2014

EcoDemics, Modelling Epidemic Spread in a Simulated Predator-Prey Evolutionary Ecosystem

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By

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A Dissertation
Submitted to the Faculty of Graduate Studies
through the Department of Computer Science
in Partial Fulfillment of the Requirements for
the Degree of Doctor of Philosophy
at the University of Windsor

Windsor, Ontario, Canada

2014

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Declaration of Originality

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Abstract

Modeling the progress of an epidemic in a population has received significant attention among various fields of science. Many epidemiological models assume random mixing of the population, homogeneous hosts, and a static environment. We are interested in modeling epidemic spread in a dynamic evolving ecosystem with behavioral models associated to its individuals. To this end, we present EcoDemics; which integrates the classical SIR (Susceptible-Infected-Removed) disease model to an individual-based evolutionary predator-prey ecosystem simulation, EcoSim. The behavioral model of each agent in EcoDemics is based on a fuzzy cognitive map (FCM) that determines the heterogeneous interactions between individuals. We present the disease model used and we demonstrate how the epidemic spread in a random mixing ecosystem differs from a heterogeneous ecosystem with its behavioral model. We observed that dynamics of the ecosystem, along with the spatial distribution of agents, play a significant role in disease progression.

Due to the high mitigation capacity and significance of the immunization intervention, we explore vaccination techniques with various time delays and population proportions in EcoDemics. Based on the herd immunity theory, the whole population can be protected against a contagious disease by vaccination of a fraction of individuals. We investigate this principle in EcoDemics and compare our results with real epidemics data.

A number of mathematical simulations have been used to analyze host-pathogen dynamics in the presence of predators; however, to the best of our knowledge, this is the first individual-based modeling study exploring the effect of predators on prey infection dynamics in a predator-prey ecosystem simulation. We used the EcoDemics framework to investigate the effect of predation on infection dynamics in EcoDemics. Our results are in agreement with both numerical and field studies.

Dedication

To My Parents for Their Love, and Endless Support

Acknowledgements

I am greatly indebted to my supervisor Dr. Robin Gras for suggesting the area of study, leading me to the world of evolutionary individual-based systems, 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. Ziad Kobti, Dr. Alioune Ngom, Dr. Jan Ciborowski, and Dr. Rob Deardon for their detailed review of my thesis and constructive criticism during the preparation of this thesis.

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Chapter 1

Introduction

1.1 Epidemic Modeling

Epidemics that spread in wide geographic areas for both animals and humans, impose a threat to global public health security. Pandemic influenza results in an estimated three to five million cases of severe illness and between 250,000 and 500,000 deaths according to different health reports [124]. Deadly infectious pandemics transmitted from animals to humans such as rabies, H1N1, and SARS had deadly effect throughout the globe. As an example, rabies is a viral disease of the central nervous system, transmitted by direct contact. The highly fatal nature of this disease resulting in approximately one death every 10 minutes, and its widespread survival that can infect any warm blooded animal and humans, makes it a great health concern worldwide. Although the final number of infections, illnesses, and deaths could vary tremendously depending on the pandemic and other multiple factors, it is certain that without adequate planning and preparations, a pandemic in the 21st century has the potential to cause enough illnesses to overwhelm public health system at all levels. This points out the great importance of modeling and simulating the spread of diseases, among both humans and animals. Recent research studies modeled and examined the effect of spread of diseases and different disease control strategies to suppress the infection.

The overwhelming majority of disease models are based on a compartmentalization of individuals or hosts according to their disease stages [2], [6], [71]. The basic models describe the number of individuals (or proportion of the population) that are susceptible to, infected with and recovered from a particular disease [68], [22]. The foundations of almost all mathematical infectious disease epidemiology are obtained by the differential equation based SIS (Susceptible-Infected-Susceptible) or SIR (Susceptible-Infected-Removed) models [6]. These mathematical models have had a long and successful history of obtaining analytical expressions for a number of interesting parameters including the total numbers of infections. These models assume homogenous hosts

meaning that each individual in the population is considered to have equal probability of contracting the disease. Additionally, random-mixing of the individuals in the population has been assumed and therefore the spatial distribution of the population has been ignored.

To overcome the inaccuracies caused by the random mixing of the individuals in the population, the use of network-based models in epidemiology has become an active topic in scientific literature. Network-based models have roots in graph theory in which nodes and edges of a graph are used to represent hosts and contacts in epidemiology [29], [67], and [82]. Several network-based models have been developed to emphasize the role of modeling heterogeneity [10], [98], clustering [86], [55], and spatial dynamics [97], [104]. These models, however, assume fixed contact structure during the course of the outbreak and the clustering is simplified by measuring the number of triangles and short cycles in the network.

In order to model heterogeneity and dynamic structure, current simulation works have incorporated a variety of techniques, including individual-based modeling and cellular automata (CA), into network simulations [42]. Mikler, Jacob, and Gunupudi have introduced the global stochastic cellular automata paradigm, addressing the issue of neighborhood saturation in a classical CA [83], [85], and [84]. Both CA and individual-based systems are bottom up approaches where the systems are described by defining the local interactions. Among existing simulators in individual-based models, EpiFast, EpiSims, and EpiSimdemics were built upon the Simdemics framework [13], [14], [16], [30], [29], and [112] to model epidemics in the human population. Contact patterns are usually modeled by census data and statistics; however, these data are often very difficult to gather [81], [68] and involve a high level of inaccuracy [119].

1.2 Thesis Motivation

In the case of animal epidemics, although several mathematical and network-based models have been developed to mimic outbreaks of diseases such as foot-and-mouth disease (FMD) [68], classical swine fever (CSF) [65] and rabies [97], far less attention has been concentrated on employing individual-based modeling of animals with

behavioral model in an ecosystem. The need for individual-based modeling has been emphasized by Real and Biek who highlighted the importance of spatial dynamics and geographical landscape to the spread of rabies [97]. One of the most frequently studied diseases in the SIR model is rabies. Several methodologies exist that help predict the local, spatial and temporal dynamics for rabies viral infection [18], [107], and [43]. These models are mainly concerned with mathematically modeling the epidemic using the available databases. However, the population properties of different animals in an ecosystem, for example, population densities, individual movements and contact rates, are extremely hard to measure [97], and data regarding which individuals are responsible for the disease transfer is difficult to gather [81]. This imposes the development of a behavioral model that determines the interaction patterns of individuals in an ecosystem.

1.3 Thesis Contribution

There are a number of artificial life systems that model evolutionary ecosystem, the most notable ones are Tierra [96], Avida [1], Echo [56], PolyWorld [118], Framsticks [57] and EcoSim [44]. None of the above systems, to our knowledge, has integrated disease progression stages. We have used EcoSim [44] which was designed to simulate agents' behavior in a dynamic, evolving ecosystem. The agents (or individuals) of EcoSim are prey and predators acting in natural simulated environment. Each individual has a behavioural model that determines its actions in the ecosystem. In this thesis, we present EcoDemics which integrates a disease model to EcoSim for studying epidemic spread in a predator-prey simulation. Here, we are not interested in modeling a specific disease in a particular ecosystem, but rather to model the influence of the behavioral model of the individuals and consequent spatial distributions on disease dynamics. We have made realistic assumptions about our virtual ecosystem and disease model and tried to make as few assumptions as possible to maintain generality and applicability of the EcoDemics model for future studies.

1.4 Thesis Outline

This thesis is organized as follows:

Chapter 2 is dedicated to the literature review of modeling infectious diseases. It describes the mathematical, network based, and individual based modeling of the epidemics.

Chapter 3 explains the individual-based predator prey evolutionary ecosystem simulation, EcoSim. It includes the design concepts regarding this simulation, and the parameters regulating the system dynamics. Also, the Neutral version of this simulation will be explained in this chapter.

Chapter 4 introduces EcoDemics, which extends EcoSim to model epidemic spread in the predator-prey ecosystem simulation. This chapter explains all the technical modifications and parameters added to the simulation to model the disease phase. The disease phase is added to both EcoSim and the Neutral version of it, and the differences will be explained extensively.

Chapter 5 is devoted to include vaccination as a powerful mitigation strategy to EcoDemics. Variations in time and in proportion of the individuals being vaccinated along with the herd immunity are discussed in this chapter.

Chapter 6 describes the effect of predation in disease dynamics. Infection with or without predators, and with predators having different attack rates are the discussion topics of this chapter. Finally in Chapter 7, conclusions and recommendations for the future work will be explained.

Chapter 2

Review of the Literature

Modeling the progress of an epidemic in a population has received significant attention among various fields of science. An epidemic model is a simplified tool to describe the transmission of contagious disease in a population of individuals. Some basic concepts in epidemiology and different epidemic modeling techniques will be discussed in this chapter.

2.1 Sources of transmission and infectiousness levels

2.1.1 Transmission of pathogens

An infectious disease is transmitted from a source. Means of transmission of infectious disease and their characteristic features, play an important role in understanding the biology of an infectious disease, and in developing proper interventions of disease control [70].Transmission may occur through several different mechanisms:

Contact: This type of diseases require direct or indirect contact.

Food or water-borne: Food or water-borne diseases are any illnesses resulting from the consumption of infected food.

Air- borne: Air-borne transmission requires inhalation of contaminated air.

Vertical transmission: In the case of some diseases such as AIDS or Hepatitis B, it is possible for the offspring of infected parents to be born infected. This type of transmission is called vertical transmission.

Vector transmission: Disease transmitted indirectly and through a vector. For example, malaria spread in individuals through mosquitoes.

2.1.2 Levels of infectiousness

The spectrum of occurrence of disease in a defined population includes:

Sporadic: occasional occurrence

Endemic: regular cases often occurring in a region

Epidemic: an unusually high number of cases in a region

Pandemic: a global epidemic or an epidemic occurring in multiple countries

2.2 Mathematical Modelling of infectious disease

2.2.1 The SIR Model

Starting point of epidemic models was carried out by Kermack and McKendrick in 1927 [71], which was followed by Bailey in 1957 [6], and Anderson & May in 1992 [2]. They considered a fixed population with three states: susceptible (S), infected (I), and recovered (R); therefore, this model is called the SIR model. The states of the disease in mathematical epidemiology are usually referred to as compartments. The pioneers of SIR model derived these differential equations:

$$\frac{dR}{dt} = \gamma I$$

$$\frac{dI}{dt} = \beta SI - \gamma I$$

$$\frac{dS}{dt} = -\beta SI$$

$$N = S(t) + I(t) + R(t)$$

Between states S and I, the transition rate is β I, where β is the contact rate, between I and R, the transition rate is γ (simply the rate of recovery).

An individual in the population N must be considered as having the same probability as every other individual of contracting the disease. The processes of transition between susceptible to infectious, and infectious to recovered, which occur simultaneously in SIR

model, are referred to as the Law of Mass Action, a widely accepted idea that the rate of contact between two groups in a population is proportional to the size of each of the concerned groups [17]. Finally, it is assumed that the rate of infection and recovery is much faster than the time scale of births and deaths and therefore, these factors are ignored in this model.

There is a threshold quantity in the SIR model which determines whether an epidemic occurs, or the disease simply dies out. This quantity is called the basic reproduction number, denoted by R_0. It can be defined as the number of secondary infections caused by a single infective introduced into a population made up entirely of susceptible individuals (S(0) =N -1) over the course of the infection of this single infective. This infected individual makes βN contacts per unit time producing new infections with a mean infectious period of 1/γ, so

$R_0 = (\beta N)/\gamma$

If $R_0 > 1$ there is an epidemic in the population. When $R_0 = 1$, the disease becomes endemic, meaning the disease remains in the population at a consistent rate, as one infected individual transmits the disease to one susceptible. If $R_0 < 1$ the infection dies out. It is worth noting that R_0 is only a threshold value and cannot be used to compare different diseases. The usefulness of R_0 is very limited as it is calculated only via a mathematical model, and rarely observed in the field.

2.2.2 Extensions of the SIR Model

There are many extensions of SIR model. This section will review some of them.

The SIRS model: It allows members of the recovered class to lose immunity and rejoin the susceptible class. The parameter *f* is the rate of loss of immunity. The differential equations are thus:

$$\frac{dS}{dt} = -\beta SI + \mu(N - S) + fR \qquad \frac{dI}{dt} = \beta SI - \gamma I - \mu I$$

$$\frac{dR}{dt} = \gamma I - \mu R - fR$$

The SEIR model: Many diseases have a latent or exposed phase, during which the individual is said to be infected but not infectious. The SEIR model includes this phase by taking parameter E into account. This parameter is the mean rate at which exposed individuals go to the infected compartment.

$\frac{dS}{dt} = B - \beta SI - \mu S$ $\frac{dE}{dt} = \beta SI - (\varepsilon + \mu)E$

$\frac{dI}{dt} = \varepsilon E - (\gamma + \mu)I$ $\frac{dR}{dt} = \gamma I - \mu R$

The MSIR model: For many infections, including measles, babies do not born into the susceptible state but are immune to the disease for the first few months of life due to protection from maternal antibodies. This added detail can be shown by including an M class (for maternally derived immunity) in the model:

$\frac{dM}{dt} = B - \delta MS - \mu M$ $\frac{dS}{dt} = \delta MS - \beta SI - \mu S$

$\frac{dI}{dt} = \beta SI - \gamma I - \mu I$ $\frac{dR}{dt} = \gamma I - \mu R$

The age-structured model: “The most specific parameter of a biological system is the age" (M. Iannelli). For some infectious diseases it has a deep influence on the dynamics spreading in a population. The simple SIR model assumes that everyone in the population has the same contact rates, regardless of age. Many of the parameters we have seen may depend on age, and especially the contact rate. In mathematical epidemic models, modeling the age-structure are very complex since we have to deal with population density through the ages of the epidemic compartments.

