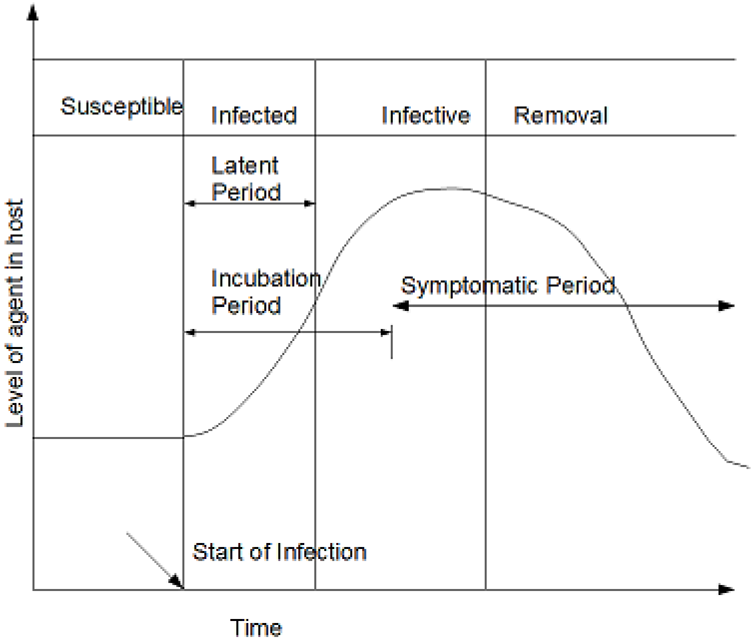


Figure 2.2: Stages of Infection [Nelson(2006)]

It is the time period between the infectious period and the onset of symptoms.

- Symptomatic Period

Symptomatic period starts after the incubation period when the symptoms shows up till the infected person stops infecting other.

Figure 2.2 depicts different stages of infection.

2.2 Mathematical Models

2.2.1 A Simple Mathematical model

The basic mathematical model SIR or Susceptible-Infected-Recovered was developed by Kermak and Mckendrik in 1927. A simple mathematical model has the following assumptions:

1. The total population is taken as a constant.

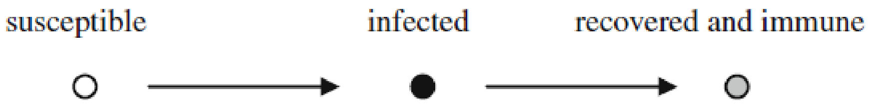


Figure 2.3: Transition of an infected individual [Kretzschmar and Wallinga(2010)]

2. An initial infected population is introduced to the total population.
3. The spread of disease to rest of population is described as a function of time.
4. The dead or recovered people in the community are counted together.

In mathematical terms, the total population can be divided to three different classes : susceptible S, who has the chance of getting infected, the infected I who represents the infected population and removed R, those who have been recovered, dead, immune or isolated until recovered. The total population can be represented as

$S \rightarrow I \rightarrow R$

These models are referred to as Susceptible-Immune-Removed or SIR models.

Figure 2.3 shows the transition of an individual from susceptible to infected to recovered and immune.

Several extensions have been made to the SIR model such as SEIR Susceptible exposed Infected Removed adding exposed stage for the latent diseases. The SIR model can be described as a function of time, that is S(t), I(t) and R(t). The SIR model has many assumptions about the equations such as

1. The increase in the infected class is proportional to number of infective and susceptible that is rSI, where r is constant.
2. The rate of removal of infective to removed class is proportional to number of infective that is aI, where a is constant and 1/a is the time spent as infected
3. The incubation period is negligible or in other words the infected person becomes infectious in no time.

4. The population is uniformly mixed.

The total population can be represented in three differential equations

$$\frac{dS}{dt} = -rSI \tag{2.1}$$

$$\frac{dI}{dt} = rSI - aI \tag{2.2}$$

$$\frac{dR}{dt} = aI \tag{2.3}$$

where r$>$ 0 is the infection rate and a$>$0 is the removal rate [Kermak and McKendrik(1927)]. Adding the equations (1), (2) and (3)

the total population is represented by

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0 \Rightarrow S(t) + R(t) + I(t) = N \tag{2.4}$$

where N is the total population. The mathematical formulation is complete with the conditions S(0)$>$0, I(0)$>$0 and R(0)$>$0.

Figure 2.4 shows the phase trajectories in Susceptible - Infective for SIR model. The relative removal rate is called as contact rate. The initial conditions for the curve are I (0) = I0 and S(0) = S0. With R(0) = 0, all trajectories start on the line S + I = N and retain inside the triangle since 0 $<$ S + I $<$ N for all time.

The basic reproduction rate Ro is defined as

$$Ro = \frac{rS0}{a} \tag{2.5}$$

The reproductive rate in other words is the number of secondary infection produced by the primary infection introduced into the total susceptible population [Murray(2002)]. 1/a is the infectious period. The calculation of reproductive rate is crucial in finding whether the epidemic is under control.

2.2.2 Early Applications of Mathematical Models

Mathematical models describe the time evolution of diseases in a population in terms of three differential equations thus dividing total population into

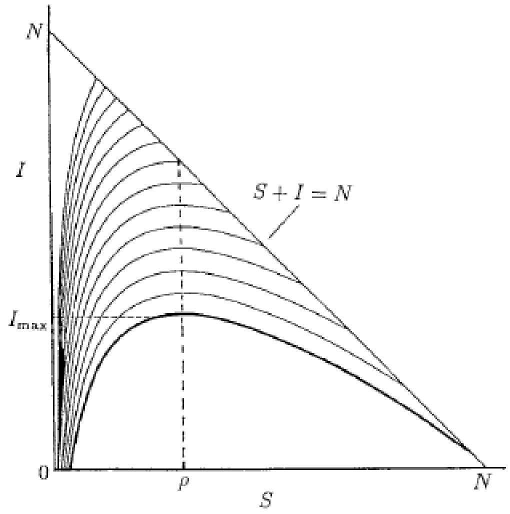


Figure 2.4: Trajectories in Susceptible -Infective [Murray(2002)].

Susceptible, Infected and Removed. Initially the infected disease is introduced to the population. They in turn infects other population when the initial infectious person may not be infectious. After the infected period the infected population may either become dead or recovered. Figure 2.5 shows how epidemic move through the stages of infection.

The earliest models of disease spread were mathematical models. The efficiency of the model depends upon how realistic the model is built. Mathematical model for evaluating the practicality in disease spread was initially used by Capasso and Paveri-Fontana for cholera epidemic in 1927. Another model involving mathematical equations for evaluating a prevention strategy was done by Bernoulli in 1760 to give an estimated value for the level of vaccination needed to epidemic outbreak. The dynamics of disease spread with use of three differential equations was done by Kermack and Mckendrick [Kermak and McKendrik(1927)]. They proposed that only if reproductive rate is greater than threshold value, then only the epidemic spread in a susceptible population. The theory aided in vaccination and thus by eradication of smallpox in 1970s [Kretzschmar and Wallinga(2010)]. It was also used for AIDS pandemic to evaluate efficient prevention strategies. Connell and Skvortsov [Connell and Skvortsov(2009)] did the model alignment

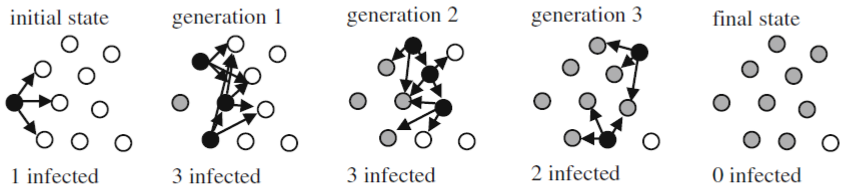


Figure 2.5: Epidemic in a population [Kretzschmar and Wallinga(2010)]

of generalized SIR mathematical model with agent based systems.

2.2.3 Advanced Mathematical Models

Mathematical models have been modified adding intermediate stages and structure to describe the dynamics of disease spread. Kretzschmar and Wallinga [Kretzschmar and Wallinga(2010)]classifies the advanced mathematical models into following subsections.

2.2.3.1 Stochastic Models

Stochastic models or models using probability distribution to predict outcomes are also used as a variation of the basic SIR mathematical model. Though in the basic model the stochastic effects are not considered, in stochastic variation, probabilities describe transition between the states. Stochastic simulations have been using Monte-Carlo simulation and Reed-Frost models [Bailey(1975)].

2.2.3.2 Continuous Age Models

Continuous age models were defined in terms of mathematical equations using partial differential equations. When compared to ordinary differential equations, partial differential equations are difficult to implement.

2.2.3.3 Complex Compartmentalized Models

Additional features such as latent period, vaccinated population were also added to mathematical system SIR for disease dissemination [Anderson and May(1991)] and [Diekmann and Heesterbeek(2000)]. Instead of uniform mixing of population groups, heterogeneity was added to population [Hethcote(2000)]. The model was used to model disease spread among sexual partners during an HIV/AIDS pandemic. Adding age structure was also done to the basic model which requires various age compartments with people passing from one age rate to other.

2.3 Network Models

2.3.1 Significance of Network Models

The mathematical models were described as mass action models by Keeling [Keeling(2005)] considering uniform mixing among population does not take into account individual details, whereas most of the disease spread occurs through networks. Disease spread has been simulated using variety of approaches using scale free networks and small world networks. It cannot model transmissions which are spread outside the networks such as flu. Read and Keeling [Read and Keeling(2003)] in their paper discuss how the social structure in the form of contact networks affect the population evolution. Analyzing disease spread in social group is an excellent way to learn population evolving model and how the routes through which the disease is spread determines the disease transmission rate.

2.3.2 A Brief History

The authors Carley *et al* [Carley et al.(2006)] in their paper argued that for bio terrorism there is no data available and terrorist may attack any population with the "weapons of mass destruction". They emphasized the importance of their work by citing the number of deaths by SARS in recent year and try to analyze, study and model the epidemic outbreaks. The authors refer to the previous works in the field [Lawson(2001)] and [Gimblett(2001)]. They also referred to the BIOSTORM project [Buckeridge et al.(2004)] as a background study for bio terrorism and also to a previous paper for medical knowledge representation of data [Miller et al.(1982)]. They criticized that most of the existing multi-agent models are applicable in the case of a single disease and that these do not take into account the social dimension of the model. They also alleged that the BIOSTORM project fails in simulating the social networks and human interactions. They used details from the previous bio terrorism attacks and disease data bases for building up the disease model. They modeled several new parameters like risk factors and symptoms. They based their social network from the GSS survey data and the agent interaction on the CONSTRUCT model [Carley(1991)]. They use the recreation rates from the from EPA Time use survey, wind data and the climate information to build respective models from the data for certain regions published in the website. They also gave a list of data repositories used in the simulation.

The authors Claude *et al* [Carley et al.(2006)]developed a multi-agent simulation for disease transmission during a bio terrorism event. They referred to BIOSTORM project [Buckeridge et al.(2004)] as a background study for bio terrorism. They alleged that the BIOSTORM project fails in simulating the social networks and human interactions. They integrated several computational models such as social networks, disease models and communication media to efficiently model the impact of an epidemic outbreak in a city. They employed real data repositories for the simulation.

Another significant contribution was made by Tian *et al*[Tian et al.(2007)] in which they proposed a new hybrid model which requires both the technologies continuous and discrete for the simulation. The authors adopted SARS outbreak case in 2003 as a basis of their study on different modeling techniques. The authors proposed a new hybrid model which requires both the technologies continuous and discrete for the simulation. They used traffic data, database knowledge and census data as the data repositories for the epidemic simulation.

Lee *et al* [Lee et al.(2008)] simulated the influenza spread taking into account a detailed social network. The authors simulated the spread of influenza. They emphasized the importance of depicting the actual social interactions between different population groups. They simulated the city of Norfalk with extensive description of individuals and their expected behavior that will serve as a "virtual laboratory" to study the effects of varying different parameters. The authors claimed that their model was built taking into account actual social interactions between different population groups rather than assumptions used by the previous models.