2.2.3 Limitations of Mathematical Models

In the mathematical models populations are considered to be uniformly distributed over the world. Also the population is well mixed meaning that there is homogeneous motion around the world. It is usually the case, however, that the number of contacts each individual has is considerably smaller than the population size, and in such circumstances, random mixing does not occur. Moreover, it can vary from place to place depending on the heterogeneity of the world or some specific properties of some individuals. Another major drawback of these models is the rapid growth of the

mathematical complexity of the systems used to describe the various aspects of phenomena in sufficient details. Therefore, many details of the progression of infection are neglected in these models.

2.3 Network Models

Unlike mathematical modeling assumption, usually the random mixing does not occur in the population; therefore, network modeling techniques has become popular. Network models include heterogeneous mixing in the population by defining the number of contacts that each host holds.

2.3.1 Standard Network Theory

Study of networks has its grounding in social sciences and graph theory. In graph theory we have nodes and edges of a graph, whereas in epidemiology, we speak of hosts and contacts. The set of contacts of a host is their 'neighbourhood' and the size of this neighbourhood is the host's degree. In order to describe the contacts in the population, an adjacency matrix can be used. An adjacency matrix A, summarizes all connections within the network. A_{ij}=1 if there is a connection for passing infection from individual i to individual j; otherwise, A_{ij}=0; and A_{ii}=0.

One interest of the network representation is that it has strong tools to analyze its properties. These properties can bring some insight about the epidemiological characteristics of the whole system. The average number of contacts that an individual has for a population of size N, is:

$$\bar{n} = \frac{1}{N}\sum_{ij} A_{ij}$$

$$= \frac{1}{N} \; ||\mathrm{A}|| \left(= \frac{1}{N} \; trace \; (\mathbf{A}^2) \; if \; non - directed\right)$$

where the trace of matrix A is defined to be the sum of the elements on the main diagonal [67]. The matrix A^m has the information about the paths of length m within the network.

As a very simple example, consider the network presented in figure 1. The adjacency matrix A, and matrix A^2 for this network are:

$$A = \begin{bmatrix} 0 & 1 & 0 & 0 \\ 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}, \qquad A^2 = \begin{bmatrix} 1 & 0 & 1 & 0 \\ 0 & 2 & 0 & 0 \\ 1 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

It can be concluded from the matrix A^2 that from individual 1 to individual 3 and vice versa there is a path of length 2 within the network.

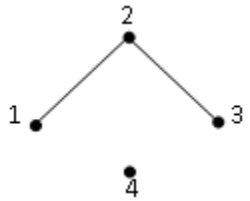

Figure 1.1. A simple network of hosts and contacts

We can calculate the number of connected pairs and triples in the graph:

number of pairs =||A|| = $\overline{n}$ N,

number of triples =$||A^2||$ - trace(A^2).

Here, ||A|| is the sum of all the elements in the matrix and n is therefore the average number of neighbours per node. The number of triples is calculated as the number of nodes which are joined by two connections, given that the nodes are distinct. Powers of the adjacency matrix are used to calculate the measures of transitivity or clustering.

As an example, the following measure is the ratio of the number of triangles (three linked nodes with the same start and end point) within the network to the number of connected triples:

$$\varphi = \frac{trace\ (A^3)}{\left|\left|A\right|\right| - trace\ (A^2)}$$

The larger this measure, the higher the level of clustering within the network. Similar measures can be defined by using squares instead of triangles but also by using longer paths.

All the population of individuals can be infected from any starting point, if the following matrix has no zero terms:

$$\sum_{m=1}^{\infty} A^m$$

Equivalently, zeros in the following matrix indicates that the network is divided into two or more separated components, which has no link to any of the others:

$$\lim_{m\to\infty}(1 + A)^m$$

Practically, a network is connected if any individual can be reached from any other by following network links; If there is a path from *individual i* to individual j, it cannot have length more than *N*-1. Hence the connectivity is determined in $\lceil \log(N\text{-}1) \rceil$ matrix multiplications.

2.3.2 Data Collection

There are three main techniques to gather network information: infection tracing, contact tracing, and diary-based studies. Each of these methods has its own benefits and purposes, and requires different resources.

Infection tracing: This method aims to identify the source of infection by constructing a transmission network. This network is built by connecting every infected individual to whom it caught the infection from, and to those whom it transmitted the infection to [51] [99].

Contact tracing: This method identifies potential transmission routes from an infected source to recognise asymptomatic infected individuals who can then be treated or quarantined [94] [27] [34]. The process of constructing the network is time consuming and requires individuals to provide complete and accurate data about personal relationships.

Diary-based studies: In this method, subjects record contacts as they occur (for example, in cattle diseases, to investigate patterns of livestock infection [38]). The great advantage of this network is that individuals are responsible for collecting the data rather than the researcher.

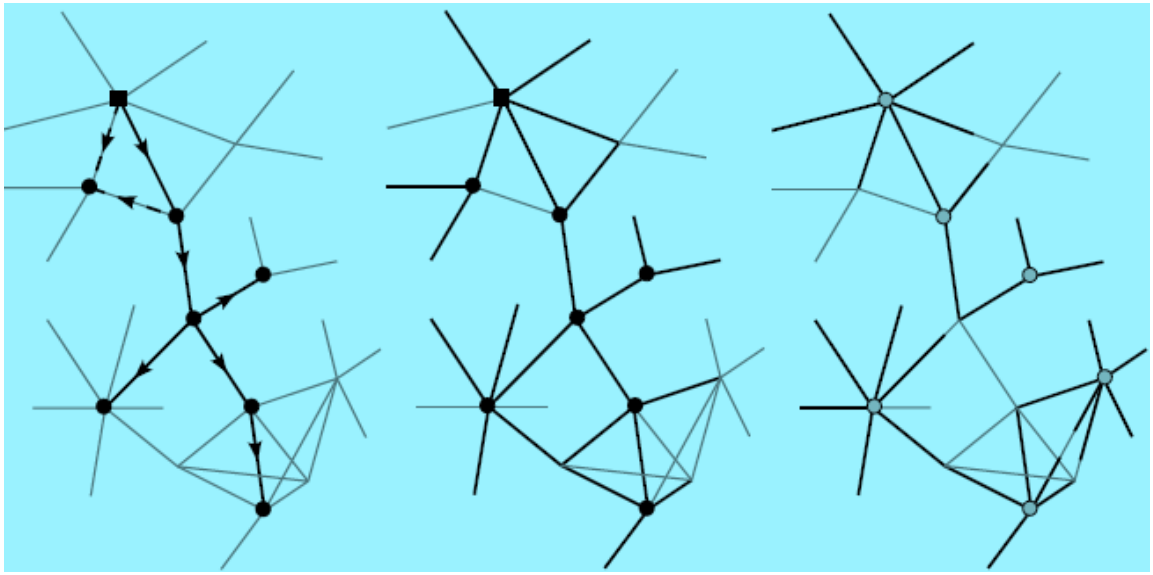

Figure 1.2. The type of network information that is achieved using infection tracing (left), contact tracing (middle) and diary-based studies (right). For infection and contact tracing, circles represent infected individuals, while the square shows the primary infectious case; for the diary-based study, those taking part are shown with open circles. For infection tracing, only sources of infection are traced and some individuals (e.g. top left) have multiple potential sources of infection. For contact tracing, a subset of all contacts from infectious individuals is traced. Finally, with a diary based study, although almost all links can be traced, the lack of a supervisor for identification means that often links from different individuals cannot be connected [68].

2.3.3 Most Popular Types of Networks

Several forms of networks have been studied for disease transmission. Here we briefly review the five most popular types for epidemic spread:

Random Networks: In this type of network connections are random and the spatial distributions of individuals are not taken into account. In other words, any two nodes are connected with a given probability p. Epidemic dynamics in random networks are equivalent to an SIR epidemic in a randomly mixed population [11].

Lattices: In this type of network, individuals are positioned on a two dimensional grid of nodes and adjacent individuals are connected. Lattices are homogeneous at the individual level and because of the localized nature of contacts are highly clustered. Two best-known examples of disease transmission through lattices are the contact process [49] and the forest-fire model [9]. The contact process models a SIS disease with "on" and "off" nodes while the forest-fire models a SIR infection: trees burn, leaving empty nodes that can be recolonized, which can be interpreted as a SIR disease with births. In lattices a wave-like spread of infection can appear, in which, from an initial node, infection spreads through a circular motion.

Small-world networks: In this type of networks, a small number of random connections are added to a lattice. The few long-range connections have a significant effect in disease spread in the way that infection can reach all parts of the lattice quickly. This type of network has received considerable attention because it includes high level of clustering as most of the infection occurs locally, but random connections enable the infection to reach other parts of the world.

Spatial networks: In this type of network, nodes are located in a given area and two nodes are connected with a probability that is defined by a connection kernel. These types of networks are very flexible as changing the location of the nodes and connection kernel generates wide variety of different networks.

Scale free networks: This type of network is constructed dynamically by adding new nodes to a network one by one. Each node that is added to the network connects preferably to the nodes with large number of contacts. The reason behind this is the fact that highly connected individuals (termed super-spreaders) are important in disease spread. Scale free networks provide extreme levels of heterogeneity to model core groups that has pivotal role in the spread and maintenance of infection. Table 2.1 summarizes the above mentioned networks according to their specifications for disease spread.

Table 2.1. Summary of network types and their specifications for epidemic spread

Network Type	Globally Connected	Clustering	Heterogeneity	Super Spreaders
Random	☑	☒	☒	☒
Lattice	☒	☑	☒	☒
Small World	☒	☑	☑	☒
Spatial	☒	☑	☑	☒
Scale Free	☒	☑	☑	☑

2.3.4 Examples of Applications of the Network Based Models

Network based models are active topics in modeling epidemics. They have been used as an explanatory tool to describe the evolution and spread of epidemics [30], [67], and [82]. Pourbohloul, et al. used contact network epidemiology to predict several control policies for a mildly contagious disease [95]. Moreover, several network-based models have been developed to emphasize the role of modeling heterogeneity [10], [98], clustering [86], [55], and spatial dynamics [97], [104]. These models, however, assume fixed contact structure during the course of the outbreak and the clustering is simplified by measuring the number of triangles and short cycles in the network. Kim, et al. presented a spatial network which focuses on the disease spread from the central point of a static vertices graph but he was not able to model the dynamics of the network structure in which the vertices and the connections are constant over time [72]

2.3.5 Limitations of Network-Based Models

In spite of the importance of having dynamic network structure for long term results, most of the network models are static, which means that the connections are constant over time. Moreover, behaviour of the population may change as a consequence of an outbreak of infection. Another important drawback is the fact that there is no simple way

to correlate the epidemiological results with the properties of the network structure. Data collection and dealing with complexity of the models are other challenges regarding the network-based models.

2.4 Agent-based models

Over the past several years, large-scale, agent-based, disaggregate models have been studied. Agent-based models are designed to capture the behavior of each unique agent (individual) with explicit interactions between these agents. An agent can have several properties, the most notable ones are as follows:

- Each agent operates independently in its environment and in its dealings with other agents.
- Agents are goal-oriented.
- Each agent is flexible and has the ability to learn and adapt its behaviors over time based on experience.
- Agents are capable of making independent decisions.
- A set of characteristics and rules exists to govern agents behavior and decision-making capability
- Meta-rules can be defined for an agent that modifies its behavioural rules during time

2.4.1 Disease Stages, Parameters, and Measurements

For an agent-based disease simulation different stages of the disease and the parameters and variables of the model has to be defined clearly. Stages of the disease describe the compartments of the infectious disease and their transition. Typical parameters and variables of the model include: population, contact, movement, type of disease, time step, and number of simulations performed for each parameter change. Also the typical measurements of an agent-based disease simulation may include:

- Number of individuals in each state of the epidemic model
- Duration of the epidemic
- Peak number of infected individuals
- Time step of the peak of the infection

- The total number and percentage of individuals infected

2.4.2 Examples of Applications of the Agent-based Models

In the past few years several epidemic models have been developed using agent-based techniques. In this section we briefly review three of the most important models. Carpenter simulated the spread of the 1918 influenza pandemic through the Norway House community in Manitoba [2]. Archival, ethnographic, epidemiological, and biological information were used to aid in designing the structure of the model and to estimate values of the model's parameters. The model was used to examine how seasonal community structures and associated population movement patterns may have influenced disease transmission and epidemic spread. An important agent-based model in the literature of epidemic modeling is called Simdemics. It is an integrated modeling environment that aids public health officials in pandemic planning [3]. Simdemics defines four models to simulate the epidemic spread: A statistical model of the population (based on age, gender or geographical density), a social interaction model, a disease model, and intervention models e.g., public policy changes, agent behavioral changes, etc. The biggest strengths of this approach are its scalability and its extensibility. An epidemiologist using the system can easily design a new intervention and run the corresponding simulation for a large urban area like Los Angeles in minutes. From data analysis she can find critical pathways as well as assess the indirect effect for example, the economic impact of certain policies. However, this model requires integrating a variety of databases from commercial and public sources to define the statistical model of the individuals which restrains the applicability of the model. The authors advocate for the necessity to have accurate individual behavioral models that reveal mobility and interaction patterns. EpiSimdemics is another simulator in literature. In this model a synthetic population was built from the United States Census, characterizing each individual with different variables [13]. Individuals are mapped to geographically located housing units and daily activities are modeled from education statistics to model school attendance and transport surveys to model mobility patterns. The disease model in EpiSimdemics consists of two parts: Within-hosts progression which is implemented by a finite state machine with probabilistic transitions, and between-hosts transmission which

is modeled by a probability function for contracting the susceptible individuals. Authors claim that straightforward simulations do not scale well, limiting the use of individual-based models to very small populations. Therefore, they tried to specifically design EpiSimdemics to scale to social networks with 100 million individuals. They demonstrated that the model scales well and can be used in policy planning.