Barett *et al* [Barrett et al.(2009)] used network models for evaluating strategic plans during an infectious disease outbreak and combined several ideas taken from computing, artificial Intelligence and network science. They divided the whole process into four parts: 1) Creating synthetic inter actors in which they created a synthetic population by combining population data sets, 2) Generation of network where they created time varying networks, 3) Developing a simulation model and finally simulating the effects of policies and adaptations of individuals. They used their model for half a dozen case studies. They used intervention policies in a case study of New River Valley region of Virginia. They conducted nine scenarios on the built model to find the effect of private and public intervention strategies on the disease diffusion

The authors Claude *et al* [Claude et al.(2009)] used the network generation algorithm [Watts and Strogatz(1998)] for building the household network. Claude *et al.* [Claude et al.(2009)] used Dijkstra's algorithm to find the shortest distance between twin streets for the agents to move. The authors used Python with the Tkinter module for the graphical representation of a city. They gave a detailed description of the graphical modules for the realistic representation of the city. They used sources such as census data and other data sources in modeling urban cities such as Dublin in Ireland. The authors claimed that the combination of agent-based and network-based approaches offer realistic simulation of epidemics within cities.

They generated a social network that includes household networks, friendship networks, and colleague networks which are linked to an overall network. The authors used Dijkstra's algorithm to find the shortest distance between twin streets for the agents to move. They used the SEIR (Susceptible-Exposed-Infected-Recovered) model to simulate the infection stages [Satsuma et al.(2004)] and added some intermediate stages between the traditional ones to allow flexibility to the model.

2.3.3 Network Simulation

The disease spread in a population was studied using lattice models small world networks and pairwise correlation models [Rhodes and Anderson(1996)]. Keeling [Keeling(2005)] in his paper has mentioned three significant steps in network based model simulation.

- Network Generation

The initial population is randomly distributed in the available space. They divided the transmission route of the disease into two types of networks in terms of their clustering: local networks which are highly connected with many social cliques and global networks with high range connection and have less cliques. Global networks are random long distance relations. Figure 2.6

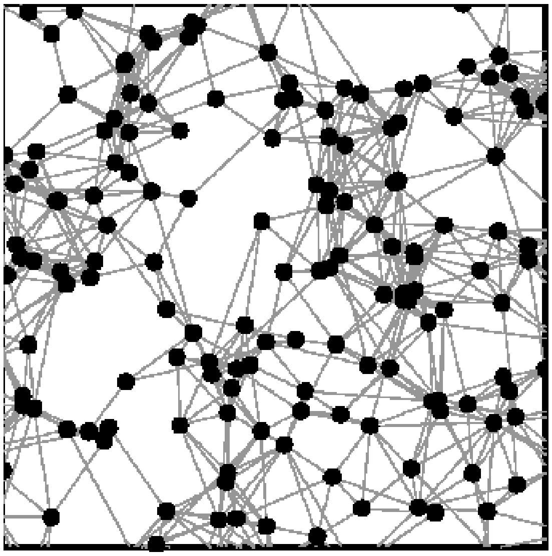


Figure 2.6: Local networks (Highly Connected)

shows local networks and Figure 2.7 (b) shows global networks. Communication in global networks is faster than local networks. Network in the space is divided to susceptible and is generated using connection kernel. Both global networks and local networks are generated with same number of contact rates that is eight contacts per node.

- Introduction of disease into generated population

Initially a single individual is infected with disease. Parameters such as rate of transmission, connection distance, infectious period are also fixed.

- Iterations until the allocated time

During the iterations births and deaths occur in the population. The number of births and deaths are decided in such a way as to maintain stability in total population.

2.3.4 A Network Generation Algorithm

In [Claude et al.(2009)] they have proposed a network generation algorithm. They have added household network between people living together, friendship network between people living in different household, colleague relations

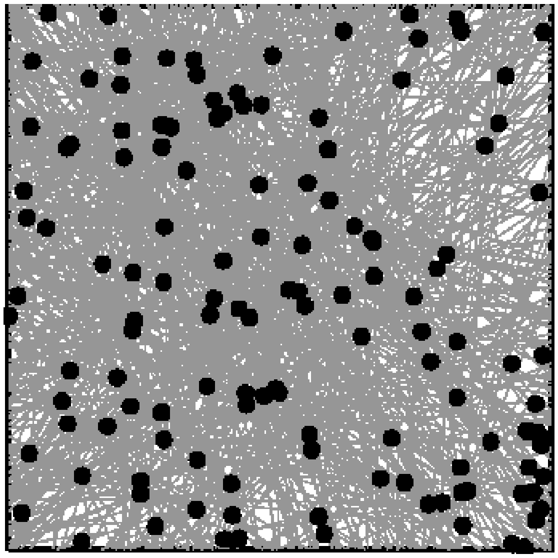


Figure 2.7: Global Networks (Loosely Connected)

between people working together. They have also considered sexual networks among the community considered. The algorithm they have proposed can be summarized as follows

1. The age and population obtained from census data is used for generating social nodes.
2. User defined data is used to generate house holds.
3. Keeling network [Keeling(2005)] is parameterized to generate house hold networks.
4. Colleague relations are added.
5. A network of sexual partners is constructed.

The household network generated is shown in figure 2.8 below.

2.4 Multi-agent Models

The multi-agent systems have been emerged as the state of the art systems in the computational epidemiology. They have been used in different areas

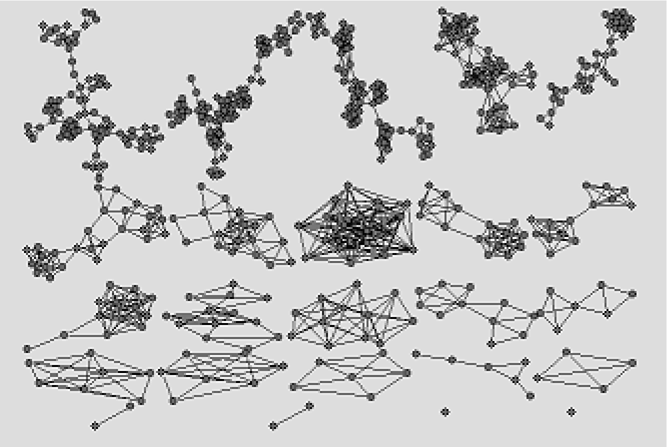


Figure 2.8: Household Network [Claude et al.(2009)]

such as micro simulation, object oriented and individual-based simulation [Drogoul et al.(2003)]. Multi-agent systems have been used for variety of applications for representation of complex software systems.

2.4.1 Basic Terminology

2.4.1.1 Agent Definition

One of the widely accepted definition of agent is by Wooldridge and Wooldridge [Woolridge and Wooldridge(2001)]which is

> An agent is a computer system that is situated in some environment, and that is capable of autonomous action in this environment in order to meet its design objectives.

Maes [Maes(1994)] defines interface agents as:

> '[C]omputer programs that employ artificial intelligence techniques in order to provide assistance to a user dealing with a particular application. . . . The metaphor is that of a personal assistant who is collaborating with the user in the same work environment.'

They have defined agent in both weak and stronger notion. In weak notion, they define agent as a hardware that has the following properties.

- Autonomy: agents act without human intervention. They have some control over their actions and state.
- Social ability: agents communicate with other agents using agent communication languages
- Reactivity: agents react to any changes that occur in their environment such as graphical user interface.
- Pro activeness: agents have goals and they act towards a common goal by taking initiative.

The authors also mention that the agents have human characteristics in stronger notion and agents can have following properties as well:

- Mobility: agents can move around
- Veracity: agents knowingly never communicate wrong information.
- Benevolence: agents do not have conflicting goals
- Rationality: agents do not act in such a way to prevent not to reach the goal.

2.4.1.2 Design of Agent Based Systems

A computer simulation includes a computer program which includes a cluster of computers that simulate a scenario. Fishwick [Fishwick(1994)] has defined computer simulation in three steps:

- Model Design
- Model Execution
- Execution Analysis

The model is designed keeping in mind the real system. The data garnered from observations and knowledge is used to build the model. The collected data is generalized using semantics or mathematical logic. The model is then run in the computer which is called model execution. Execution analysis involves analyzing the results obtained from the program and the behavior

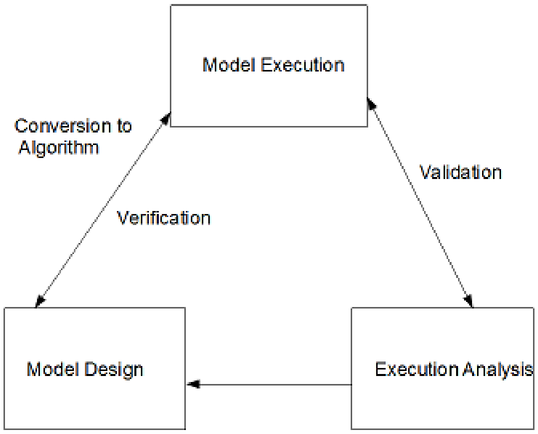


Figure 2.9: Computer Simulation[Fishwick(1994)]

indicated through the execution process. Figure 2.9 shows computer simulation steps.

Gilbert and Troitzsch [Gilbert and Troitzsch(2005)] added a model building step which includes writing a computer simulation program. Drogoul *et al* [Drogoul et al.(2003)] mention that writing an algorithm is significant that involves well structured efficient program with proper debugging, good graphics libraries etc. Figure 2.10 shows computer simulation steps as defined by Drogoul *et al* [Drogoul et al.(2003)].

2.4.1.3 Agent Applications

The multi-agent systems have been used in various fields of research. They have been used to solve real life problems by simulating artificial world. These include but not limited to following

- Manufacturing [Cetnarowicz and Kozlak(2002)]
- Traffic Control [Balaji and Srinivasan(2010)]
- Social Science [Yamada et al.(2006)]
- Health care [Kobti et al.(2006)]

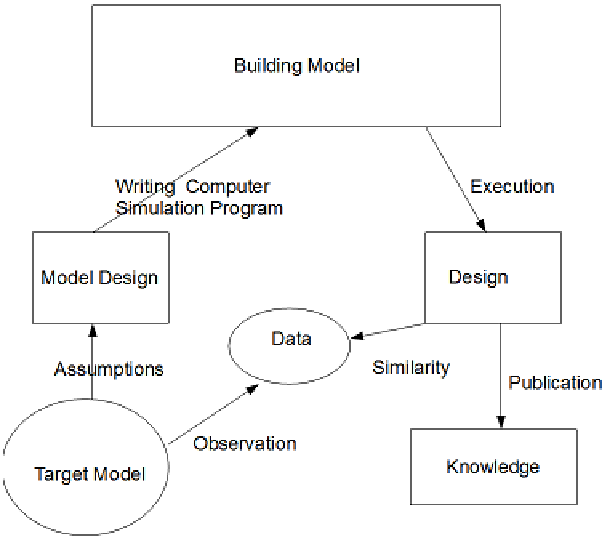


Figure 2.10: Computer simulation [Gilbert and Troitzsch(2005)]

- BioTerrorism [Carley et al.(2006)]
- Process Control [Schwuttke and Quan(1993)]

Cetnarowicz and Ko´zlak [Cetnarowicz and Kozlak(2002)] use multi-agent system for real time management of production process. The multi-agent system introduced by the authors enables efficient production system management. Balaji and Srinivasan [Balaji and Srinivasan(2010)] use multi-agent system to simulate complex traffic in Singapore. They implement intelligent process control by the agent architecture. Yamada [Yamada et al.(2006)] have implemented socially intelligent agents to simulate emotionally supportive agents. Kobti *et al* [Kobti et al.(2006)] have implemented child vehicle safety system for preventing injuries by improper use of child safety seats. They use cultural algorithms to implement population evolution. Carley *et al.* [Carley et al.(2006)] use agent based architecture to simulate social networks during a bio terrorism event.

2.4.1.4 Agent Theories

Agent theories represent how agent theorists represent properties of agents as per Wooldridge and Jennings[Woolridge and Wooldridge(2001)]. In agents as intentional systems, agents are represented using attitudes such as believing, needing something etc. The attitudes are called intentional notions and are of two different types: information attitude and pro attitude. The information attitude includes belief and knowledge and pro attitude include desire, intention, obligation, commitment, choice etc. The intentional notions are represented by language of formulation such as modal language which contains modal operators or meta language and semantic model. The semantic model approach is to use possible worlds to represent agents belief, knowledge goals etc. A complete agent theory must define the relation between different agent properties. Below mentioned are the theories of agency [Woolridge and Wooldridge(2001)]

- Moore *et al.* [Moore(1990)] Knowledge and action

Moore formalized an agent theory in terms of knowledge and actions. He suggested that knowledge represents what an agent knows in order to perform an action. Thus an agent performs action in order to achieve a goal and that an agent has incomplete information about reaching the goal.