2.4.3 Advantages and Challenges of Agent-Based Models

Agent-based models are able to capture complexity of individual behavior with the use of a bottom-up approach. An epidemic can be introduced into a dynamic environment with detailed social context which overcomes the limitations of static network models. The stochastic nature of the modeling technique ensures that randomness is involved in the model which is a significant factor in infection spread. In agent-based models, several experiments can be made to examine contributing factors to specific outcomes. This again outperforms the limitations of previous disease models: In the mathematical SIR models it is rough trying to simulate complex scenarios (for example spatially inhomogeneous populations or special events, etc.) ([20], [109]); in network-based models it is difficult to answer "what if" questions or to correlate the epidemiological results to the properties of the network structure [67].

On the other hand, there is a trade-off in agent-based models between simplicity and complexity: the model should be simple enough to yield useful insights and complex enough not to misrepresent what is going on in the real world. There is also a challenge in adequate relevance to reality, which can be overcome by the use of empirical data for parameter values, behaviors, and decision rules.

Chapter 3

Underlying Platform for Ecosystem Simulation

In order to model disease in an individual-based ecosystem simulation, we used EcoSim [44] as an underlying platform. EcoSim was designed to simulate agents' behavior in a dynamic, evolving ecosystem. The agents (or individuals) of EcoSim are prey and predators acting in a simulated environment.

This chapter presents EcoSim, and a simplified version of this ecosystem simulation, the Neutral model along with the protocol to describe these models.

3.1 EcoSim

In this section we explain EcoSim using the updated 7-points Overview-Design concepts-Details (ODD) standard protocol [45], [46] for describing the individual-based models.

3.1.1 Purpose

EcoSim is an individual-based predator-prey ecosystem simulation which was designed to simulate agents' behavior in a dynamic, evolving ecosystem. The main purpose of EcoSim is to study biological and ecological theories by constructing a complex adaptive system which leads to a generic ecosystem with behaviors similar to those found in existing ecosystems. Due to complexity in real nature, and long time and difficult process required to observe and study such theories, the role of these kinds of tools are crucial. EcoSim uses, for the first time, a fuzzy cognitive map (FCM) to model each agent behavior. The FCM of each agent, being coded in its genome, allows the evolution of the agent behavior through the epochs of the simulation.

EcoSim as a virtual ecosystem has shown coherent behaviors of the whole simulation with the emergence of patterns also observed in existing ecosystems providing a general framework for the study of several specific ecological problems. Several studies have been done using EcoSim. Devaurs et al. [24] have shown that the behaviour of this model is realistic by comparing the species abundance patterns observed in the simulation with

real communities of species. Furthermore, the complexity has been evaluated [77] and the chaotic behaviour [42] and multi-fractal property [40] of the system, have been proven. These kind of behaviours and properties as it has been observed in real ecosystems as well. Golestani et al. [41] have also measured the effect of small geographic barriers on the speciation in EcoSim.

It can be also used in studying important phenomena in nature such as speciation [79], extinction [54], sexual selection mechanism, and etc. which gives new and more realistic insight about them.

3.1.2 Entities, state variables, and scales

Individuals: EcoDemics has two types of individuals: predator and prey. Each individual possesses several characteristics (see Table 3.1) such as: age, minimum age for breeding, speed, vision distance, level of energy, and amount of energy transmitted to the offspring. Energy is provided to the individuals by the resources (food) they find in their environment. Prey consumes grass, which is dynamic in quantity and location, whereas predator hunts for prey individuals. Each individual performs one unique action during a time step, based on its perception of the environment. Each agent possesses its own FCM that represents its genome and also its behaviors are determined by the interaction between the FCM and the environment.

Table 3.1. Several physical and life history characteristics of individuals from 10 independent runs.

Characteristic	Predator	Prey
Maximum age	42 time steps (+/- 6)	46 time steps (+/-18)
Minimum age of reproduction	8 time steps	6 time steps
Maximum speed	11 cells / time step	6 cells / time step
Vision distance	25 cells maximum	20 cells maximum
Level of energy at initialization of the system	1000 units	650 units
Average speed	1.4 cells / time step (+/- 0.3)	1.2 cells / time step (+/- 0.2)
Average level of energy	415 units (+/- 82)	350 units (+/- 57)
Maximum level of energy	1000 units	650 units

Average number of reproduction action during life	1.14 (+/- 0.11)	1.49 (+/- 0.17)
Average length of life	16 time steps (+/- 5)	12 time steps (+/- 3)

The energy is provided by the primary or secondary resources found in their environment. For example, prey individuals gain 250 units of energy by eating one unit of grass and predators gain 500 units of energy by eating one prey. At each time step, each agent spends energy depending on its action (e.g. breeding, eating, running) and on the complexity of its behavioral model (number of existing edges in its FCM). On average, a movement action such as escape and exploration requires 50 units of energy, a reproduction action uses 110 units of energy and the choice of no action results in a small expenditure of 18 units of energy.

Cells and virtual world: The smallest units of the environment are cells. Each cell represents a large space which may contain an unlimited number of individuals and/or some amount of food. The virtual world consists of a matrix of 1000×1000 cells. The world is large enough in order to observe migration patterns, an individual moving in the same direction during its whole life cannot even cross half of the world. The virtual world wraps around to remove any spatial bias. In addition, the dimensions of the world are adjustable but dimensions growth can increases the computation complexity of the simulation by allowing more individuals to co-exist.

Time step: Each time step involves the time needed for each agent to perceive its environment, make a decision, perform its action, as well as the time required to update the species membership, including speciation events and record relevant parameters (e.g. the quantity of available food). In terms of computational time, the speed of simulation per generation is related to the number of individuals. Recent executions of the simulation with an average of 250,000 individuals produced approximately 15,000 time steps in 35 days.

Population and Species:

In average in every time step of the simulation, there are 250,000 individuals each of one or more species. A species is a set of individuals with similar genome.

3.1.3 Process overview and scheduling

The possible actions for the prey agents are: perceive the environment to obtain information of the vicinity in terms of grass, predators, and sexual partner, evasion (escape from predator), search for food (if there is not enough grass available in the its habitat cell, prey can move to another cell to find grass), socialization (moving to the closest prey in the vicinity), exploration, resting (to save energy), eating and breeding. Predator also perceive the environment to gather information used to choose an action among: hunting (to catch a prey), search for food, socialization, exploration, resting, eating and breeding. For every individual, after doing one action, the energy is adjusted. Updating the age of every individual at each time step is also another process. There are also two environmental processes: after all individuals perform their actions, the amount of grass and meat are adjusted.

At each time step, the value of the state variables of individuals and cells are updated. The overview and scheduling of every time step is as follows:

1. For every prey:
   1.1. Perception of the environment
   1.2. Computation of the next action
   1.3. Performing their actions and update of the energy level
   1.4. Updating the list of prey
   1.5. Updating prey species
2. For every predator
   2.1. Perception of the environment
   2.2. Computation of the next action
   2.3. Performing their action and update of the energy level
   2.4. Updating the list of predators and prey
   2.5. Updating predator species
3. For every cell in the world
   3.1 Updating the grass level
   3.2 Updating the meat level
4. Updating of the age of the individuals

The complexity of the simulation algorithm is mostly linear in the number of individuals. If we consider that there are N1 preys and N2 predators then the complexity of part 1 and part 2 of the above algorithm, including the clustering algorithm used for speciation, will be O(N1) and O(N2) respectively [4]. This virtual world of the simulation has 1000×1000 cells, therefore the complexity of part 3 will be O(k = 1000×1000). The complexity of part 4 will be O(N1 + N2). As a result the overall complexity of the algorithm will be calculated as O(2N1 + 2N2 + k), which is O(N = 2N1 +2N2).

3.1.4 Design concepts

3.1.4.1 Basic principles

To observe the evolution of individual behaviour and ultimately ecosystems over thousands of generations, several conditions need to be fulfilled: (i) every individual should possess genomic information; (ii) this genetic material should affect the individual behaviour and consequently its fitness; (iii) the inheritance of the genetic material has to be done with the possibility of modification; (iv) a sufficiently high number of individuals should coexist at any time step and their behavioural model should allow for complex interactions and organizations to emerge; (v) a model for species identification, based on a measure of genomic similarity, has to be defined; and (vi) a large number of time steps need to be performed. These complex conditions pose computational challenges and require the use of a model which allies the compactness and easiness of computation with a high potential of complex representation.

In EcoSim, a Fuzzy Cognitive Map [74] is the base for describing and computing the agent behaviors. Each agent possesses a FCM to compute its next action. Their FCM is represented in their genome which is assigned to each individual at birth. A FCM is a directed graph containing nodes representing concepts and edges representing the influence of concepts on each other (Figure 3.1). When a new offspring is created, it is given a genome which is a combination of the genomes of its parents with some possible mutations.

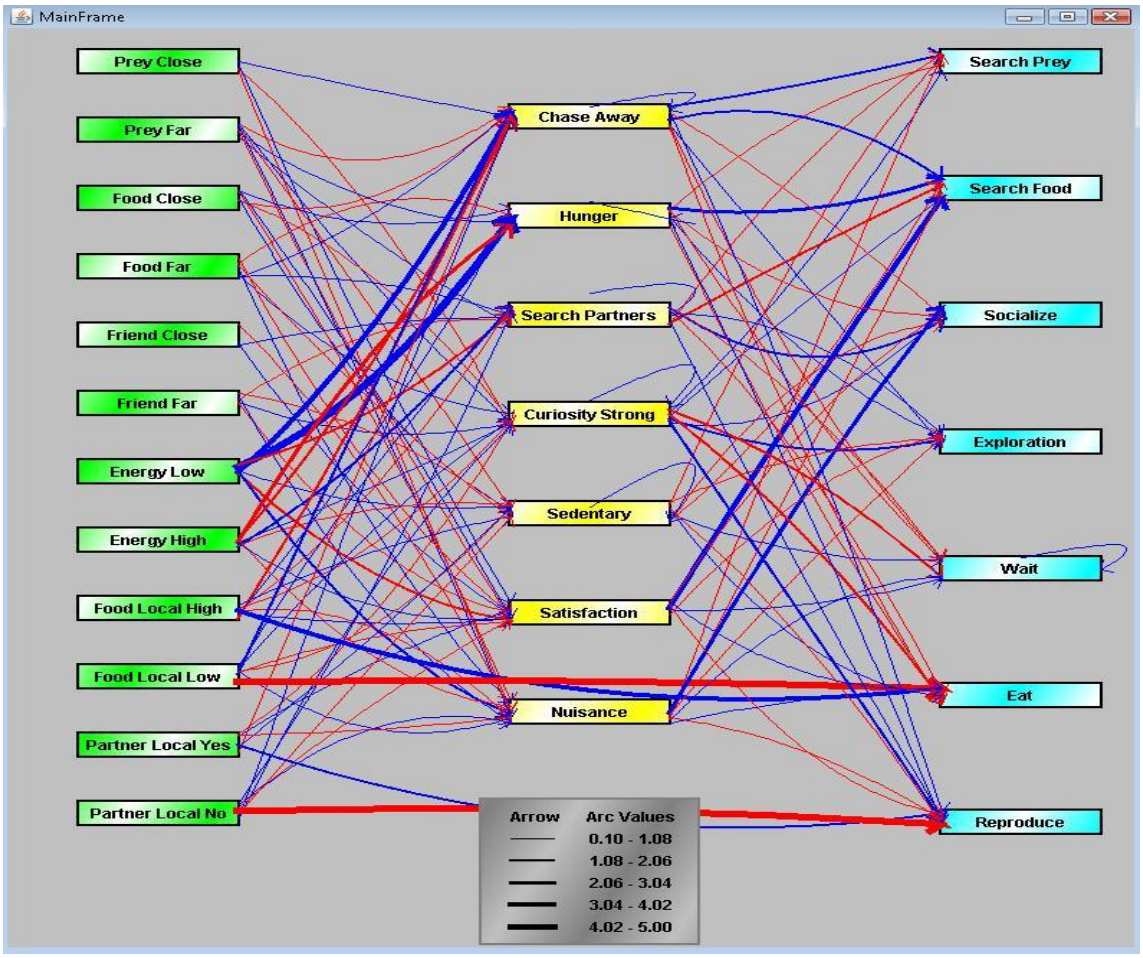

Figure 3.1. A sample of Predator's FCM including concepts and edges. The width of each edge shows the influence value of that edge. Color of an edge shows inhibitory (red) or excitatory (blue) effects.