- Cohen and Levesque [Cohen and Levesque(1990)]— Intention

The theory suggested by Cohen and Levesque prove successful in reasoning about agents. They suggest that intentions make agents achieve a goal. The agents track their actions and try if their attempts fail. Agents believe that their intentions are possible.

- Rao and Georgeff [Rao and Georgeff(1991)]— belief, desire, intention architectures

  They developed an agent theory based on belief, desire and intention. They introduced the notion of realism, which is how an agent's belief about the future in turn influences its desires and intentions.

- Singh [Singh(1994)]

Singh developed a theory with a family of logics to represent intentions, beliefs, knowledge and communication between the agents.

- Wooldridge [Wooldridge(1992)] modeling multi–agent systems

In his PhD thesis, Wooldridge developed a simple model for multi-agent systems and proved how different attempts in execution helps in formulation of belief logics.

2.4.1.5 Agent Architecture

Agent architecture represents how we construct computer systems from the specifications. They can be defined as engineering representation of software agents. Maes [Maes(1994)] defines agent architecture as follows

> particular methodology for building [agents]. It specifies how ... the agent can be decomposed into the construction of a set of component modules and how these modules should be made to interact. The total set of modules and their interactions has to provide an answer to the question of how the sensor data and the current internal state of the agent determine the actions ... and future internal state of the agent. An architecture encompasses techniques and algorithms that support this methodology.

The agent architectures include agent architectures based on attitude [Bratman et al.(1988)]. The architecture suggested has four data structures which include plan library, belief, desire and intention. An alternative approach is by Vere and Bickmore [Vere and Bickmore(1990)], in which they develop an agent with linguistic ability, planning, acting characteristics and autonomocity.

2.4.2 Early Applications in Epidemiology

Perrin *et al* [Perrin et al.(2006)] used multi-agent systems for immune modeling. They recognized the importance of understanding the level of invasion of HIV virus in immune system, testing against clinical data and the formulation of efficient health policies. The authors try to understand the cell interactions in human body which may eventually lead to a destruction of immune system. They used Message Passing Interface (MPI) for communication between computer nodes. They used a single agent to model a lymph node which interacts with a neighborhood of other cells.

The vector borne transmission was also modeled used agent based systems by Roche *et al* [Roche et al.(2008)]. They categorized the models in simulating disease outbreak into four groups which are reaction diffusion [Tran and Raffy(2006)], network models [Hufnagel et al.(2004)] to study the network properties, meta population theory [Hanski and Gilpin(1997)] and multi-agent systems. They implemented the parallelism in such a way that the computer nodes can be replaced by chip set which communicate using internal memory when compared to the socket communication between computer nodes. They integrated real world data using extraction of data from GIS which in turn will be helpful in learning disease dynamics. They also used evolutionary dynamics to study the evolution of pathogens.

Agent based systems for simulating disease spread across ship was first used by Gutierrez [Gutiterrez(2005)]. He pointed out that the tools which can clearly depict the course and direction of disease outbreak can help the medical sector in taking sufficient actions and evaluating the effectiveness of precautionary measures used in the critical situation. He modeled the airborne, water borne and contact borne diseases. He referred to previous models such as mathematical model [Wang and Ruan(2004)], stochastic models [Muller et al.(2003)], [Aschwanden(2004)] and [Paterson(2002)] which demonstrated similar characteristics. The model was run to address three different diseases small pox, SARS and norovirus.

Understanding the significance of protecting Health Care Workers (HCW), Cooley *et al.* [Cooley et al.(2010)] simulated the multi-agent system taking into consideration data pertaining to HCW. The authors referred to a previous method [Beckman et al.(1996)] for extraction of Census data. They also refer to previous Models of Infectious Disease Agent Study (MIDAS) [Ferguson et al.(2006)] and [Germann et al.(2006)] as a basis for their model and models other than MIDAS models [Glass et al.(2006)], [Habler et al.(2007)] and [Longini et al.(2004)]. The authors also ventured in triggering a research on simulating the attack rates, the effects of delaying vaccination and varying immunization coverage in HCW. They used the standard SIR(Susceptible-Infected -Recovered) framework.

Mysore *et al* [MYSORE et al.(2005)] developed a multi-agent based system for modeling and analysis of Brazilian food poisoning scenario. They used the XSSYS tool [Antoniotti et al.(2003)] for temporal logic trace analysis. The authors took into account the people's behavior and hospital behavior while building the model. The authors used the food poisoning outbreak in Brazil in 1918 [Do Carmo et al.(2004)]] to simulate the disease outbreak. They used repast, a multi-agent based tool for simulating the epidemic scenario. The authors conducted experiments with varying parameters like number of hospitals, communication, grid size, number of people and triage. They also did the trace analysis with the help of Triage which could read the repast traces. The authors claimed that the model they created had all elements essential to model a typical catastrophic event and that with the help of efficient tools like repast and XSSYS their model could evaluate different strategic plans which could in turn help in taking proper polices in advance.

A multi-agent model which can read directly from Geographic Information systems was developed by Patlolla *et al* [Patlolla et al.(2006)]. They developed a computational tool to study and analyze the disease diffusion, strategic plans and spread visualization. The authors extracted Tuberculosis related data from Geographic Information System (GIS) to model the outbreak and predict the level of disease diffusion.

The agent based systems for modeling disease spread in developing countries was done by Sutiono *et al* [Sutiono et al.(2007)] and Yergens *et al* [Yergens et al.(2006)]. The authors Sutiono *et al* simulated the typhoid scenario with Netlogo, a multi-agent based tool for the simulation. They simulated the real population, the patches or environments where people live and their inter- actions. With the help of screen shots from the Netlogo, they explain how to make predictions about the behavior of disease in a community. They suggested that the interface shows valuable information to epidemiologist such as number of population, healthy people, infected people etc.

Pita and Neto developed a game in Vidya multi-agent platform motivated to develop a disease dissemination simulation model [Pita and Pit(2007)]. They claimed that the original game consists of players called jivas and how they survive through complex environment.

Nyulas et al [Nyulas et al.(2008)] claim to be the first to use ontology for all characteristics for agent based system. The early works on using ontology on building multi-agent systems are semantic knowledge model [Laclavik et al.(2006)], ontology to share and reuse information [Tran and Raffy(2006)], generic multi-agent task oriented architecture [Sandru et al.(2005)] system based on UPML [Gomez et al.(2001)] and reuse library [Hajnal et al.(2007)]. The authors proposed a new architecture based on JADE platform for deploying a network of agents. They divided their system to three layers: 1)knowledge layer which contain different ontologies and problem solving library, 2)an agent platform which generates controller agents to generate all necessary information and congurator agents which instructs the agents and

3)data source layer which represents the agent's environment.

Chen *et al* [Chen et al.(2004)] did model alignment of agent based systems with mathematical models. They claimed that their model combined the concepts of agent based and network based models for simulation. The agents modeled as residents go through their regular routine till they become susceptible. When they come in the vicinity of the infected agents, they become infected and are unable to perform their routine functions. Instead of three stages of infection in traditional model they used seven infection stages susceptible, incubation, infected not infectious, prodrome, contagious, not quarantined, contagious but quarantined, population that die and population that recover.

Skvortsov *et al* [Skvortsov et al.(2007)] developed an agent based system to simulate an epidemic outbreak. They developed a model called CROWD created a urban environment with modern buildings and other infrastructure so that they resemble an urban life. For modeling the urban environment they used Advanced Urban Environment, system for modeling a synthetic population that resembles the real urban environment. They simulated an Australian town with the real census data and that they were able to reproduce the household, workplace and other infrastructure in the town.

Connell *et al* [Connell and Skvortsov(2009)] referred to the previous agent based models such as Episims [Eubank et al.(2004)] and BioWar [Carley et al.(2006)]. They used CROWD agent based model for building up the complex terrain and physical features of an Australian town used in the case study. They simulated the town with the data extracted from the census data along with the businesses, workplaces, households, schools buildings and interactions between individuals in their routine life. They created an artificial epidemic outbreak in the city and produced graphical results based on the data fed. They compared and contrast the results with the SIR model with the help of graphs. They claimed that the results obtained from agent based simulation and SIR based simulation are nearly similar. They argued that the minute difference in values occurs due to the interaction level of people are different in SIR that assumes that people interact uniformly.

Gonza'lez et al [Gomez et al.(2001)] proposed a new architecture that integrated a set of components for knowledge representation, epidemiological analysis, knowledge acquisition, multi-agent simulation and evaluation of strategies for the prevention and control of infectious diseases. The authors proposed that the expert component has an expert Graphic User Interface (GUI) for user interaction, an expert module for knowledge base representation, a knowledge acquisition module for knowledge base editing, an explanatory module and a control module for exchange of information among different components.

2.5 Evolutionary computation

Evolutionary computation is a branch of artificial intelligence to use social intelligence to solve optimization problems. R.G Reynolds [Reynolds et al.(2004)]defines Evolutionary Computation as

> “ the metaphorical use of concepts, principles, and mechanisms extracted from our understanding of how natural systems evolve to help solve complex computational problems”.

The following sections brief on evolutionary algorithms, cultural algorithms and early applications on cultural algorithms.

Evolutionary algorithms have been used extensively to explain genetic evolution. Cultural evolution also enables a learning society similar to biological evolution in which people learn from others and evolve. Ant Colony Optimization (ACO) [Dorigo et al.(2006)] and Particle Swarm Optimization (PSO) [Eberhart and Kennedy(1995)] are other two population learning algorithms used for optimization problems. Both of the algorithms employ social interactions between agents in a population to solve optimization problems. PSO was developed by Kennedy and Eberhart in 1995 inspired by the bird flocking phenomena. PSO is initialized with particles and searches for optimum solution. Each particle keeps track of their best performance and uses this information to do their next step. In every iteration, each particle keeps track of two values which are the best value obtained by the particle and the best performance by any other particle in the total population. Thus they move through the problem space and try to reach the global optima. Ant Colony Optimization was developed inspired by ant colony formation by Dorigo et al [Dorigo et al.(2006)]. Ants deposit a chemical substance called pheromone and each ant follows trail which is rich in pheromone deposit. In the ACO model, each agent use the knowledge which is the pheromone density to find path. ACO is used extensively in path finding problems such as traveling salesman problem. Cultural Algorithms [Reynolds et al.(2004)] are another set of population learning algorithm developed by Reynolds inspired by cultural evolution in nature.

2.5.1 Cultural algorithms

Cultural Algorithms are a way to use social intelligence to solve optimization problems. It is an extension to genetic algorithms. Cultural Algorithm has three main components:

- Population Space.
- Belief Space.
- Protocol that defines knowledge exchange between population space and Belief Space [Reynolds et al.(2004)].

The communication between global belief space and population space is through two functions: acceptance and influence functions. The selected individuals from the population space are selected to global belief space through acceptance function. The population space is influenced by global belief space using influence function. The cultural knowledge can be of at least five categories: situational, normative, topographic, historic and domain knowledge [Kobti et al.(2006)]. Figure 2.11 shows the Cultural Algorithm framework.

2.5.3 Applications of Cultural Algorithm

Cultural Algorithms were used in variety of applications such as optimization problems [Reynolds and Zhu(2001)], artificial society simulation [Reynolds et al.(2005)] agriculture simulation, manufacturing [Rychtyckyj and Reynolds(2002)], agent-based modeling of price incentive systems [Ostrowski and Reynolds(2004)] etc. Figure 2.12 shows how the experience by the agents whether successful or failed is used to update the local memory.

Multi-agent systems were used to find out the disappearance of Pueblo Indians of Mesa Verde region from South west Colorado. They simulated an artificial society with farming practices used, settlement, family practices using the data obtained from archaeological sites. They used a model in which agents keep track of exchanges made between fellow agents use cultural algorithm to learn successful strategies to make generalizations about which relative is most likely to successfully respond to a request [Reynolds et al.(2005)].

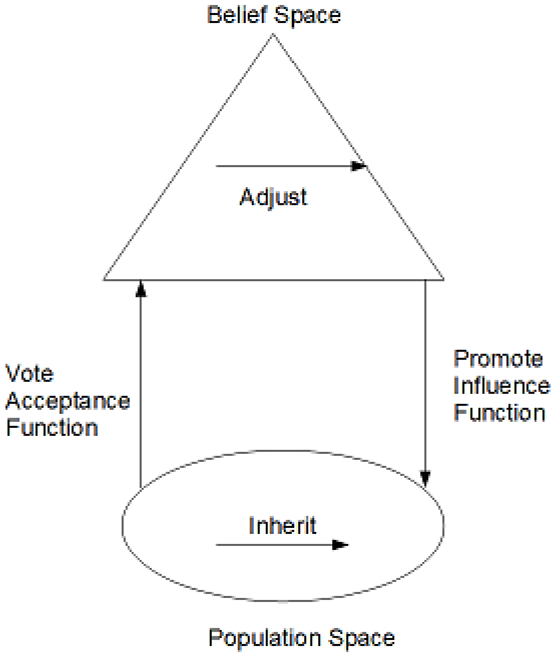


Figure 2.11: Cultural algorithm Framework [Kobti et al.(2006)]

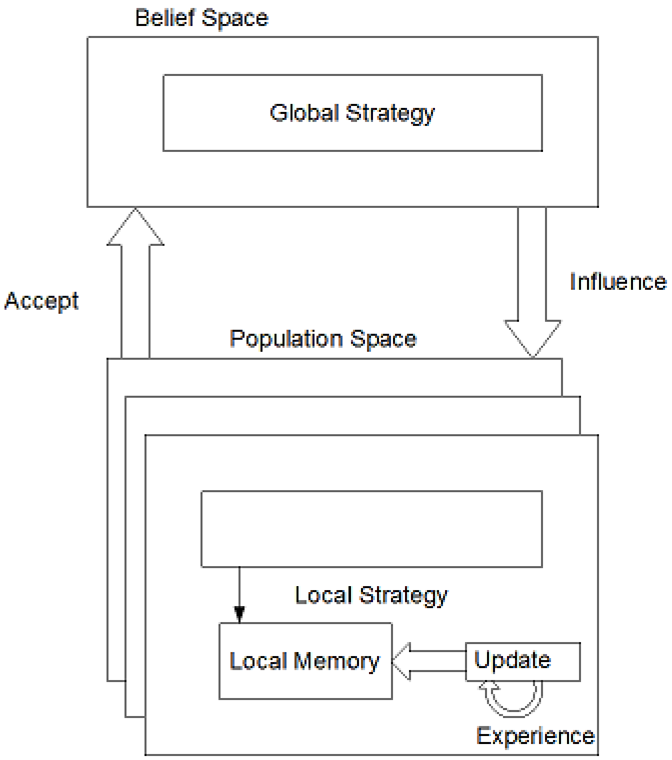


Figure 2.12: Belief Space and Population Space [Kobti et al.(2004)]

Chapter 3

Problem Specification and Methodology

3.1 Knowledge Aware SIR

In this research we investigate the effect of knowledge in reducing number of infected during an epidemic spread by modifying the basic mathematical model of epidemic spread. Kermak and Mckendrik [Kermak and McKendrik(1927)] introduced the concept of representing population affected by epidemic in terms of mathematical equations. They represented the population in terms of three equations : Susceptible, Infected and Removed. Though there are a number of epidemiological models developed, the mathematical models still remain as the simplest and fastest method to predict the effect of infectious disease. In the basic SIR model susceptible population moved to infected population based upon equations and does not take into consideration of prevention behaviors and knowledge held by people. This may result in wrong results during risk assessment. There has been many extensions to the traditional model adding intermediate stages between SIR. Little research has been done in mathematical models considering the influence of knowledge and culture held by people during such an infectious spread. Research [Yap et al.(2010)] shows that people's actions are influenced by the society in which they are living in. Mathematical equations without taking into account these details may fail in producing reasonable results.

We take the basic mathematical framework and extend it to knowledge aware SIR model. Figure 3.1 shows proposed knowledge aware framework.

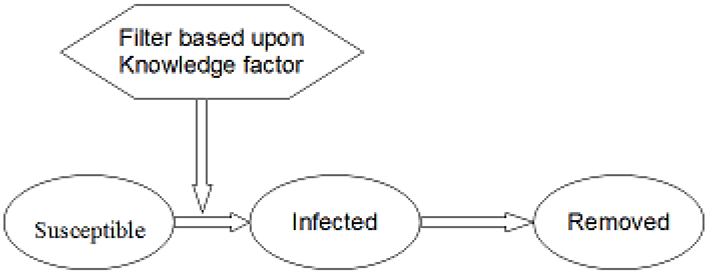


Figure 3.1: Knowledge Aware SIR

In the proposed framework, susceptible population moves to Infected status depending upon the knowledge factor. This framework is built based upon the study [Yap et al.(2010)] that knowledge and culture influence behavior practices of people during an epidemic.

In this research, we try to investigate how knowledge and culture influence the preventive behavior of people during an epidemic outbreak. We believe that this kind of modeling helps health care practitioners to do risk assessment and in making more accurate predictions during an epidemic spread. The case study described in chapter 4 is an attempt to find out the significance of knowledge in disease prevention. Using Cultural Algorithms (CA), an agent based model has been built where people in the population contribute and accept new strategies from the belief space.

3.2 KSIR Algorithm

We propose an algorithm for making risk assessment during an epidemic spread in terms of mathematical equations. The knowledge held by people which is a deciding factor in making accurate predictions are also taken into considerations. Algorithm for the Knowledge aware SIR has been described below. The model has following assumptions: 1) 1/ alpha is a measure of the time spent in the infectious state 2) The incubation period is neglected that is, a susceptible who gets infected is infectious from the moment he contracts disease 3) The population is homogeneous; that is population is uniformly mixed 4) The population is closed; that is no one enters or leaves the population 5) Permanent immunity that is persons once recovered never contracts disease again.

Let beta be rate of infection to contacts, alpha be the rate of recovery, N be total population, reproductive rate be r0, S represents the Susceptible, I represents Infected, R represents removed which includes dead or immune and K represents Knowledge Factor that is knowledge held by people.

1. Divide the total population to Susceptible, Infected, Recovered.
2. Initialize S(0),R(0),I(0) Repeat following steps until termination t, where t represents number of time steps

- Compute S(t) = S(t-1) + (-beta *S*I*K);
- Compute I (t) =I(t-1) - (S(t)+R(t));
- Compute R (t)= R(t-1) + alpha *I;
- Compute r0 = beta* alpha /N*K.

Knowledge factor or K is the measure of reduction in the number of infected agents during an epidemic spread caused by the knowledge held by people. This knowledge is the preventive knowledge held by people during a disease spread. It can be specific to a particular disease. For example, during a flu epidemic, people can have knowledge such as getting a flu shot done can it turn cause prevention of disease. Its value has been computed from experimental results. It can have the range of values 1.2 to 3.8. For example, the number of infected agents at the end of 5th time step in SIR and KSIR are compared and the knowledge factor value is 1.2. Also at the end of 40th day or time step the number of infected agents in SIR and KSIR are computed and knowledge factor is computed as 3.8. The impact of approximation introduces computational complexity.

3.3 Culturally Sensitive KSIR

We also make an extension to the K-SIR model or Kc -SIR model where Kc represents culturally evolved knowledge. The cultural algorithms are used

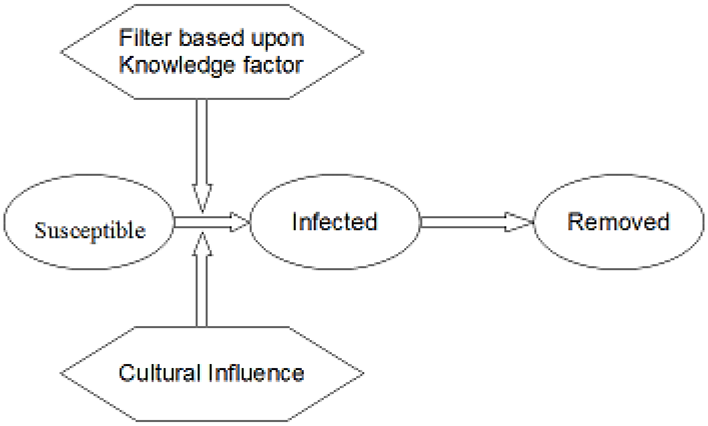


Figure 3.2: Culturally Sensitive SIR

to represent evolution of knowledge in a social setting. The variable K or Knowledge factor in computation of S(t), I(t), R(t) and r0 is replaced by Kc or knowledge held by people learning from the society.

Figure 3.2 represents culturally sensitive knowledge SIR. In the culturally sensitive SIR model, apart from knowledge held by people, cultural factor also comes to picture. Cultural knowledge is evolved from interaction with other people which may influence ones action in deciding actions during an epidemic.

3.4 Kc SIR Algorithm

Let beta be rate of infection to contacts, alpha be the rate of recovery, N be total population, reproductive rate be r0, S represents the Susceptible, I represents Infected, R represents removed which includes dead or immune and Kc represents Cultural Knowledge Factor that is knowledge held by people learning from the society.

1. Divide the total population to Susceptible, Infected, Recovered.

2. Initialize S(0),R(0),I(0) Repeat following steps until termination t, where t represents number of time steps

- Compute S(t) = S(t-1) + (-beta *S*I*Kc);
- Compute I (t) =I(t-1) - (S(t)+R(t));
- Compute R (t)= R(t-1) + alpha *I;
- Compute r0 = beta* alpha /N*Kc.

Culturally sensitive Knowledge factor or Kc is the measure of reduction in the number of infected agents during an epidemic spread caused by the cultural knowledge held by people. This cultural knowledge can be learnt, exchanged and evolved from a society. It varies with disease type. For example, during a flu epidemic, people can get influenced by behaviors of the society such as coughing and sneezing to your arm, getting flu shot etc. An incidence of disease in a contact group of a person can cause increased awareness which in turn decreases the chance of getting disease. Kc differs from K in the fact that Kc is individual knowledge about disease prevention coupled with cultural knowledge in the society. The cultural knowledge represents the dominant knowledge in the society. During an epidemic, public health officials can have prevention campaign or seminars which can cause a shift in cultural knowledge of a person during a disease outbreak. Its value has been computed from experimental results. It can have the range of values 1.3 to 4.6. For example, the number of infected agents at the end of 5th time step in SIR and KcSIR are compared and the knowledge factor value is 1.3 Also at the end of 40th day or time step the number of infected agents in SIR and KcSIR are computed and knowledge factor is computed as 4.6. The knowledge factor differs from the culturally evolved factor in the fact that the culturally evolved knowledge changes or evolves with more popular beliefs and prevention behaviors. Knowledge factor comprises of only self acquired knowledge.

3.5 Components of multi-agent system based on culturally sensitive SIR

In this research a multi-agent system has been built based upon culturally sensitive SIR to evaluate it. Intelligent agents have been used in a multi-agent platform and an infectious disease has been introduced to the population. The agents interact and spread disease along their path. Following are the major components of the multi-agent system built.

1. Multi-agent Population: The population is represented by a number of intelligent agents interacting with each other.
2. Cultural setting: Multi-agents learn from others while updating their individual belief space.
3. Kc SIR model

3.5.1 Multi-agent Population

The population space consists of a number of autonomous agents acting to achieve its goals and objectives. Wooldridge [Woolridge and Wooldridge(2001)] defined an agent as

> an agent is a computer system, situated in some environment, that is capable of flexible autonomous action in order to meet its design objectives.

An agent has three important characteristics which are

1. Situatedness: Agent is aware of its environment and receives some input from the environment. It can perform some actions to change the environment in which it is situated.
2. Autonomy: An agent has its own actions and states. It acts on its own and human does not have control over its actions.
3. Flexibility: Flexibility in the sense that the agent is responsive towards the environment, goal oriented and social.

The system is implemented using cultural algorithm, a population based algorithm. Population based algorithms imitate natural evolution. They are used to find solutions to optimization problems. Ant colony optimization and particle swarm optimization are population based optimization algorithms. Particle swarm optimization is used to mimic social behavior. The movement of particles or swarms in a bird flock moving in a search space is updated so as to find global optima. In ant colony optimization, ants move around randomly in search of food. They lay down pheromone deposits on the way which is most likely to be followed by another ant in search of food. The longer a pheromone stays the faster it evaporates and eventually a shorter path will be visited by ants more frequently.