Formally, an FCM is a graph which contains a set of nodes C, each node C_i being a concept, and a set of edges I, each edge I_{ij} representing the influence of the concept C_i on the concept C_j. A positive weight associated with the edge I_{ij} corresponds to an excitation of the concept C_j from the concept C_i, whereas a negative weight is related to an inhibition (a zero value indicates that there is no influence of C_i on C_j). The influence of the concepts in the FCM can be represented in an n×n matrix, L, in which L_{ij} is the influence of the concept C_i on the concept C_j. If $L_{ij} = 0$, there is no edge between C_i and C_j.

3.1.4.2 Emergence

In each FCM, three kinds of concepts are defined: sensitivity-based (such as distance to foe or food, amount of energy, etc.), internal-based (fear, hunger, curiosity, satisfaction,

etc.), and motor-based (evasion, socialization, exploration, breeding, etc.). The activation level of a sensitivity-based concept is computed by performing a fuzzification of the information the individual perceives in the environment. For an internal-based or motor-based concept C, the activation level is computed by applying the defuzzification function on the weighted sum of the current activation level of all the concepts having an edge directed toward C. Finally, the action of an individual is selected based on the maximum value of motor-based concepts' activation level. Activation levels of the motor-based concepts are used to determine the next action of the individual. For example in Figure 3.2 there are two sensitivity-based concepts (foeClose and foeFar), one internal-based (fear), and one motor-based (evasion). There are also three influence edges: closeness to a foe excites fear, distance to a foe inhibits fear, and fear causes evasion. Activations of the concepts foeClose and foeFar are computed by fuzzification of the real value of the distance to the foe, and the defuzzification of the activation of evasion tells us about the speed of the evasion.

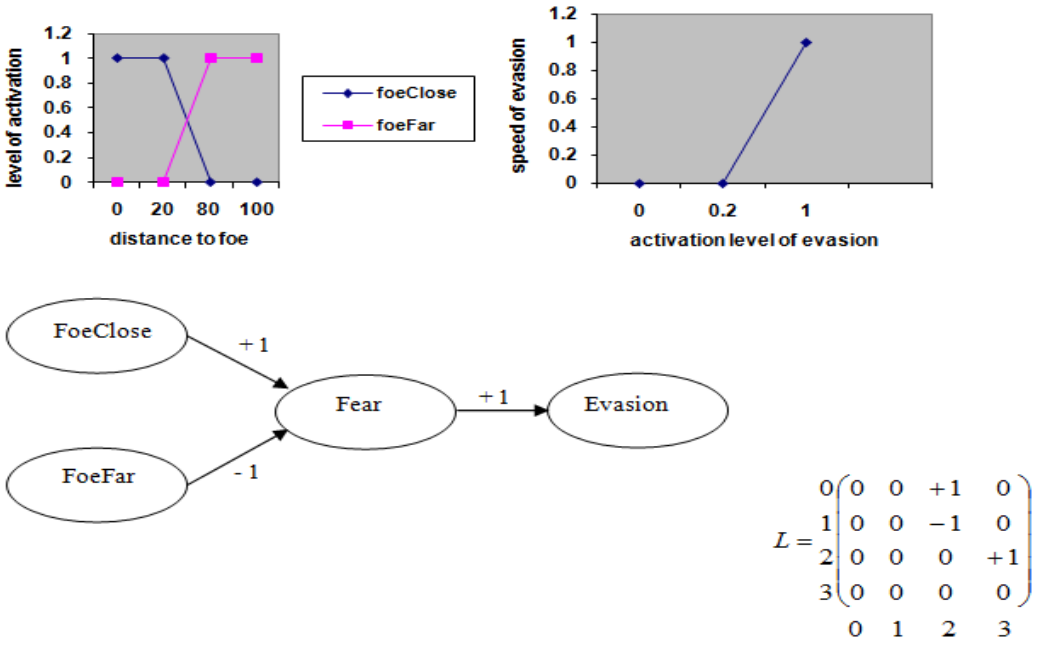

Figure 3.2. An FCM for detection of foe (predator) and decision to evade with its corresponding matrix (0 for 'Foe close', 1 for 'Foe far', 2 for 'Fear' and 3 for 'Evasion') and the fuzzification and defuzzification functions[108].

At the initiation of the simulation prey and predators scattered randomly all around the virtual world. Through the epochs of the simulation, distribution of the individuals in the world is changed drastically based on many different factors: prey escape from predators, individuals socialize and form groups, individuals migrate gradually to find sources of food, species emerge, etc. Figure 3.3 shows an example of a snapshot of the virtual world after thousands of time steps with emerging grouping patterns.

It has been shown that the data generated by EcoSim present the same kind of multifractal properties as the ones observed in real ecosystems [103]. Individuals' distribution forming spiral waves is one property of prey-predator models. The prey near the wave break has the capacity to escape from the predators sideways. A subpopulation of prey then finds itself in a region relatively free from predators. In this predator-free zone, prey starts expanding intensively and form a circular expanding region. The whole pressure process and spiral formation will be applied to this subpopulation of prey and predators again leading to the formation of a second scale [40]. This process repeats over and over and this is a common property of self-similar processes [15]. Because there are consecutive interactions between prey and predators during time, the same pattern repeats over and over and then self-similarity emerges in spatial distribution of individuals.

As can be seen in the figure individuals grouped together, and different species emerged. In addition migration phenomena can be observed, as relocation of the individuals leads to the redistribution in the population.

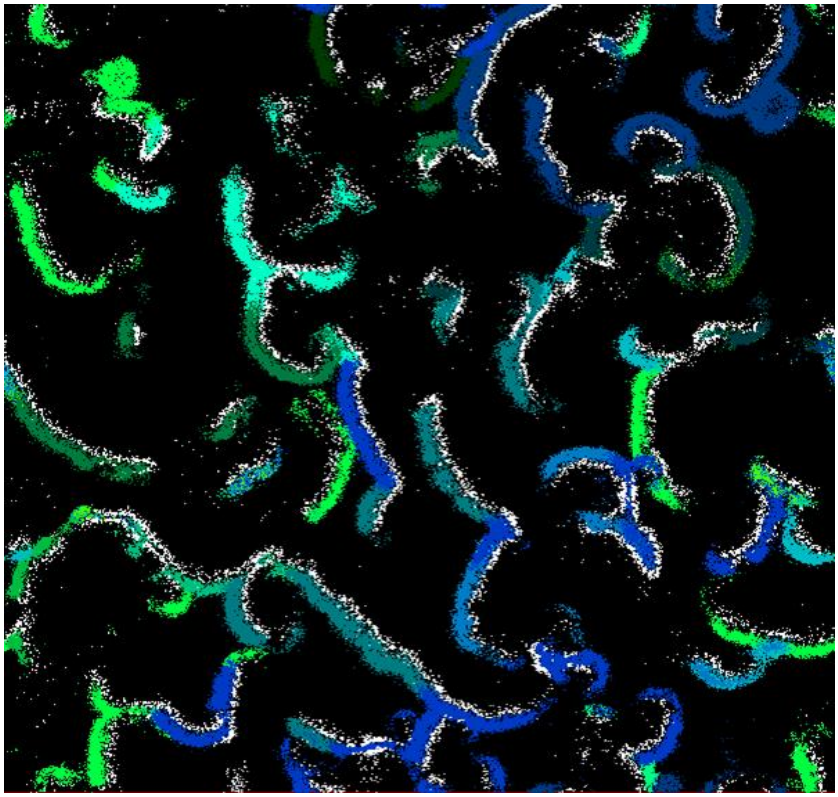

Figure 3.3: The snapshot of the virtual world in one specific time step, white color represents predator species and the other colors show different prey species

3.1.4.3 Adaptation

The genome maximal length is fixed (390 sites), where each site corresponds to an edge between two concepts of the FCM. But, as many edges have an initial value of zero, only 114 edges for prey and 107 edges for predators exist at initialization. One more gene is used to code for the amount of energy which is transmitted for the parent to their child at birth. The value of a site, which is a real number, corresponds to the intensity of the influence between the two concepts. The genome of an individual is transmitted to its offspring after being combined with the one of the other parent and after the possible addition of some mutations. The behavior model of each individual is therefore unique. Step after step as more individuals are created, changes in the FCM occur due to the formation of new edges (with probability of 0.001), removal of existing edges (with probability of 0.0005) and changes in the weights associate to existing edges (with probability of 0.005). New genes may emerge from among the 265 initial edges of zero value. This emergence and disappearance of the genes in FCM is due to environmental changes and genetic drift which lead to adaptability of individuals.

3.1.4.4 Fitness

We calculate the fitness for every species as the average fitness of its individuals. The fitness of an individual is defined as the age of death of the individual plus the sum of the age of death of its direct offspring. Accordingly, the fitness value mirrors the individual's capability to survive longer and produce high number of strong adaptive offspring. There is no pre-defined explicit fitness-seeking process in the simulation but rather it is a consequence of natural selection. Individuals that are more adapt to the environment live longer, have a higher level of energy, and therefore are able to have more offspring, and can transfer them efficient genomes.

3.1.4.5 Prediction

So far, there is no learning mechanism for individuals and they cannot predict the consequences of their decision. The only available information for every individual to make decision is the information coming from their perceptions at the current time step and the value of the activation level of the internal-based and motor-based concepts at the previous time steps. The activation levels of the concepts of an individual are never reset during its life. As the previous time step activation level of a concept is involved in the computation of its next activation level, this means that all previous states of an individual during its life participate in the computation of its current state. It means therefore that an individual has a basic memory of its own past that will influence its future states. As the action undertaken by an individual at a given time step depends on the current activation level of its motor-based concepts, the global behavior of an individual dynamically depends on a complex combination of the information it currently receives from its environment, its current internal states, and the past states it went through during its life.

3.1.4.6 Sensing

Every individual in EcoSim is able to sense its local environment inside of its vision range. For instance, every prey can sense the five closest foes, cells with food units and mates within the vision range, the number of grass units in its cell, and the number of possible mates in its cell. Moreover, every individual is capable of recognizing its current level of energy.

It should be noticed that the FCM process explained in section 3.1.4.2, enables for example, to distinguish between perception and sensation: the sensation is the real value coming from the environment, and the perception is the sensation modified by the internal states. For example, it is possible to add three edges to the previous map: one autoexcitatory edge from the concept fear to itself, one excitatory edge from fear to foeClose, and one inhibitory edge from fear to foeFar (Figure 3.4). A given real distance to the foe seems higher or lower to the individual depending on the activation level of fear. Also, the fact that the individual is frightened at time t influences the level of fear of the individual at time t + 1. This kind of mechanism gives the possibility of modeling a degree of paranoia and a degree of stress for the individual. It also allows the individual to memorize information from previous time steps: fear maintains fear. It is therefore possible to build very complex dynamic systems involving feedback and memory using an FCM, which is needed to model complex behaviors and abilities to learn from evolution.

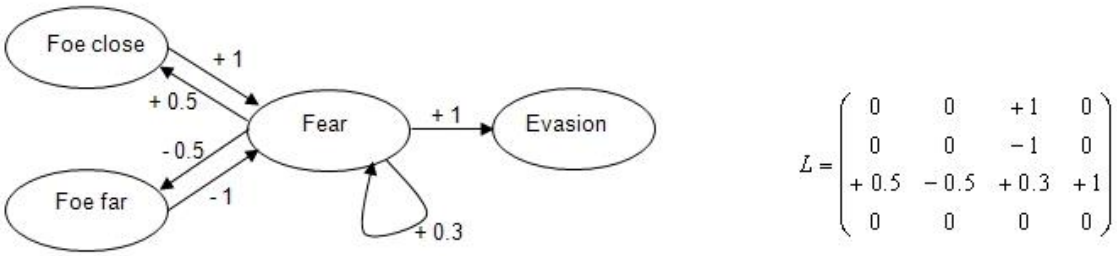

Figure 3.4. An FCM for detection of foe (predator) - difference between perception and sensation[108].

3.1.4.7 Interaction

The only action that requires a coordinate decision of two individuals is reproduction. For reproduction to be successful, the two parents need to be in the same cell, to have enough energy, to choose the reproduction action and to be genetically similar. The individuals cannot determine their genetic similarity with their potential partner. They try to mate and if the partner is too dissimilar, that is the dissimilarity between the two genomes is greater than a threshold (half of the speciation threshold), the reproduction fails.

Predator's hunting introduces another type of interaction in the simulation. For a predator to succeed in the hunting action, its distance to the closest prey requires to be less than

one. When a predator's hunting action succeeds, a new meat unit is added in the corresponding cell and the energy level of the predator is also increased by one unit of meat energy.

Furthermore, there is a competition for prey and predators for food. For example, if in a given cell there is only one food unit and two agents have chosen the action of eating, the younger will act first, and so it will be the only one that can eat (in this cell) at this time step. This is a way to simulate the fact that the older help the younger to survive.

3.1.4.8 Stochasticity

To produce variability in the ecosystem simulation, several processes include stochasticity. For instance, at initialization time the number of grass units is randomly determined for each cell. Moreover, the maximum age of an individual is determined randomly at birth from a uniform distribution centered at a value associated with the type of agent. Stochasticity is also included in several actions of the individuals; in evasion and socialization: if there is no predator or partner respectively in the vision range of the individual, the direction of the movement would be random. Furthermore, the direction of the exploration action is always random.

Moreover, to understand what is the amount of randomness in EcoSim, Golestani et al. [42] examined whether a chaotic behavior exists in signals (time series) generated by the simulation. To enforce the result, they used four different methods: Higuchi fractal dimension, correlation dimension, largest Lyapunov exponent, P&H method. For each of them, in order to obtain a statistically significant evaluation, they applied the surrogate test method on 24 samplings of the considered data. According to the results obtained after applying these different methods, all of them providing clear predictions, they concluded that behavior of simulation is non-random and chaotic.

3.1.4.9 Collectives

In EcoSim, the notion of species is implemented in a way that species emerge from the evolving population of agents. Species can become extinct if all of their members die. EcoSim implements a species concept directly related to the genotypic cluster definition [78] in which a species is a set of individuals sharing a high level of genomic similarity. In addition, in EcoSim, each species is associated with the average of the genetic characteristics of its members, called the 'species genome' or the 'species center'. The

speciation mechanism implemented in EcoSim is based on the gradual divergence of individual genomes. The speciation method begins by finding the individual in a species S with the greatest distance from the species center. If this distance is greater than a predefined threshold for speciation (which is two time greater than the threshold for reproduction), a 2-means clustering is performed [4]. Otherwise, species S remains unchanged. If clustering is to be performed, two new species are created – one centered on a random individual, denoted I_r, and another centered on the individual which is the most genetically different from I_r. Subsequently, all remaining individuals in S are added to one of the two new sister species – whichever species the individual is more genetically similar. After recalculating the new centers for the two new species, the process of clustering is repeated for convergence.

Several studies have been made in EcoSim at the level of species. Devaurs et al. [24] have compared the species abundance patterns emerging from EcoSim with those observed in natural ecosystems using Fisher's logseries [33]. Species abundance is a key component of macroecological theories and Fisher's logseries is one of the most classical models of species abundance distribution. The results of this study proved that at any level in sample size, EcoSim gives coherent results in terms of relative species abundance, when compared with classical ecological results. In another study, Golestani et al. [41] investigated how small, randomly distributed physical obstacles influence the distribution of populations and species. They added various numbers of obstacles in the world and observed a direct and continuous increase in the speed of evolution (e.g. the rate of speciation). The spatial distribution of species was also more compact in the world with obstacles than in the world without obstacles (see figure 3.5). These results suggest that environmental heterogeneity and other factors affecting demographic stochasticity can directly influence speciation and extinction rates.

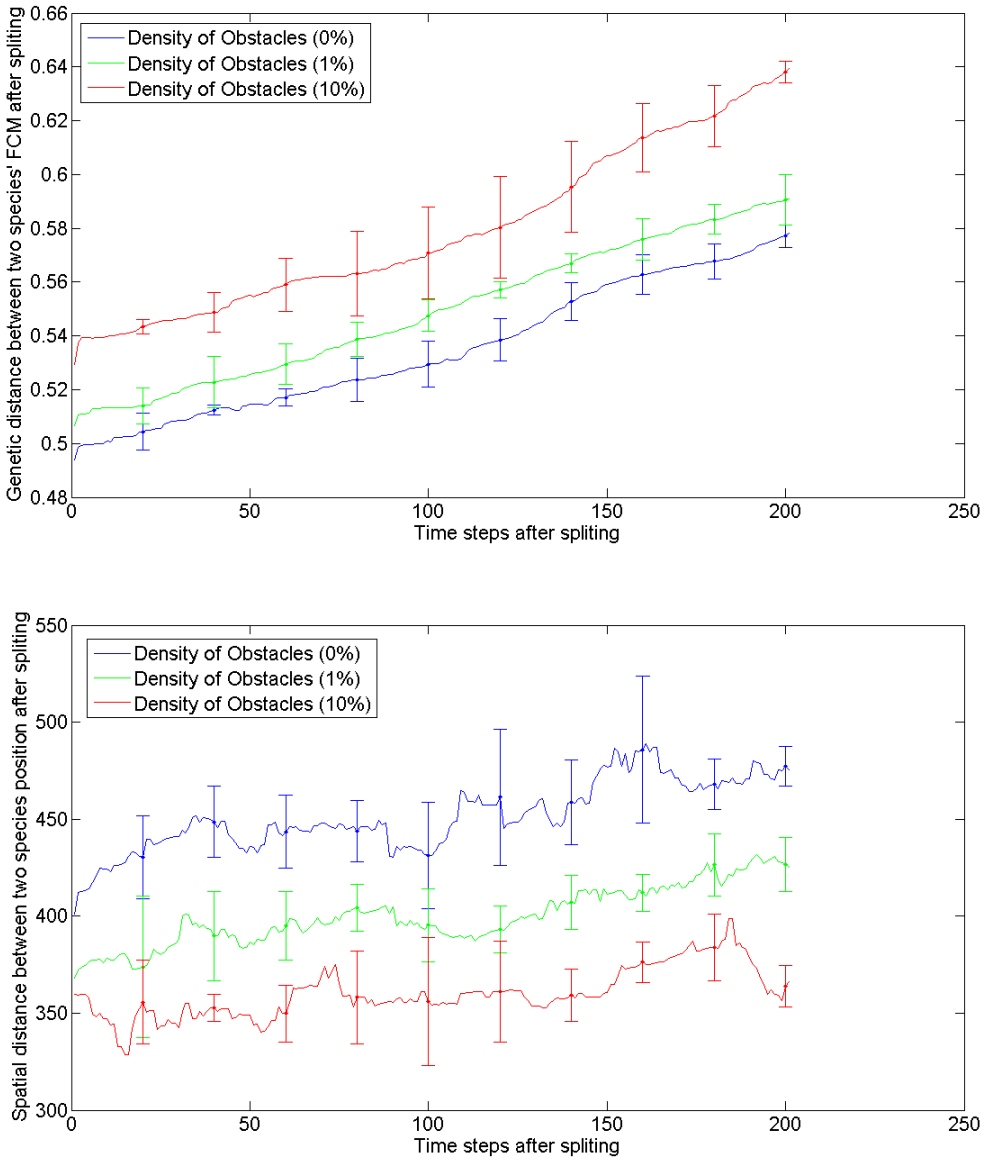

Figure 3.5 Genetic (top) and spatial (bottom) distance between two species after splitting

In another study, the fitness values of hybrid and non-hybrid individuals have been compared. This study concluded that hybrid individuals demonstrated lower values of fitness during their lifetime (see figure 3.6).

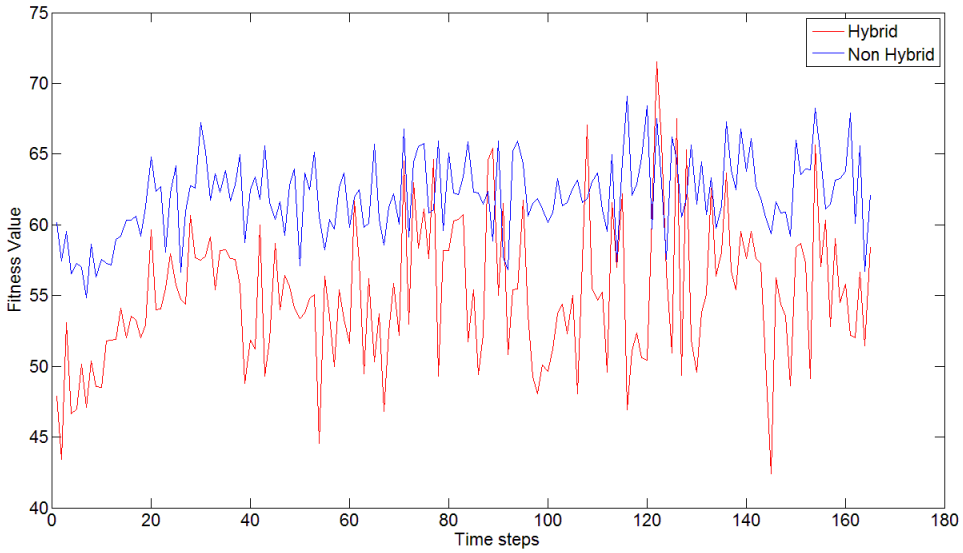

Figure 3.6 Comparison of fitness value between hybrid and non-hybrid individuals

3.1.4.10 Observation

EcoSim produces a large amount of data in every time step, including number of individuals, new and extinct species, geographical and internal characteristics of every individual, and status of the cells of the virtual world. Information regarding each individual includes position, level of energy, choice of action, specie, parents, FCM, etc. Information about the individuals and species are stored in one file with an average size of 30MB, and information for the virtual world is stored in another file with an average size of 5MB. Also there is a possibility to store all of the values of every variable in the current state of the simulation in a separate file, giving the possibility to restore the simulation from that state afterwards. The overall size of this file, which is only stored once in a while during a run of a simulation, is a few hundred MBs depending on the size of population and species. All the data is stored in a compact special format, to facilitate the storage and future analysis. There is a program which can be used to extract all the data. This program reads one file at a time and extracts all the required variables with a linear complexity for different analysis.

3.1.5 Initialization and input data

A parameter file is defined for EcoSim which is used to assign the values for each state variable at initial time of the simulation. These parameters are as follows: width and

height of the world, initial numbers of individuals, threshold of genetic distance for prey/predator speciation, maximum age, energy, speed, vision range, and initial values of FCM for prey/predator. Any of these parameters can be changes for specific experiments and scenarios. An example of a list of most common user specified parameters for initially running the EcoSim are presented in Table 3.2.

Table 3.2.Values for user specified parameters.

User Specified Parameter	Used Value
Number of Prey	12000
Number of Predators	500
Grass Quantity	5790000
Maximum Age Prey	46
Maximum Age Predator	42
Prey Maximum Speed	6
Predator Maximum Speed	11
Prey Energy	650
Predator Energy	1000
Distance for Prey Vision	20
Distance for Predator Vision	25
Reproduction Age for Prey	6
Reproduction Age for Predator	8

3.1.6 Submodels

As mentioned earlier, each individual performs one unique action during a time step based on its perception of the environment. EcoSim iterates continuously, and each time step consists of the computation of the activation level of the concepts, the choice and application of an action for every individual. A time step also includes the update of the world: emergence and extinction of species and growth and diffusion of grass, or decay of meat.

At initialization time there is no meat in the world and the number of grass units is randomly determined for each cell. For each cell, there is a probability, probaGrass, that the initial number of units is strictly greater than 0. In this case, the initial number is generated uniformly between 1 and maxGrass. Each unit provides a fixed amount of energy to the agent that eats it. The preys can only eat the grass, and the predators have two modes of predation: hunting and scavenging. When a predator's hunting action succeeds, a new meat unit is added in the corresponding cell and the predator is considered consuming another one. When a predator's eating action succeeds (which can be viewed as a scavenging action), one unit of meat is removed in the corresponding cell. The amount of energy is energyGrass for one grass unit when eaten by a prey and is energyMeat for one meat unit eaten by a predator. The number of grass units grows at each time step, and when a prey dies in a cell, the number of meat units in this cell increases by 2. The number of grass units in a cell decreases by 1 when a prey eats, and the number of meat units decreases by 1 when a predator eats. The number of meat units in a cell also decreases at each time step, even if no meat has been eaten in this cell.

1. Evasion (for prey only). The evasion direction is the direction opposite to the direction of the barycenter of the 5 closets foes within the vision range of the prey, with respect to the current position of the prey. If no predator is within the vision range of the prey, the direction is chosen randomly. Then the new position of the prey is computed using the speed of the prey and the direction. The current activation level of fear is divided by 2.

2. Hunting (for Predator only). The predator selects the closest cell (including its current cell) that contains at least one prey and moves towards that cell. If it reaches the corresponding cell based on its speed, the predator kills the prey, eating one unit of food and having another unit of food added to the cell. When there are several prey in the destination cell, one of them is chosen randomly. If the speed of the predator is not enough to reach the prey, it moves at its speed toward this prey. If there is no prey in the current cell and in the vicinity or it does not have enough energy to reach to a prey, hunting action is failed.

3. Search for food. The direction toward the closest food (grass or meat) within the vision range is computed. If the speed of the agent is high enough to reach the food, the agent is

placed on the cell containing this food. Otherwise, the agent moves at its speed toward this food.

4. Socialization. The direction toward the closest possible mate within the vision range is computed. If the speed of the agent is high enough to reach the mate, the agent is placed on the cell containing this mate, and the current activation level of sexualNeeds is divided by 3. Otherwise, the agent moves at its speed toward this mate. If no possible mate is within the vision range of the agent, the direction is chosen randomly.

5. Exploration. The direction is computed randomly. The agent moves at its speed in this direction. The activation level of curiosity is divided by 1.5.

6. Resting. Nothing happens.

7. Eating. If the current number of grass (or meat) units is greater than 1, then this number is decreased by 1 and the prey's (predator's) energy level is increased by energyGrass (energyMeat). Its activation level for hunger is divided by 4. Otherwise nothing happens.