3.5.2 Cultural Setting

In cultural algorithm, the global belief space contains the successful strategies of individuals. Each agent will have its own characteristics and traits. Agents will have their individual belief space which will be updated based upon the global belief space. Successful candidates and their strategies are selected to the global belief space using accept function and people gets influenced by global belief space using influence function. The pseudo code developed by Reynolds [Reynolds et al.(2004)] is as follows.

- begin t=0;
- Initialize Population POP(0);
- Initialize Belief Network BLF(0);
- Initialize Communication Channel CHL(0);
- Evaluate (POP(0)); t=1;
- repeat Communicate (POP(0), BLF(t));
- Adjust (BLF(t));
- Communicate (BLF(t), POP(t));
- Modulate Fitness (BLF(t), POP(t)); t = t+1;
- Select POP(t) from POP(t-1);
- Evolve (POP(t));
- Evaluate (POP(t)); until (termination condition)
- end

At any given point of time, there are a set of individuals in population space. The performance of each agent is evaluated. The most general belief will be the prevailing belief space. The individual belief space will be adjusted according to the dominant belief. The performance function is called fitness function. The basic functions of cultural algorithm are

1. Acceptance Function: Evaluated successful individuals are selected to global belief space.
2. Influence Function: Function through which global belief space influence individuals
3. Performance Function: Individuals are evaluated according to this function
4. Reproduction Function: Individuals in belief space are mutated

The cultural algorithm setting is depicted in figure 3.3 with these four functions.

3.5.3 SIR model

In the basic SIR model, susceptible population moves to infected population and infected population moves to removed population according to predefined mathematical equations.

3.5.4 Knowledge Aware SIR Model

In the proposed method a knowledge factor is added as an extension to the basic SIR model in which knowledge factor represents the preventive behavior of people during an epidemic. Figure 3.4 shows the effective knowledge of an individual resulting after being influenced by general or dominant cultural beliefs in the society.

The algorithm for disease spread simulation with culturally evolved knowledge is described in following steps:

- Initialize Population Space
- Initialize Belief Space

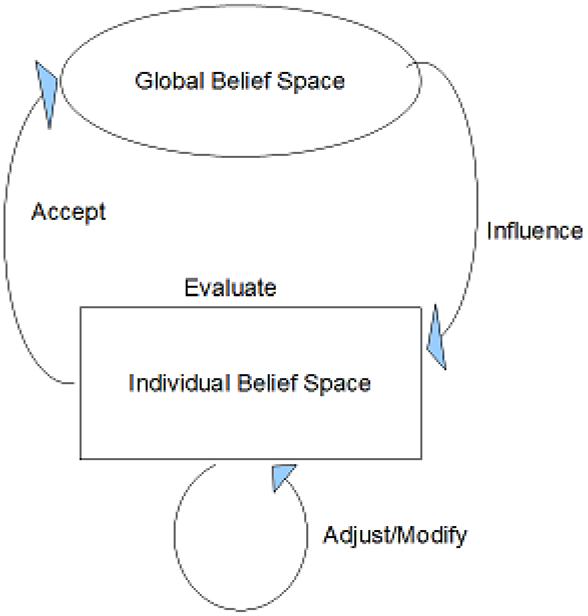


Figure 3.3: Cultural Algorithm -Setting

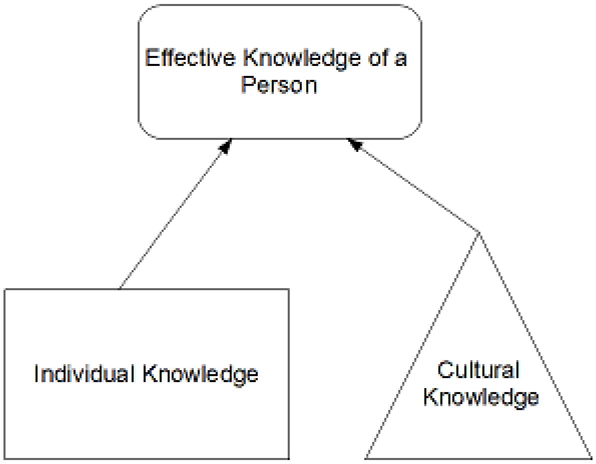


Figure 3.4: Effective Knowledge

- Divide the total population in terms of profession, culture and contact group
- Repeat steps 1-13 until termination condition is met.

1. Introduce Infectious Disease to an agent
2. Patients and close contacts seek Knowledge from others
3. Get neighbors of the Patient
4. Calculate the matching score. If fitness is less than 4 go to step 5 else go to step 12
5. Neighbor of infected person gets disease
6. Patients and close contacts of infected person seek knowledge
7. Check the period of illness of infected agents, if greater than threshold go to step 8 else go to step 12
8. Calculate the probability of recovery
9. If probability is one, go to step 11 else go to step 10
10. Agent is removed from the infection cycle
11. Agent is recovered
12. Move
13. If Agents fitness is greater than exemplars in the global belief space, agent is added to the belief space .

Chapter 4

Case Study

An extended mathematical model has been designed in the previous chapter. An algorithm for disease spread has been proposed. To verify and demonstrate, a basic agent based model based on the extended mathematical model has been designed and built. The model uses the SIR concept together with the knowledge factor. Cultural Algorithms are used to enable a population learning model. A case study on a cross cultural survey done on Singapore military is utilized for real life data to use in the model. The multi-agent based system developed is built upon the knowledge aware SIR model. Multi-agent system is built using Repast simulation toolkit. The design and implementation of the agent based system has been presented in details in following section.

The section is organized as follows:

1. Motivation for Epidemic Modeling
2. Epidemic Research Background
3. Computer Modeling
4. Design of Knowledge Aware SIR model
5. Parameters and agents in the model
6. Flow chart and Sequence Diagrams of the framework
7. Detailed Knowledge Representation
8. Functions used in system.

Test results are discussed in next chapter.

4.1 Motivation for Epidemic Modeling

Epidemiology is a science that provides health professionals information on risk assessment which is vital in decision making during a epidemic spread. It ranges from infectious diseases to other aspects of health care. Newly emerging and re-emerging diseases have made epidemiology significant in recent years. That includes AIDS, Tuberculosis and influenza to name a few. SARS, influenza and tuberculosis also cause millions of deaths around the world. Recent attacks of bio terrorism also necessitated the need for epidemiological models. To make right decision at right time makes an important task for public health systems. A timely decision can save many lives in the case of an epidemic spread. With more people traveling worldwide and the dynamic nature of world demands just in time systems to predict a disaster. Though mathematical tools have been in the scenario for a while, it is a less efficient tool when thought in terms of individual evaluation. Bio terrorism necessitated network based tools which create small world networks. Multi-agent based system is quite effective since it can mimic real world scenarios and predict the impending disaster. Modern technologies such as Geographic information systems or GIS is also used to visualize the disease spread across a geographic region. Agent based tools when coupled with the visualization tools opens up a new way to analyze and monitor a disease outbreak.

Studies show that [Jefferson et al.(2008)] pandemic influenza with 50% incidence rate has caused 36, 000 deaths in United States alone annually. Epidemic such as severe acute respiratory syndrome (SARS) caused 8000 people across the world. 2009 showed the first pandemic wave in 21st century. The public health agency of Canada reports that in province of Ontario 3636 laboratory confirmed cases were reported during H1N1 pandemic. 7% of worlds total death relate to respiratory related diseases. The prevention strategies include isolation of people, use of antivirals and quarantine of contacts. Several studies have been conducted to prevent a second wave of pandemic.

In order to find out the prevention strategies during an influenza epidemic World Health Organization [Group(2006)] conducted surveys on effectiveness of each prevention strategies. They include:

- Isolation of patients and Quarantine of contacts

Reports show that isolation of patients do not prevent the pandemic spread completely since mild cases will not be noticed and due to the failure to report to health care officials. In Canadian province of Alberta, isolation and quarantine could prevent only 60% of influenza spread. During 1918 epidemic, isolation and quarantine could not stop disease transmission but could reduce the number of causalities. In closed settings such as military or dormitories, early detection and quarantine was not much effective in preventing epidemic spread.

- Social distancing measures

Less number of causalities in rural areas in an epidemic made a conclusion that avoiding crowding during an epidemic can be an efficient strategy to reduce epidemic spread. Closing down schools during an epidemic was another strategy that was found to be effective. A teachers strike in Israel during a epidemic in 2000 caused a considerable reduction in the number of cases. Vaccination is another prevention strategy used. In Michigan when 86% of students vaccinated, it had one third of illness rate when compared to not vaccinated place.

- Measures on person entering or exiting an infected area

Control on persons entering or leaving an infected area was found to be effective in some instances. In Australia in 1919, there were controls at interstate borders to protect areas from already affected areas. Canada also has history in which people were restricted to enter an infected areas by banning tickets to the area [Group(2006)].

- Personal protection and Hygiene measures

Personal protection and hygiene measures include

- Wearing Masks in Public

During 1918 pandemic, mask use was mandated. No controlled studies assess the effect of mask during an epidemic spread. Influence of multiple measures were computed, but the influence of mask alone in preventing is not studied. But studies indicate that use of masks during epidemic can cause epidemic to subside.

- Hygiene and Disinfection

Personal hygiene factors include covering ones mouth while sneezing or coughing, hygiene etiquette, avoiding spitting etc. Hand washing is another personal etiquette that is found to be quite effective among prevention ethics.

The WHO report stresses on the importance of hygiene practices for prevention of epidemic spread. That includes promoting hand washing habits and posters in school and public places.

4.2 Epidemic Research Background

An agent based model is implemented using data from a knowledge, attitude and practice survey done in Singapore military during an influenza epidemic (H1N1) epidemic which consists of four exposure groups confirmed cases, close contacts of cases, health care workers and general personnel [Yap et al.(2010)]. Following a H1N1 epidemic outbreak in Singapore in the first week of August 2009, military initiated cross cultural survey from August 2009 to early October 2009 among military people. Surveys have been distributed to military people, their close contacts and health care workers. Questionnaire included a quest to peoples personal hygiene behavior and social behavior such as covering mouth and nose or wearing a mask during a disease spread. The survey aimed at investigating behavioral practices of people and thereby educating people during a future epidemic.

4.3 Computer Modeling

Computer Modeling has been used extensively in the fields of science and technology in order to find solutions to analytical problems. Following sections brief on the computer modeling techniques used in the proposed model.

4.3.1 Repast

The Recursive Porous Agent Simulation Toolkit is the agent modeling toolkit used for multi-agent simulation. Repast has more features from swarm and other predecessors such as genetic algorithms. Repast was developed in University of Chicago by researchers Sallach, Collier, Howe, North and others. It has been maintained by organizations like Argonne National Laboratory. Repast is now managed by the non-profit volunteer Repast Organization for Architecture and Development (ROAD). Repast has three implementations which are Repast for Java(Repast J), Repast for Microsoft .Net framework (Repast.Net) and Repast for python (Repast Py) among which Repast J offers core services. Repast 3 has following features but are not limited to

- Object oriented
- Available on all new computing platforms
- Supports social networking tools
- Has libraries for random number generation, neural networking, Monte Carlo simulation and genetic algorithms
- Has results logging and graphing tools as built in facilities
- Provides event scheduler
- Implemented in Java, C#
- Provides run time alteration of agent properties

4.3.2 Repast Setup

In Repast, agent based simulation has two steps which are preparing for the simulation and running of the simulation. In running each action is represented by terminology called ticks. Repast should have at least two classes one for describing agent characteristics or behavior which is agent class and other for model description which is model class. The class SimpleModel is inherited by our model where we override needed methods provided by our model. These methods are buildModel() and setup(). setup() is called when setup button is clicked. buildModel() function is called when the simulation is run. It creates the agents needed for the simulation. Building a repast model requires writing two classes: Agent Class and Model Class.

The agent class contains simulation specific details. The model class extends SimModelImpl. A model class has following parts

- Infrastructure and Representation Variables

Infrastructure variables include schedule and display variables and representation variables include initial parameters for a model run. Numberofagents is an example of representation variables.

- Repast Template Methods

Repast template methods include

1. buildModel() - It is used to create the model. Agent and its environment is created here. It also collects data.
2. buildDisplay() - It is used to create displays. Batch run will not have display.
3. buildSchedule() -It defines what objects need to be called and when.

- Get and set Accessor Methods

Get methods are used to receive set of parameters and set method is used to modify a parameter.