8. Breeding. The following algorithm is applied to the agent A:

if A.energyLevel > 0.125 × maxEnergyPrey then

for all A of the same type in the same cell

if A.energyLevel > 0.125 × maxEnergyPrey and D(A,A) < T and

A′ has not acted at this time step yet and

A's choice of action is also breeding

then

interbreeding(A,A)

A.sexualNeeds ← 0

A.sexualNeeds ← 0

If A' satisfies all the criteria, the loop is canceled

If none of the A' agents satisfies all the criteria, the breeding action of A fails.

For every action requiring that the agent move, its speed is computed by the formula

Speed = Ca _× maxSpeedPrey => for the preys

Speed = Ca × maxSpeedPredator => for the predators

with Ca the current activation level of the motor-based concept associated with this action.

The process of generating a new offspring (interbreeding function) consists of following steps. First, the value of birthEnergyPrey is transmitted with possible mutations from one randomly chosen parent to the offspring. Second, the edges' values are transmitted with possible mutations, and the initial energy of the offspring is computed. To model the crossover mechanism, the edges are transmitted by block from one parent to the offspring. For each concept, its incident edges' values are transmitted together from the same randomly chosen parent. Third, the maximum age of the offspring is computed. Finally, the energy level of the two parents is updated.

3.2 Neutral model

In order to understand the importance of behavioural model and its consequence in different aspects of EcoSim, in this section we define a simplified model of our simulation, which includes random mixing at the predator-prey level. This model is derived from the "unified neutral theory of biodiversity" by ecologist Stephen Hubbell [59]. Hubbell's theory treats individuals in the population as essentially identical in their per capita probabilities of giving birth, dying, migration, and speciation. This implies a random behaviour at the individual level.

In the neutral version of the simulation, the Neural model, the behavioural model responsible for different actions of each individual is removed and the actions of the individuals are narrowed down to movement and reproduction:

- Movement of the individuals in the virtual world is random; however, the distribution of movements and the size of the world are kept the same as in the EcoSim.
- Predator-Prey population dynamics are determined by the Lotka-Volterra competition model [76], [113], and [114]. This model controls the number of births and deaths of individuals at each time step. The following formulas have been used to compute the variation in number of both of prey and predators:

  $$\frac{dn_1}{dt} = r_1.\left(1 - \frac{n_1}{k_1}\right).n_1 - a_1.n_1.n_2$$

  $$\frac{dn_2}{dt} = r_2.n_2 - a_2.n_1.n_2$$

  Where n_2 is the number of predator, n_1 is the number of prey, dn_1/dt and dn_2/dt represent the variation of the two populations with time, t represents the time; and r_1, a_1, r_2, a_2 and k_1 are parameters representing the interaction of the two species. The individuals that die are randomly selected.
- Reproduction action is also random, and unlike EcoSim there is no need for genetic similarity of the parents. The parents and the offspring's initial location are also randomly chosen.

For the sake of consistency, all of the initial parameters are identical, or as close as possible to those in the EcoSim. Also the evolutionary process of the EcoSim has been preserved in the Neutral model, but without having the natural selection pressure. The complexity of the Neutral model is also maintained as linear with the number of individuals.

In order to investigate the characteristics of individuals' positions in our simulations, we compare the spatial distribution of the individuals in both the Neutral model and EcoSim (Figure 3.7 (a), and 3.7 (b)). Compared to the emerging herd patterns observed in the original simulation (3.7 (b)), the spatial distribution of individuals in the neutral model of the simulation seems somehow random. Complex patterns of population variations and species organization do not emerged in the Neutral model.

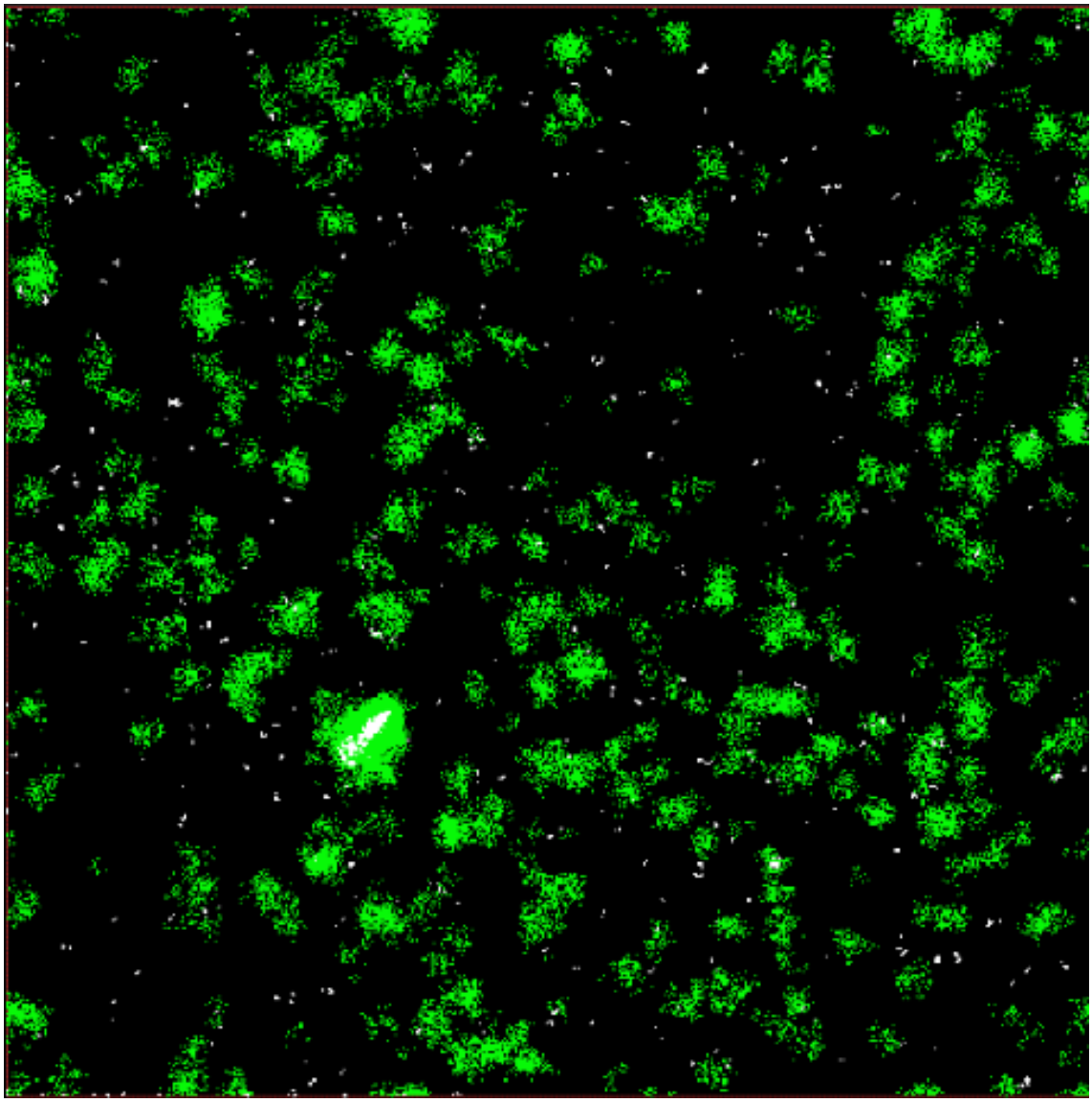

Figure 3.7 (a) Spatial distribution of Individuals in the Neutral model

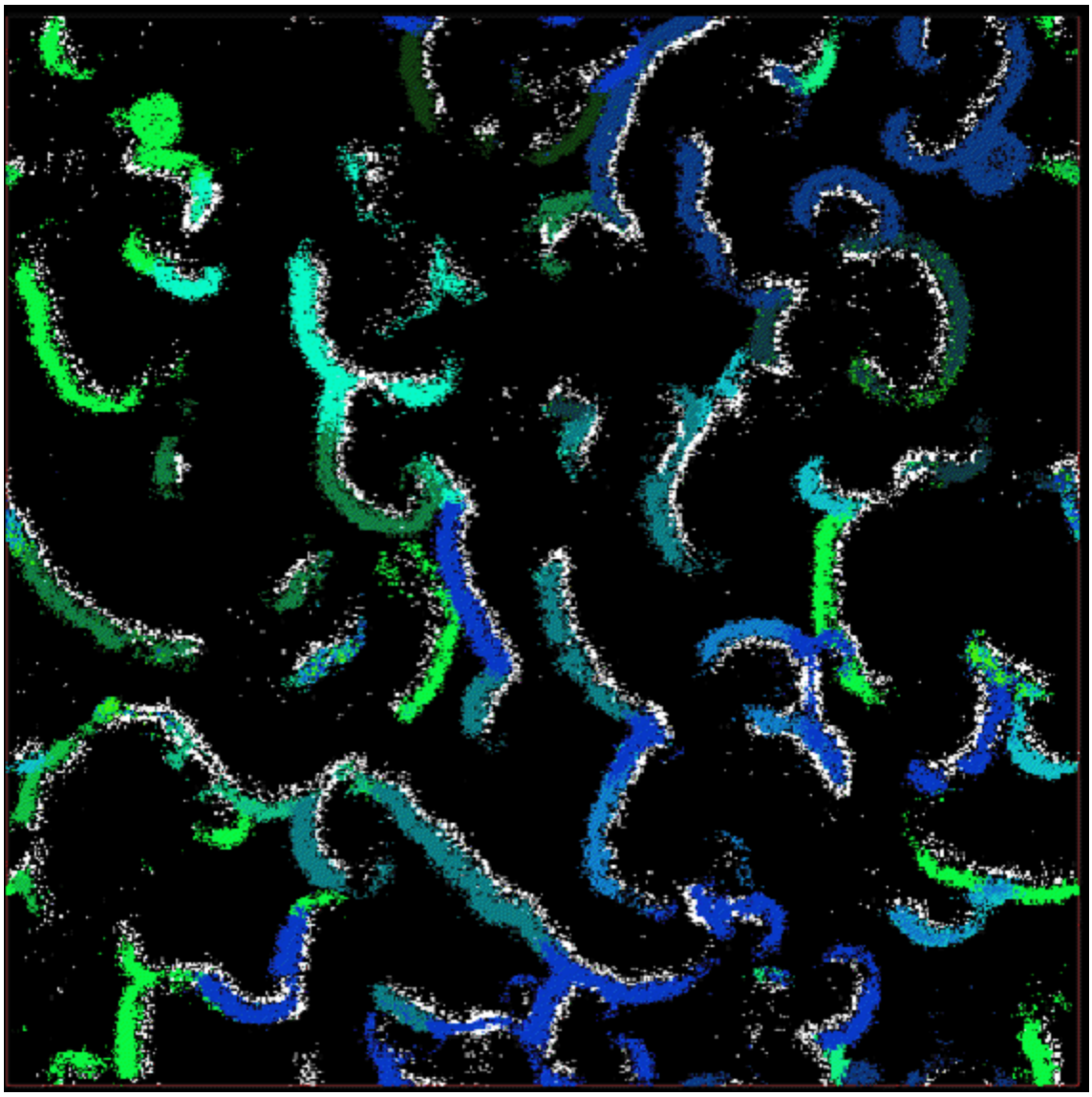

Figure 3.7 (b) Spatial distribution of Individuals in the EcoSim

3.3 Appendix 1

Table 3.3 The initial parameters of the EcoSim.