- Interface methods

To implement SimModel interface the model should have following methods

1. public String[] getInitParam(): It contains the initial set of model parameters and they are displayed in the repast tool bar.
2. public void begin(): It is called whenever the start button in Repast tool bar is clicked. It has also three build methods: buildModel(), buildDisplay() and buildSchedule(). In essence begin() method initializes the model.
3. public void setup(): setup() method is called when setup button in Repast tool bar is clicked. It is used to set objects which are created to null as well as disposing the display surfaces.
4. public Schedule getSchedule(): It returns schedule associated with the model.
5. public String getName(): It returns the model name. It is displayed as the title of the model.

- Simulation Specific Methods: It specifies the methods that are specific to a model. It includes methods that write data to a file.
- Main Method: Main method creates an instance of the model that is created.

4.3.3 Repast Run

Repast can be run in different operating systems such as Windows, Unix or Mac operating system. In Windows, Repast can be run by double clicking repast.jar file. It can be run on command line in Windows as well from other operating systems. Repast suite comes with many demonstration models. The demonstration models has to be loaded and can be run via repast tool bar. Repast runs are of two types: batch run and non-batch run. Batch run are done using parameter file which contains the starting and ending value of parameters and the total number of runs to complete the simulation. A non-batch uses graphical user interface to start and end the simulation. It also allows to manipulate the agent states during model run.

4.3.4 Repast Display and Charts

Repast uses three types of classes for the graphical representation of agents used in the class Spaces, Displays and a display surface. For displaying, the objects needed to be displayed must be created. The agents and environment are created in buildModel(). In buildDisplay(), appropriate display is created. The display is created and added to Display surface which is created in Setup() method. When the DisplaySurface gets the method call UpdateDisplay, it gets the list of display objects in space, gets drawing information for the objects to be drawn.

4.3.5 Repast Scheduling

Repast scheduling is done using Schedule object. It is responsible for any change in simulation. It can be used to schedule some actions to occur at a particular tick or iteration, in equal interval, every iteration or the end of simulation. Scheduling is done by making method calls at some iteration. These method calls must use BasicAction class. A BasicAction class must implement execute() method and the variables used by the method.

4.3.6 Repast Tool bars

Repast can be run either through command line or as java application. Repast GUI helps user to start, stop and play the simulation. Figure 4.1

Figure 4.1: Repast-Toolbar1

shows repast tool bar 1. It has options to start multi run, start, step, initialize, stop, pause, setup, load model, view settings, load model and exit. To run a simulation you need to click either start, initialize or step button.

Figure 4.2 is the repast tool bar 2. It shows the parameters used in the model. It also has custom actions tab and repast actions tab. Repast actions include making a movie, taking snapshot of the run, output to console etc.

4.4 Design of Knowledge Aware SIR model

4.4.1 Agents in the model

The agents used in the model have characteristics such as

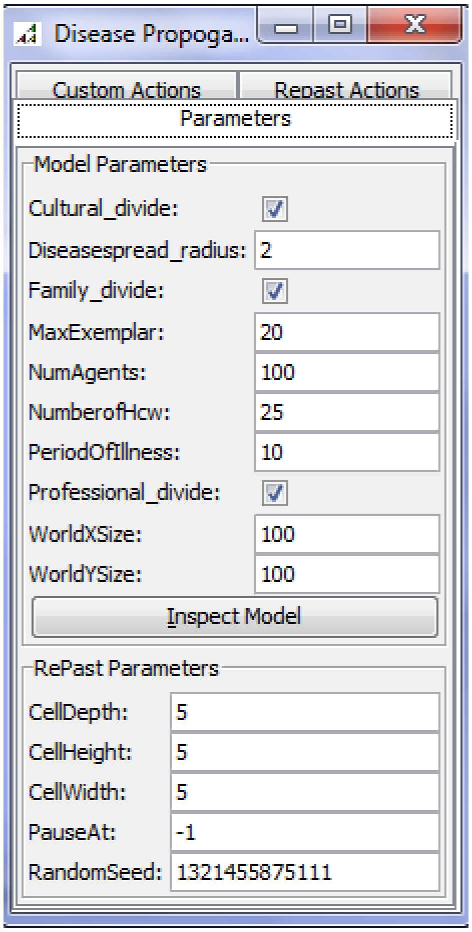
- Health condition

Health condition of an agent changes when simulation runs. After the infectious disease is introduced to the population, neighboring agents get disease from infectious agent. Health condition of an agent can be susceptible, infected or dead. Health condition is a integer variable and can have values 0 which means susceptible or the initial condition, 1 or infected and 2 dead or recovered.

- Family Tag:

It represents contact group in which agent belongs to. In order to understand the influence of disease prevention behaviors on patients close contacts, the agent population is divided to different contact groups in which each contact group is of ten members. When a patient of the contact group contracts disease the members in the contact group seek knowledge and prevention strategies and becomes well aware of the flu prevention behaviors.

- Cultural Score : Score specific to a cultural community



Cultural_divide: ☑
Diseasespread_radius: 2
Family_divide: ☑
MaxExemplar: 20
NumAgents: 100
NumberofHcw: 25
PeriodOfIllness: 10
Professional_divide: ☑
WorldXSize: 100
WorldYSize: 100

CellDepth: 5
CellHeight: 5
CellWidth: 5
PauseAt: -1
RandomSeed: 1321455875111

Figure 4.2: Repast -Toolbar2

Cultural Score is specific to a particular community. Depending upon community's specific cultural behaviors, cultural score is computed.

- Knowledge Score: score based on knowledge held by patients

Knowledge score is computed from the knowledge held by agents. The computation of knowledge score along with examples are detailed in section 4.4.3.

- Profession

Professionally, an agent can be health care worker, Military Personnel or general people. The number of Health care workers is initialized to be one fourth of total population.

4.4.2 Parameters

Table 4.1 represents the parameters used in the model. The number of agents is initialized to 100. Period of illness represents the time period needed for recovery or in other words time to remove an agent from the infection cycle. It can recovered or dead. The Diseasespread radius is the minimum infection distance for a neighboring agent.The boolean variable cultural divide is the boolean variable used to divide the population to different cultures. The Maxememplar is the maximum number of exemplars. In this particular case study we have used 20 exemplars. The boolean variable professional divide is used to divide population to professions and the boolean variable Family divide is used to divide population to different contact groups.

4.4.3 Knowledge Definition and Design

The knowledge held by people is represented by an array. Each bit in the array represents each piece of information. The knowledge of how to prevent flu has been taken from Public Health Agency of Canadahttp://www.fightflu.ca website. The preventive behavior includes:

1. Get your flu shot
2. Eat Healthy Food
3. Wash your hands frequently
4. Keep your hands away from face

Parameter used in the model	Description
numberofsusceptibleagents	number of susceptible
numberofinfectedagents	number of infected
diseasespread_radius	Minimum distance to get infected
PeriodOfIllness	Time period to get recovered or dead
CA_enable	Flag to set cultural algorithm on or off
cultural_divide	Flag to set cultural division on or off
agents_have_knowledge	Flag to set knowledge enabling on or off
NumberofAgentsDeadorRecovered	number of removed agents
family_divide	Flag to set family division on or off
DiseaseInfect	Flag to set infection spread on or off
NumberofAgentsSaved	number of agents saved
NumberofAgentsLearnt	number of agents learnt
dayinfected	day in which agent is infected

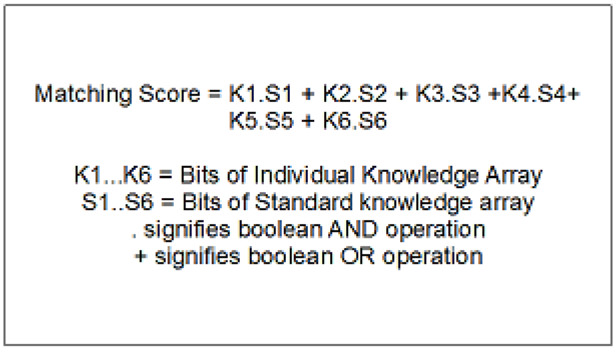
Table 4.1: Parameters used in the model

5. Cough and Sneeze to your arm
6. If you get sick stay home
7. Wear a mask if infected.

A multi-agent system has been implemented in which agents move randomly and spread disease across the way. Knowledge score of agents are initialized and gets evolved when simulation runs. An agent who is within the infection distance gets disease depending upon their knowledge score. These bits of knowledge is represented in the form of an array. Each bit of array represents each bit of information.

4.4.3.1 Knowledge Score Computation

Knowledge score is computed by ANDing and ORing the knowledge array bits with the standard knowledge array or array with all ones. For example if an agent knows the fact that to prevent flu, one must get your flu shot done and wash hands frequently and wear a mask but unaware of other facts, his knowledge array is represented by 1010001. His knowledge score is computed by comparing with the perfect score that is all ones. Perform AND operation with the perfect score and then performing an OR function. In the above



Matching Score = K1.S1 + K2.S2 + K3.S3 +K4.S4+
K5.S5 + K6.S6

K1...K6 = Bits of Individual Knowledge Array
S1..S6 = Bits of Standard knowledge array
. signifies boolean AND operation
+ signifies boolean OR operation

Figure 4.3: Knowledge Score Computation

example, knowledge score is computed as 3. Depending upon knowledge score an agent contracts disease from an infected one. The threshold of matching score is kept to be 4. If the matching score is less than 4 then agent gets disease if the agent is within the infection distance.

4.4.4 Cultural Algorithm

Cultural algorithm is deployed using following three functions:

- Initialize

In initialize function, the global belief space is initialized with health care workers. The knowledge array is initialized with values obtained from survey.

- Influence

In Influence function, an individual's belief space is replaced with exemplars knowledge array. The belief space contains exemplars and a randomly selected exemplar is used to influence an individual agent. Figure 4.3 depicts the influence function. E1, E2 ... En represent exemplars in the belief space. In this example number of exemplars is set to 20. For example in the case study, lets say an individual has knowledge bits as 1, 0, 0 in the case of a 3 bit knowledge array. If the individual seek knowledge from an exemplar who has the knowledge array 1, 1, 0, then the individual's knowlede array becomes 1, 1, 0. In other words the knowledge array is replaced with those with exemplar.

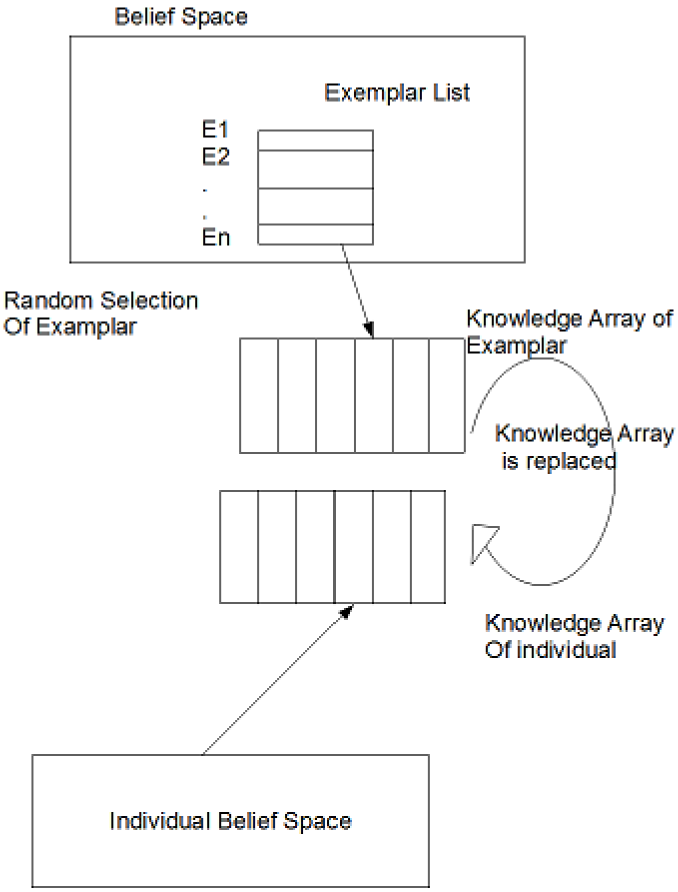


Figure 4.4: Influence Function

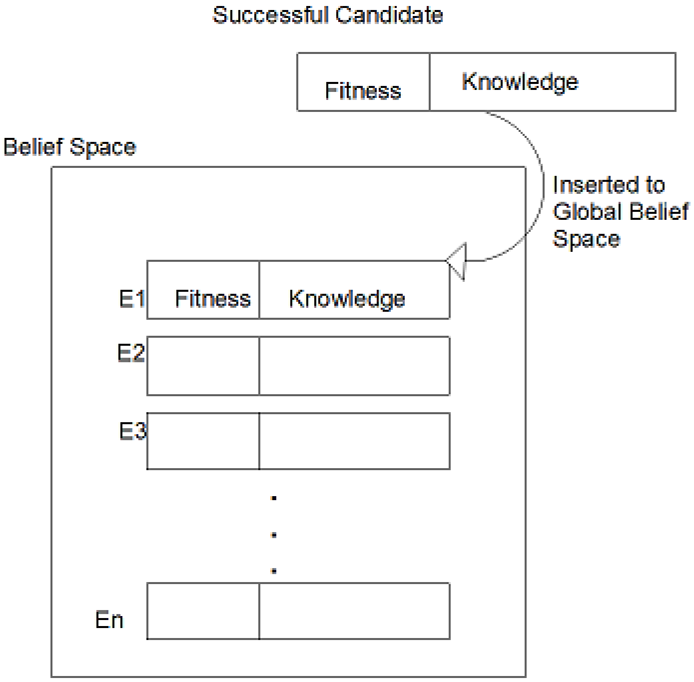


Figure 4.5: Accept Function

- Accept

In Accept function, an individual's fitness is computed. An exemplar has two parts:

1. Fitness
2. Knowledge

If the individual agents fitness is greater than the one in exemplar list, then it is inserted to the global belief space. The exemplar having lowest fitness is removed from the belief space using insertion sort.