Parameter	Initial Value	Comments
Width	1000	width of the world
Height	1000	height of the world
ProbaGrass	0.187	initial probability of grass per cell
ProbaGrowGrass	0.0028	probability of diffusion of grass
ValueGrass	250	energy value for a consumed grass
ValuePrey	500	energy value for a consumed prey
MaxGrass	8	maximum number of grass in a cell
SpeedGrowGrass	0.5	speed of growing grass
MaxMeat	8	maximum number of meat in a cell
NbResources	2	number of food resources in the world
ProbaMut	0.005	probability of mutation to a nonzero gene
ProbaMutLow	0.001	probability of mutation to a zero gene
MinArc	0.075	threshold for an arc to be counted as nonzero
InitNbPrey	12000	initial number of prey
InitNbPredator	2000	initial number of predator
DistanceSpeciesPrey	1.5	threshold of genetic distance for prey species
DistanceSpeciesPred	1.3	threshold of genetic distance for predator species
AgeMaxPrey	46	maximum age for prey
AgeMaxPred	42	maximum age for predator
AgeReprodPrey	6	minimum reproduction age for prey
AgeReprodPred	8	Minimum reproduction age for predator
ClusterPrey	10	number of prey per clusters at initialization
ClusterPredator	20	number of predators per clusters at initialization
RadiusCluster	5	radius in number of cell of each initial cluster
EnergyPrey	650	maximum energy of prey
EnergyPredator	1000	maximum energy of predator
SpeedPrey	6	maximum speed of prey
SpeedPredator	11	maximum speed of predator
VisionPrey	20	maximum vision of prey
VisionPredator	25	maximum vision of predator
StateBirthPrey	30	initial parental energy investment for prey
StateBirthPred	40	initial parental energy investment for predator
nbSensPrey	12	number of sensitivity-based concepts in prey
nbConceptsPrey	7	number of internal-based concepts in prey
nbMotorPrey	7	number of motor-based concepts in prey
nbSensPredator	12	number of sensitivity-based concepts in predator

nbConceptsPredator	7	number of internal-based concepts in predator
nbMotorPredator	7	number of motor-based concepts in predator
Restore	1	0-no restore, 1-restore
MaxSave	500	0-no save, #-save every # states
MinSave	0	0-no save, #-save every # states
WorldSave	0	0-no save, 1-save world

Table 3.4 Initial FCM values for Prey (See the abbreviation table):

	FR	HG	SP	CU	SD	ST	NU	ES	SF	SC	XP	WT	ET	RP
PC	4	0	0	0.1	0	-1	1	0	0	0	0	0	0	0
PF	-4	0	0	0	0	0.5	-0.5	0	0	0	0	0	0	0
OC	0	0.5	0	-0.1	0.1	0.5	-0.5	0	0	0	0	0	0	0
OF	0	0	-0.4	0.2	-0.2	-0.7	0.7	0	0	0	0	0	0	0
FC	0	0	0.5	-0.1	0.1	0.5	-0.5	0	0	0	0	0	0	0
FF	0	0	-0.4	0.2	-0.2	-0.5	0.5	0	0	0	0	0	0	0
EL	0.4	4	-1.5	0	0	-2.2	2.2	0	0	0	0	0	0	0
EH	0	-1	1.5	0.2	-0.2	1.5	-1.5	0	0	0	0	0	0	0
OH	0	-0.2	0	-0.3	0.3	1.1	-1.1	0	0	0	0	0	2.6	0
OL	0	0.2	0	1	-1	-1.1	1.1	0	0	0	0	0	-4	0
PY	0	0	0	-0.4	0.4	0.5	-0.5	0	0	0	0	0	0	1.5
PN	0	0	0.5	0.3	-0.3	-0.8	0.8	0	0	0	0	0	0	-4
FR	0.5	0	0	0	0	0	0	1.5	-0.8	-1	0.3	-1	-1	-1
HG	0	0.3	0	0	0	0	0	-0.8	2.1	-0.7	0.7	-0.5	4	-1.8
SP	0	0	0.2	0	0	0	0	-0.2	0	1.5	0.5	-0.3	-0.4	3
CU	0	0	0	0.1	0	0	0	-0.1	0.5	0.3	1.5	-0.2	-0.3	-0.2
SD	0	0	0	0	0.1	0	0	0	-0.5	-0.3	-1.2	0.2	0.3	0.2
ST	0	0	0	0	0	0	0	-0.1	-0.8	-0.2	-2	1.5	0.8	0.7
NU	0	0	0	0	0	0	0	0.4	1	0.2	2	-1.2	-0.7	-0.7
ES	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SF	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SC	0	0	0	0	0	0	0	0	0	0	0	0	0	0
XP	0	0	0	0	0	0	0	0	0	0	0	0	0	0
WT	0	0	0	0	0	0	0	0	0	0	0	0.2	0	0
ET	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RP	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 3.5 Prey/predator FCM abbreviation table:

NodeName	Abbreviation	NodeName	Abbreviation
Fear	FR	PredClose	PC
Hunger	HG	PredFar	PF
SearchPartner	SP	FoodClose	OC
CuriosityStrong	CU	FoodFar	OF
Sedentary	SD	FriendClose	FC
Satisfaction	ST	FriendFar	FF
Nuisance	NU	EnergyLow	EL
Escape	ES	EnergyHigh	EH
SearchFood	SF	FoodLocalHigh	OH
Socialize	SC	FoodLocalLow	OL
Exploration	XP	PartnerLocalYes	PY
Wait	WT	PartnerLocalNo	PN
Eat	ET	PreyClose	YC
Reproduce	RP	PreyFar	YF
ChaseAway	CA		
SearchPrey	SY		

3.6 Parameters of prey defuzzification function (see figure A1):

NodeName	Activation	Fuzzy Parameter1	Fuzzy Parameter2	Fuzzy Parameter3
PredClose	0	1	3.5	3.5
PredFar	0	2	3.5	3.5
FoodClose	0	1	6	6
FoodFar	0	2	6	6
FriendClose	0	1	5	5
FriendFar	0	2	5	5
EnergyLow	0	1	4	4
EnergyHigh	0	2	4	4
FoodLocalHigh	0	2	4	4
FoodLocalLow	0	1	4	4
PartnerLocalYes	0	2	1000	20
PartnerLocalLow	0	1	1000	20
Fear	0	0	1	3.5
Hunger	0	0	1	3
SearchPartner	0	0	1	3

Curiosity	0	0	1	2.5
Sedentary	0	0	1	2.5
Satisfaction	0	0	1	3
Nuisance	0	0	1	3
Escape	0	0	1	3.5
SearchFood	0	0	2	3
Socialize	0	0	4	3
Exploration	0	0	6	2.5
Wait	0	0	7	3
Eat	0	0	8	3.5
Reproduce	0	0	10	3.5

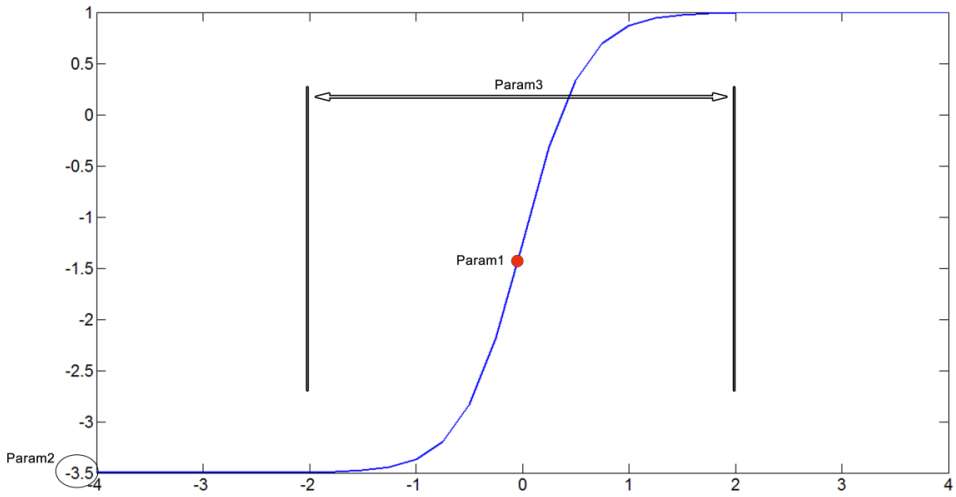

Figure 3.8. The three parameters that specify the shape of the curve. The first parameter specifies the center of curve in the horizontal axis, the second parameter specifies the lower band of curve in the vertical axis and the third parameter specifies the width of curve.

Table 3.7 Initial FCM for Predator (See the abbreviation table):

	CA	HG	SP	CU	SD	ST	NU	SY	SF	SC	XP	WT	ET	RP
YC	0.7	0	0	-0.1	0	0.5	-0.5	0	0	0	0	0	0	0
YF	-0.5	0.7	0.1	0.4	-0.4	-0.5	0.5	0	0	0	0	0	0	0
OC	-0.5	0.7	0	-0.1	0.1	0.5	-0.5	0	0	0	0	0	0	0
OF	0.8	-0.2	0.1	0.2	-0.2	-0.6	0.6	0	0	0	0	0	0	0
FC	0	0	0.7	0	0	0.4	-0.4	0	0	0	0	0	0	0
FF	0	0	-0.5	0.3	-0.3	-0.4	0.4	0	0	0	0	0	0	0
EL	3.5	5	-1.2	0	0.2	-1.5	1.5	0	0	0	0	0	0	0
EH	-2	-3	1.4	0.3	-0.3	1	-1	0	0	0	0	0	0	0
OH	-1.5	0.3	-0.2	-0.3	0.3	1	-1	0	0	0	0	0	4	0
OL	1.7	0	0.2	1	-1	-1	1	0	0	0	0	0	-5	0
PY	-0.3	0	0	-0.4	0.4	0.8	-0.8	0	0	0	0	0	0	2
PN	0.3	0	0.5	0.3	-0.3	-0.8	0.8	0	0	0	0	0	0	-5
CA	0.2	0	0	0	0	0	0	1.5	-0.2	-0.4	0.3	-0.4	0	-0.4
HG	0	0.3	0	0	0	0	0	4	2.5	-1.2	0.3	-0.4	3.5	-0.8
SP	0	0	0.2	0	0	0	0	-0.8	-0.8	1.5	0.3	-0.5	-0.6	3
CU	0	0	0	0.1	0	0	0	0.3	0.3	0.3	1.5	-0.4	-0.3	-0.2
SD	0	0	0	0	0.1	0	0	-0.3	-0.3	-0.3	-1.5	0.4	0.3	0.2
ST	0	0	0	0	0	0	0	-0.8	-0.8	-0.2	-1.8	1	0.8	0.8
NU	0	0	0	0	0	0	0	1	0.8	0.2	2	-1	-0.6	-0.8
SY	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SF	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SC	0	0	0	0	0	0	0	0	0	0	0	0	0	0
XP	0	0	0	0	0	0	0	0	0	0	0	0	0	0
WT	0	0	0	0	0	0	0	0	0	0	0	0.2	0	0
ET	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RP	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 3.8 Parameters of predator defuzzification function (see figure A1):

NodeName	Activation	Fuzzy Parameter1	Fuzzy Parameter2	Fuzzy Parameter3
PreyClose	0	1	4	4
PreyFar	0	2	4	4
FoodClose	0	1	5	5
FoodFar	0	2	5	5
FriendClose	0	1	5	5
FriendFar	0	2	5	5

EnergyLow	0	1	4.5	4.5
EnergyHigh	0	2	4.5	4.5
FoodLocalHigh	0	2	1000	20
FoodLocalLow	0	1	1000	20
PartnerLocalYes	0	2	1000	20
PartnerLocalNo	0	1	1000	20
ChaseAway	0	0	1	3
Hunger	0	0	1	3.5
SearchPartner	0	0	1	3
Curiosity	0	0	1	2.5
Sedementary	0	0	1	2.5
Satisfaction	0	0	1	3
Nuisance	0	0	1	3
SearchPrey	0	0	1	3
SearchFood	0	0	3	3.5
Socialize	0	0	5	3
Exploration	0	0	7	2.5
Wait	0	0	8	3
Eat	0	0	9	3.5
Reproduce	0	0	11	3.5

Chapter 4

EcoDemics: Modeling Epidemic Spread in EcoSim

Modeling the progress of an epidemic in a population has received significant attention among various fields of science. Many epidemiological models assume random mixing of the population, homogeneous hosts, and a static environment. We are interested in modeling epidemic spread in a dynamic evolving ecosystem with a behavioral model for the individuals. In this chapter, we present EcoDemics; which integrates the classical SIR (Susceptible-Infected-Removed) disease model with EcoSim. We present the disease model used and we demonstrate how the epidemic spread in a random mixing ecosystem differs from a heterogeneous ecosystem with behavioral model. We further validate our results by comparing it against an EcoDemics Neutral model, classical SIR results and real field data.

4.1 Introduction

Several mathematical and network-based models have been developed to mimic outbreaks of animal epidemics such as foot-and-mouth disease (FMD) [120], [121], [68], classical swine fever (CSF) [65], porcine high fever disease (PHFD) [123], and rabies [97]; however, far less attention has been concentrated on employing individual-based modeling of animals with behavioral model in an ecosystem. The need for individual-based modeling has been emphasized by Real and Biek who highlighted the importance of spatial dynamics and geographical landscape on the spread of rabies [97]. One of the most frequently studied diseases in the SIR model is rabies. Rabies is a viral disease of the central nervous system, transmitted by direct contact. The highly fatal nature of rabies and its widespread prevalence that can infect any warm blooded animal and humans, makes it a great health concern worldwide. Several methods exist that help predict the local, spatial and temporal dynamics for this viral infection [18], [107], and [43]. These models are mainly concerned with mathematically modeling the epidemic using the available databases; however, the population properties of different animals in

an ecosystem, for example, population densities, individual movements and contact rates, are extremely hard to measure [97], and data regarding which individuals are responsible for the disease transfer is difficult to gather [81]. This points out the development of a behavioral model that determines the interaction patterns of individuals in an ecosystem and that can be integrated in a simulation. There are a number of artificial life systems that model evolutionary ecosystem, the most notable ones are Tierra [96], Avida [1], Echo [56], PolyWorld [118], Framsticks [57] and EcoSim [44]. None of the above systems, to our knowledge, has integrated notions of disease progression. In this chapter, we present EcoDemics which integrates a disease model with EcoSim for studying epidemic spread in a predator-prey simulation. Here, we are not interested in modeling a specific disease in a particular ecosystem, but rather to model the influence of the behavioral model of the individuals and their consequent spatial distributions on disease dynamics. We have made realistic assumptions about our virtual ecosystem and disease model and tried to make as few assumptions as possible to maintain generality and applicability of the EcoDemics model for multiple future studies.

The rest of the chapter is organized as follows. The next two sections are dedicated to a brief description of the ecosystem simulation. We present the disease model used, and the neutral model in Section 3, followed by the experiments and results. We then conclude and discuss our future plans in the conclusion section.