4.4.5 Belief Space

The number of exemplars is initialized to 20. The exemplars or successful candidates to belief space.

4.4.6 Model design and Flow Chart

Our proposed model investigates the disease spread in a closed population. An agent based model has been implemented with parameters such as infection distance or the minimum distance to get infected from an infected person, Knowledge array or the array containing the knowledge for infectious disease prevention, alpha or the rate of recovery, beta or the infection rate (not a constant, depends on distance), total population group, number of days per simulation and period of illness.

Agents move randomly across a closed surface. The total population is divided into susceptible, infected and recovered population. The probability that a person gets a disease from an infected agent depends upon knowledge score which is computed from the knowledge held by individuals. An infected person is either recovered or dead depending upon probability of recovery. Agents have characteristics such as health information, cultural group it belongs to and profession. An agent has a close contact group and have different professions including health care workers. Agents learn from others and periodically update their belief space. Agents having more knowledge score are added to global belief space and in turn influence other agents in the society. Close contact's knowledge score increases if there is a newly infected person in the group and depending upon their knowledge score, are added to the belief space replacing agents having low knowledge score.

Figure 4.5 depicts the flow chart1 of disease transmission. Initially the infectious disease is introduced to the population. Close contacts of the patient seek knowledge on how to prevent the flu from others. Neighbors of the infected person are found. Any agent within radius of infection distance is susceptible to disease. In addition the matching score of the neighbor is computed. Calculation of matching score is discussed in previous section.

Figure 4.6 depicts part two of disease transmission flow chart. If the matching score of neighboring agent is less than 4 neighbor gets disease. Consequently, the patient and the close contact seek knowledge from neighbors and contacts. If matching score is greater than 4 the agent is saved. The ill period of patient is calculated and if it is greater than recovery period,

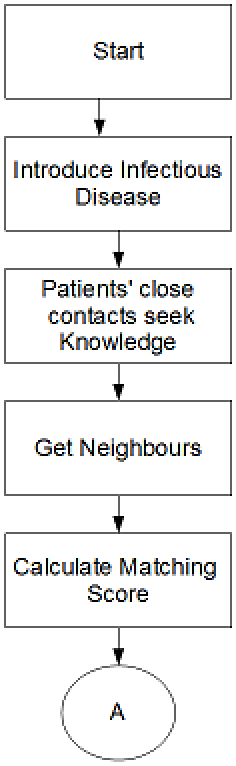


Figure 4.6: Flowchart1-Disease Spread Algorithm

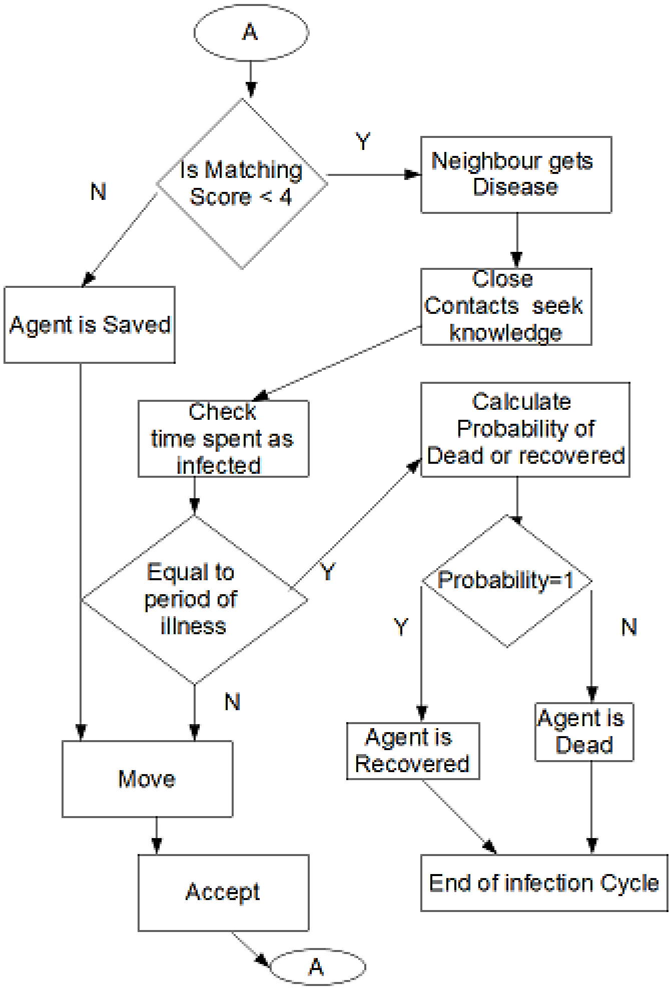


Figure 4.7: Flowchart2-Disease Spread Algorithm

the agent continues its movement. The agent also accepts new strategies of successful exemplars from the belief space. The probability of getting disease is computed. If probability is 1, then the agent is recovered else the agent is removed from the infection cycle.

The total population is represented in terms of three groups: number of Susceptible people (S), number of Infected People (I), number of Removed (R) and number of Dead People. The total population is divided to general, military, patients, close contact and health care workers.

A multi-agent based model is built with 100 agents in a 100 * 100 grid. The assumptions made for the model design are:

1. The population is a closed one
2. Each time step corresponds to one day
3. The agents move randomly across the grid
4. The infectious agents spread disease to the neighboring agents
5. The neighbors of infectious agents get disease depending upon knowledge score.
6. The period of recovery is taken as 10 days.

Chapter 5

Testing and Validation

5.1 Test Results

We ran the simulation 10 times in three different settings and calculated the number of susceptible, infected and recovered number of agents in each run. The number of agents was set to 100. The agents move randomly along the grid.

In the first setting, the agents get the disease from infected agents if they are within a constant infection distance. When the disease was introduced to one of the agents, it becomes infectious and start infecting other neighbor agents irrespective of the behavioral practices of the neighboring agents.

The resulting graph is plotted with the number of infected agents in the Y-axis and time steps on the X-axis. Figure 5.1 shows the graph plotted with the number of infected agents without knowledge and without learning.

In the second setting, agents get infected with the disease depending upon their knowledge score. The knowledge represents the knowledge held by agents on how to prevent the spread. The agents do not learn from others. Figure 5.2 shows the graph plotted with the number of infected agents with the knowledge and without learning in Y axis and time steps in X axis.

In the third setting, agents get the disease depending upon the culturally evolved knowledge. Figure 5.3 shows a graph plotted with the following measures in a culturally sensitive K-SIR in Y axis and time steps in X axis.

- Number of Susceptible(S)
- Number of Dead or Recovered(R)

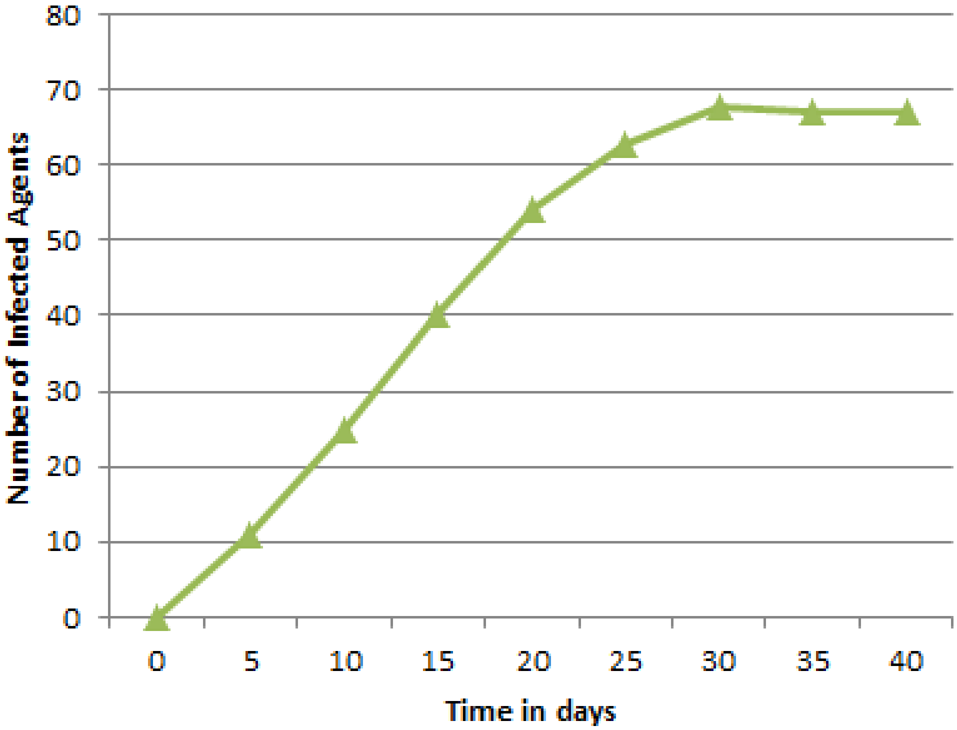


Figure 5.1: Infected agents over time in the first setting

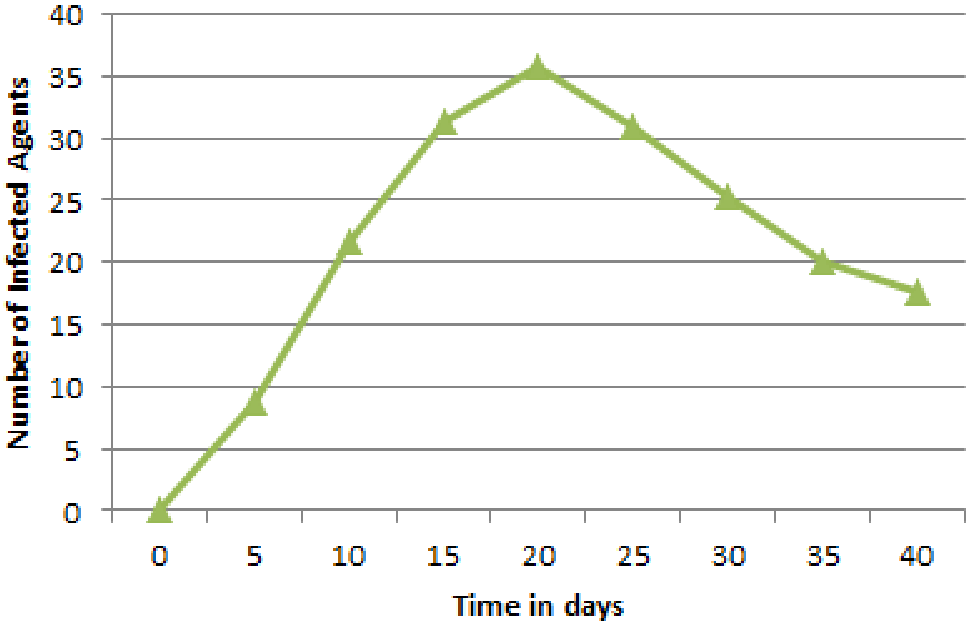


Figure 5.2: Infected agents over time in the second setting

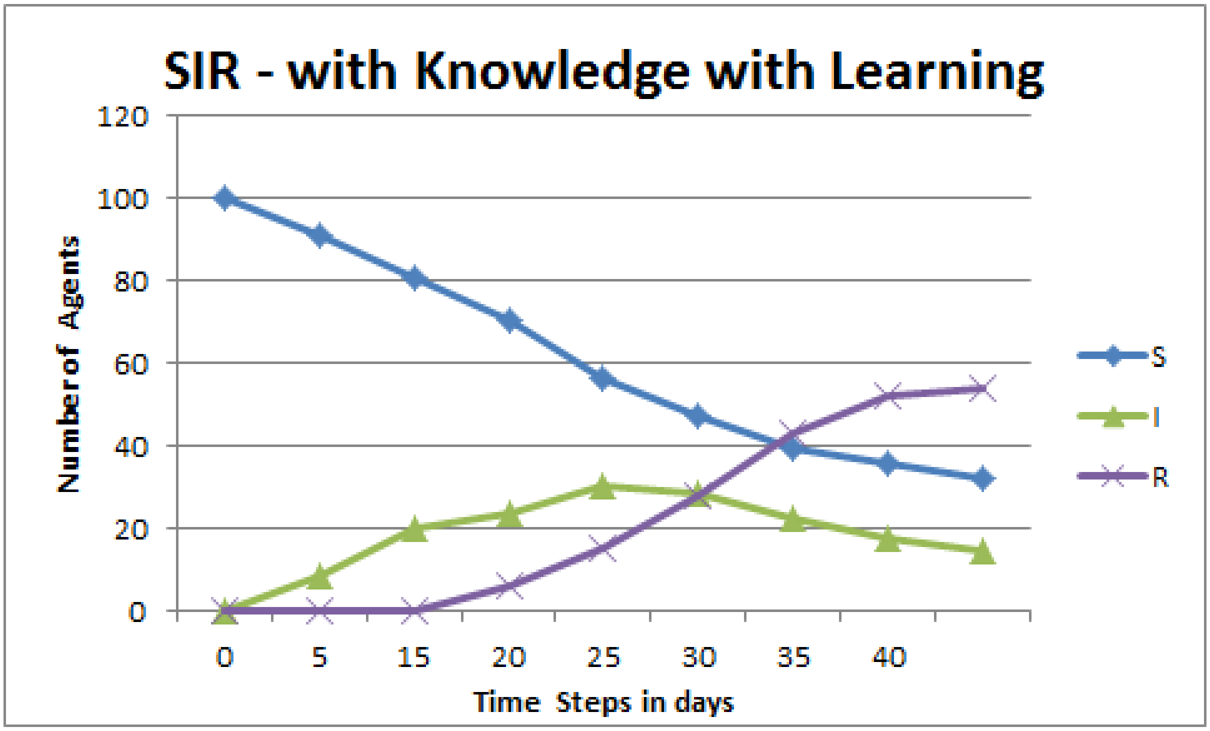


Figure 5.3: SIR with knowledge with learning over time

- Number of Infected agents with knowledge and learning (I).

Susceptible agents are 100 at the beginning of the simulation. After 10 time steps, infected agents become either dead or recovered. The total number of susceptible, infected and recovered forms the total population.

Infected number of agents in intervals of ten time steps is shown in the table. The multi-agent system implemented with the data specific to the case study affirms the importance of knowledge in calculating risk or in formulation of intervention policies. Studies show that a third of infection cases [Group(2006)] have been reduced as a result of educating people about behavior practices during an epidemic. The results obtained from the Kc-SIR simulation yield results close to the real epidemic data in the case study. [Jefferson et al.(2008)].

Table 5.1 shows the results of infected number of agents in the first setting. The number of agents after 5 time steps are computed and is printed to an output file. Table 5.2 shows the standard deviation of values of infected

Table 5.1: Infected number of agents without knowledge and without learning

Time	Run1	Run2	Run3	Run4	Run5	Run6	Run7	Run8	Run9	Run10
0	0	0	0	0	0	0	0	0	0	0
5	10	10	10	10	10	10	20	10	10	10
10	25	20	20	22	27	18	40	30	26	20
15	38	30	40	48	33	35	50	50	45	32
20	52	50	60	60	45	46	55	55	65	52
25	60	52	70	78	61	50	52	68	75	60
30	67	60	72	75	63	66	55	70	78	70
35	68	62	68	78	64	73	55	62	70	72
40	68	68	59	75	65	71	62	68	65	73

Table 5.2: Setting1- Standard Deviation of 10 runs

Time	Average	Standard Deviation
0	0	0
5	11	3
10	24.8	6.2
15	40.1	7.3
20	54	6.0
25	62.6	9.3
30	67.6	6.6
35	67.2	6.3
40	67	4.6

Table 5.3: Infected number of Agents with knowledge

Time	Run1	Run2	Run3	Run4	Run5	Run6	Run7	Run8	Run9	Run10
0	0	0	0	0	0	0	0	0	0	0
5	9	10	9	6	10	12	8	8	8	8
10	19	20	19	30	20	33	18	17	20	20
15	22	48	21	38	28	45	30	35	28	20
20	29	49	21	50	30	48	36	35	30	30
25	23	30	20	50	32	40	22	32	30	31
30	22	22	19	25	38	30	22	33	22	19
35	20	20	19	13	28	22	21	21	19	18
40	18	20	19	11	20	20	19	17	16	16

Table 5.4: Setting2- Standard Deviation of 10 runs

Time	Average	Standard Deviation
0	0	0
5	8.8	1.5
10	21.6	5.1
15	31.5	9.3
20	35.8	9.44
25	31	8.4
30	25.2	6.0
35	20.1	3.5
40	17.6	2.7

Table 5.5: Infected Agents with knowledge and with learning

Time	Run1	Run2	Run3	Run4	Run5	Run6	Run7	Run8	Run9	Run10
0	0	0	0	0	0	0	0	0	0	0
5	10	9	8	6	9	10	8	8	9	8
10	17	18	18	30	17	30	12	20	23	16
15	20	21	20	30	20	35	20	22	21	21
20	25	27	20	50	29	40	48	26	22	20
25	22	22	19	50	29	30	32	40	22	19
30	22	20	18	25	28	25	22	30	19	18
35	20	18	17	13	19	18	20	10	19	19
40	18	16	17	11	10	15	20	10	15	13

Table 5.6: Setting3- Standard Deviation of runs

Time	Average	Standard Deviation
0	0	0
5	8.5	1.1
10	20.1	5.6
15	23.8	6.4
20	30.7	10.6
25	28.5	9.6
30	22.7	3.9
35	17.3	3.1
40	14.5	3.3

Table 5.7: Knowledge Score

Type of person	Knowledge Score
Patients	69.0
Contact	71.7
Health care workers	69.6
General Servicemen	68.8
Overall	69.7

number of agents in ten runs.

Table 5.3 shows the results of infected number of agents in the second setting. Table 5.4 shows the standard deviation of values of infected number of agents in ten runs in the second setting.

Table 5.5 shows the results of infected number of agents in the third setting. Table 5.6 shows the standard deviation of values of infected number of agents in ten runs in third setting.

5.2 Validation

The study conducted on Singapore military [Yap et al.(2010)] surveyed on people's basic knowledge such as information about pandemic influenza, questions about mask usage, vaccination usage and avoidance behavior knowledge such as avoiding crowded places, avoiding people with flu symptoms and personal habits such as, covering one's mouth while sneezing, washing hands regularly with soap and water and avoiding people when infected. The questionnaire also included practice behaviors such as if they have worn mask at home and in public places or avoided infected people. Table 5.4 shows the knowledge score obtained from the survey.

Figure 5.4 shows the average number of infected agents taken in all three settings compared with the real case study results.

The overall knowledge score of the people involved in the survey is 69.70%. The knowledge score in the case study results shows the level of knowledge owned by an individual about pandemic influenza. Comparison of results proves that the simulated results produce closer results to real case study results and could help in accurate risk assessment during an epidemic. Finer results may be obtained in addition of further details such as influence of

Figure 5.4: Comparison of Results

Time	Infected in SIR	Infected in KSIR	Infected in KcSIR	Real case study results
0	0	0	0	0
10	24.8	21.6	20.0	7.5
20	54.0	35.8	30.2	16.7
30	67.6	25.2	22.6	20.5
40	67.0	17.6	14.4	20.3

cross cultural factor in disease prevention behavior.

Chapter 6

Discussion

An algorithm for disease transmission has been proposed. A basic agent based model has been built. Three different settings have been implemented. The test results are analyzed and results are compared. Section 6.1 discusses the first experiment with agents do not learn and do not hold any knowledge. Section 6.2 discusses the second setting with agents hold knowledge but do not learn from others. Section 6.3 discusses the third setting where agents have knowledge and also learn from others. Section 6.4 discusses the comparison of results obtained from three settings and real case study results.

6.1 Experiment1 with no learning and knowledge

In setting one agents do not learn from others. Table 5.1 shows the number of infected agents with equal time intervals of 5 time steps or days in this example in ten consecutive runs. Figure 5.1 shows the infected number of agents over time. Initially the number of susceptible agents was 100. In the basic SIR where agents move from one stage to another was implemented, the number of infected agents was high.

6.2 Experiment2 with knowledge no learning

In setting two agents do not learn from others but they hold knowledge about prevention behavior during an epidemic and this knowledge prevents agents from getting infected from an already infected agent. Table 5.2 shows the number of infected agents with time intervals of 5 time steps in ten consecutive runs. Figure 5.2 shows the infected number of agents over time. Initially the number of susceptible agents was 100. When K-SIR was implemented, there is a drastic decrease in the number of infected agents when compared to the basic SIR.

6.3 Experiment3 with knowledge with learning

In third setting agents have knowledge and they learn from others. The dominant knowledge that is prevailing in the society about the prevention behavior during an epidemic is used to influence agent's actions. Table 5.3 shows the number of infected agents with equal time intervals of 5 time steps in ten consecutive runs. Figure 5.3 shows the susceptible, infected and recovered number of agents over time. Initially the number of susceptible agents was 100. Based upon the results, when the culturally sensitive SIR was implemented, the number of infected agents decreased again.

6.4 Comparison of Results

The number of infected agents in three settings taken in time difference of 10 time steps or 10 days are compared with the case study results. Figure 5.4 shows the comparison of results. The actual results are closer to the simulated results when time progresses i.e when more people learn and exchange knowledge about disease prevention in a cultural setting. The results affirm the importance of knowledge as a deciding factor in risk assessment and strategic decision making during an epidemic.

Chapter 7

Conclusion and Future work

The aim of this study was to extend the basic SIR mathematical model to enable the role of knowledge in the simulated human population. This knowledge can be learned, exchanged and applied by individuals interacting in a simulated social setting. In addition to individual evolution, population evolution can be enabled specific to knowledge based SIR with the use of a custom Cultural Algorithm.

By using a mathematical model it is possible to do the risk assessment and help public authorities in taking strategic decisions during a spread. The model should be easy to build since time plays a significant role in an epidemic spread. Though various extensions have been made to the traditional model, none has considered the influence of cultural knowledge. As per the studies [Yap et al.(2010)], the cultural knowledge alters actions of people and makes risk assessment impossible. During an epidemic spread, the highest knowledge is held by close contacts of the patients followed by health care agents. We believe that by deploying knowledge factor specific to each group of people in the SIR model helps in yielding more realistic results.

In this paper, an extension to the traditional model has been proposed that takes into consideration, the preventive behavior of people during disease spread. Current focus is made on extending the framework to add cultural specific details to the existing disease spread algorithm, thereby creating close results. Encouraging results have been obtained in successive runs of the simulation.

Ethnicity also plays a role in determining peoples action [Yap et al.(2010)]. Research shows [Montgomery and Jones Schubart(2010)] that socio-cultural differences specific to particular community also contribute to preventive practices by people. Different cultures behave differently in a disease spread and are decided by factors such as individualism versus collectivism, time orientation, poverty, language barriers and communication styles. These specific details must be taken into consideration while making predictions during an epidemic. As a future work we plan to extend the culturally sensitive SIR with more culturally diverse characteristics.

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