4.2 Disease model in EcoDemics

We modified EcoSim by integrating a disease model to study disease outbreak. As described in Chapter 2, in the SIR (Susceptible-Infected-Removed) model, an individual passes from susceptible to infected to removed (removed includes both those that develop immunity and recover and those that are dead). The interest of EcoDemics is that the spatial distribution and interactions of the individuals emerge naturally from the behavioural model itself. For the study of disease we focus on patterns of epidemic outbreaks in prey as they have higher populations. We have not set our parameters for a specific disease, but in the experiments section, we will compare the pattern of the infection curve generated by the EcoDemics with the field data corresponding to the rabid infected raccoons and cats in different parts of USA. The disease model we use is a

probabilistic time-controlled model. The system is based on a plug and play architecture, which simplifies the addition, modification, or removal of the disease phases.

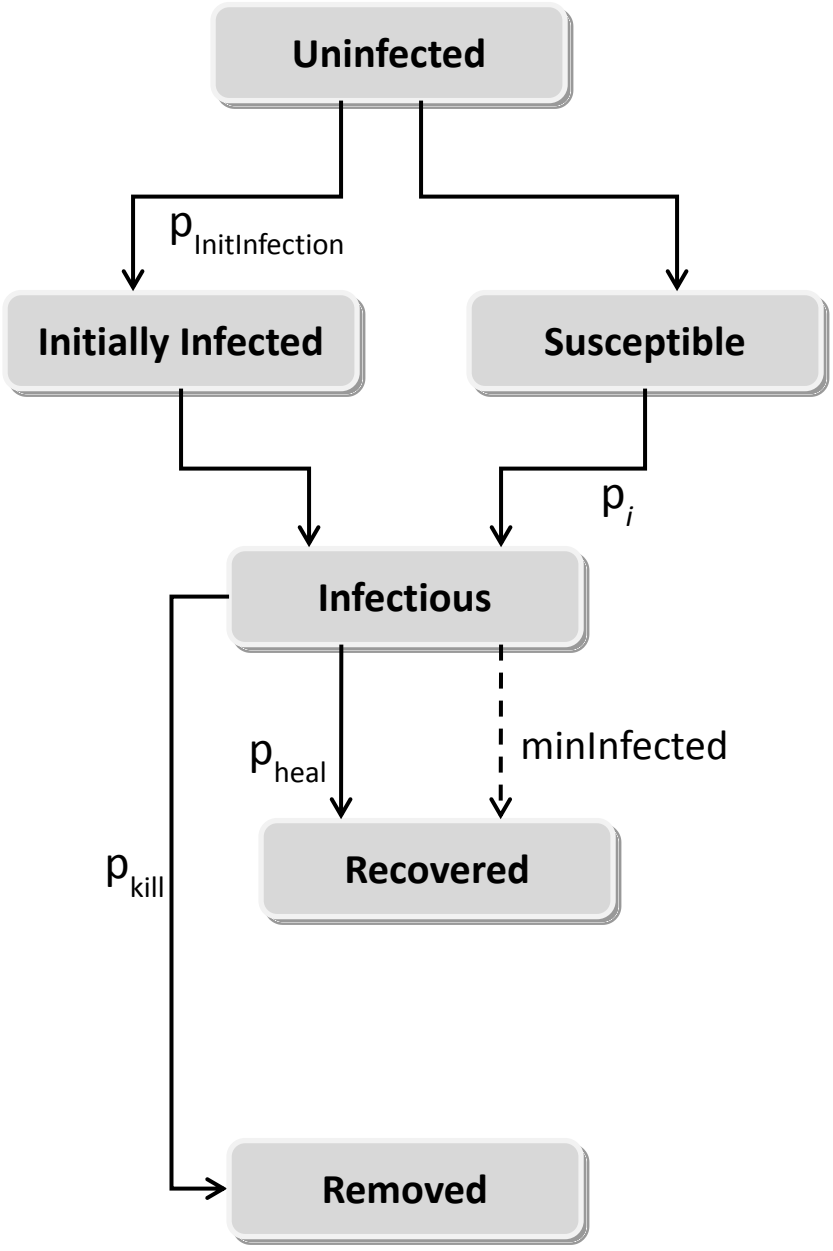

Figure 4.1 The disease model representing different states of within host disease progression. The solid lines represent the transition between states along with their probabilities. The dotted line represents the time controlled state transition along with the affecting parameters.

The disease starts at a user specified time step and not from the beginning of the simulation. This provides the system with a chance to stabilize and for individuals to group together. The initial location of the infection is set afterwards, and prey individuals are infected according to the probability $p_{InitInfection}$. The window in which the initial infection happens is 1/256 of the size of the world. This location is not completely random as it should be occupied and surrounded with a reasonable number of individuals based on the total population size (at least 1/200 of the total number of prey). This process of randomly selecting a location and checking the density of individuals continues until a suitable location for initially spreading the disease is found. This only happens once in the simulation and the spread of the disease is monitored at each time step. Individuals subject to the disease become infected based on a probability function presented later in equation (4.1). The infected individuals then enter different SIR disease stages; infected and then recovered based on the probabilities presented in Table 4.1.

In addition, we set a minimum time (*minInfected*) for the individual to carry the disease before it can recover. This time represents both the subclinically infectious state (shedding individual without visible signs of disease) and clinically infectious state (shedding individual with visible signs of disease). In more detail, individuals are given immunity to disease according to a probability p_{immune}. Infected individuals can spread the disease to other individuals in the same cell and to the 8 closest adjacent cells (Moore neighborhood). The interaction between individuals comes from the fact that individuals belonging to the same species tend to group together: individuals from the same prey species are not randomly distributed in the world but are spatially close to each other [4]. At each time step, the uninfected individuals have the possibility to be infected based on a probability function p_i introduced in equation (4.1). The function parameters vary according to the individual's characteristics. These function variables provide the disease model with more details to account for real life characteristics. These variables are the number of infected individuals surrounding the susceptible individual, and the susceptible individual's age, which determines the risk of contracting the disease. We chose to include age structure in our disease model since for some infectious diseases, it has a significant influence on the dynamics of the epidemic in the population.

Table 4.1 Probabilities of the disease model along with their description.

Name	Description
$p_{InitInfection}$	Probability of initially infecting an individual with the disease. It is only used at initialization of the simulation.
p_{immune}	Probability of the individual being immune to the disease.
p_{heal}	Probability of recovering from infection.
p_{kill}	Probability for the infected individual to be killed by the disease at each time step.

In our experiment, the life span of an individual is from 1 to *maxAge*, where *maxAge* is computed randomly for each individual to be centered around 46. Individuals are divided into two groups:

- High risk are in age range of 1-15 or 31-*maxAge*
- Low risk are in age range of 16-30

The probability p_i is the probability of individual *i* being infected with the disease and is:

$$p_i = \begin{cases} 0, & \sum s + \sum r = 0 \\ 1/(1 + \beta \exp(\alpha(2\sum s + \sum r - 1))), & \sum s + \sum r \neq 0 \end{cases} \quad (4.1)$$

This equation specifies the probability that a particular susceptible individual, *i* is infected at a specific time and location, where *s* is the number of infected individuals in the same cell as *i*, and r represents the number of infected individuals in the adjacent cells. Each cell is a square, and has 8 adjacent cells including the cells located at the corners. If there is no infected individual in the adjacent cells, the disease transmission probability will be zero.

In our experiment, a higher weight is given to the number of infected individuals in the same cell as *i*, than to the number of infected individuals in nearby cells. The values of α

and β are the parameters of the infection, where β determines the minimum probability of getting the disease having the smallest number of adjacent infections (compare figure 4.2(a) and 4.2(b) to see the effect of two different β values), and α affects the slope of the probability function that determines how the number of adjacent infections increase the probability of new infection (compare figure 4.2(a) and 4.2(b) to see the effect of two different α values). This mechanism allows one to finely vary the transmissibility level of the disease. We define different values of α and β for the two age groups. Figure 4.2 (a) and (b) show the described functions for high risk individuals, with α = -0.2 and β = 2, and low risk individuals, with α = -0.15 and β = 4, respectively.

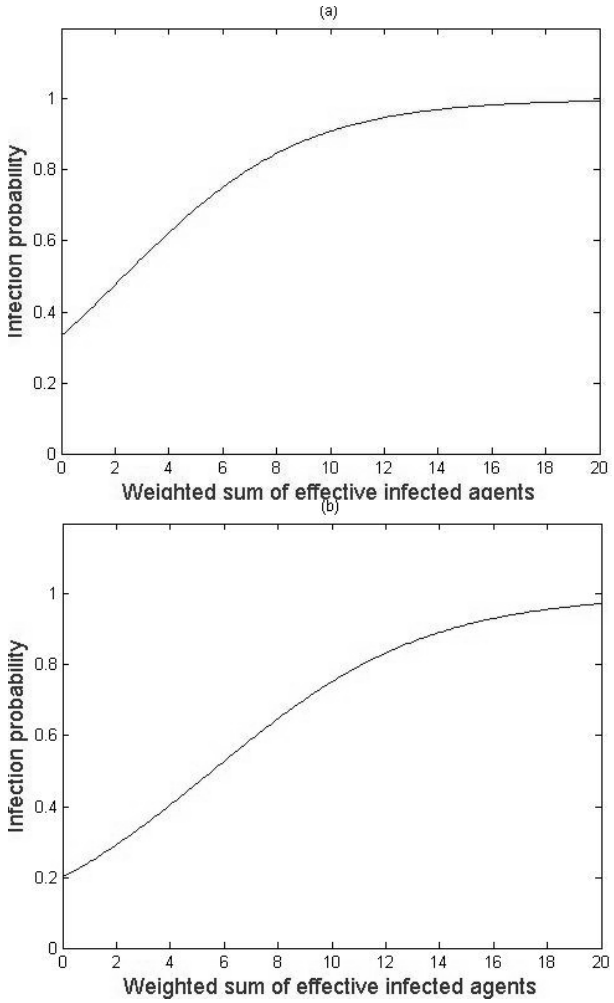

Figure 4.2. Probability of getting the infection for (a) high risk individuals and (b) low risk individuals.

At each time step, some individuals will recover based on the probability parameter p_{heal}, given that they have passed the minimum time to carry the disease (*minInfected*). This model is based on the SIR-type epidemic, which is characterized by the fact that recovered individuals will become immune to the disease. In addition, individuals can die from the disease based on the probability parameter p_{kill}. Each individual in the ecosystem is given a unique to enable tracing his behaviour throughout his life. For each time step, we save the state of the simulation, including major information about all individuals, in a file. This enables us to keep track of all of the individuals, and study different interesting aspects with minimum computational time and complexity.

Our model overcomes limitations found in mathematical and differential equations modeling such as random mixing of the population, and the difficulty of capturing individual level interactions. The computational complexity of this model remains reasonable as it is linear relative to the population size, and it is able to capture many characteristics of the environment along with the individuals' behavior. The complications faced by network based systems to maintain dynamics of the networks is easily overcome in our model as the dynamics are integrated into the model through the dynamic environment and evolution of individuals over time. Our model makes some improvements compared to other individual based modeling systems because it contains a higher level of detail by modeling predator-prey behavior and uses an evolutionary process. These properties will permit us to enhance epidemiological studies by investigating the effect of a disease's spread on different aspects of evolution; however, these subjects are beyond the scope of this thesis.

The shape of the environment plays a great role in the epidemic spread as the density of regions affect the magnitude of the disease spread. As individuals from the same species tend to be found in a connected region, species population and densities play a role in the spreading of disease. The predators also force the escape of prey, which affects the migration of prey species from one place to another. The predator-prey interaction had its share of interest in biological studies as it has a direct effect on population dynamics, adaptation, behavior and biodiversity of communities [47], and [61]. EcoDemics is able to model hundreds of thousands of individuals during tens of thousands of time steps. The

birth and death of individuals are included in the mathematical models by including birth and death rates in the differential equations that express the models. Therefore, these mathematical models fall short in capturing any behavior or individual interactions, and model birth and death only as global functions. In our simulation, a birth is associated with the transmission of genomic information with crossover and mutation, allowing model evolution. The death of an individual is linked to a specific reason, including individual fitness and environment, which can be further studied, such as lack of energy, reaching maximum age or being eaten by a predator. In order to highlight the importance of predator-prey interactions, and the significance of the behavioral model of each individual in forming the population regions as well as its consequence on spreading the infection, we present the epidemic spread in the Neutral model as well. We have developed the same disease model in the neutral version of the simulation, and we have compared the infection behaviour and the patterns of spread with the one in EcoDemics in the next section. For the sake of consistency, all of the initial parameters are identical, or as close as possible to those in the EcoDemics model, including the number of individuals, and the time of initiation of the infection.

4.3 Implementation, analysis, and comparison

In this section we compare the infection dynamics in EcoDemics and the Neutral model. The objective of this section is to understand the effect of individuals' behavior and spatial distribution in the disease spread. At the end of this section, we will present the results of the mathematical modeling of the SIR model and a real field data epidemic, and compare them to the EcoDemics and the Neutral model.

4.3.1 Parameters and initialization of the simulation

The simulation is implemented in C++ and all experiments are performed on Sharcnet [105] using the Linux XC cluster. Although this simulation models complex behaviors, its global complexity is still linear and each of the experiments is done in only a few hours. Due to the large number of parameters in the EcoDemics, numerous scenarios can be defined and experimented on. In order to determine the appropriate values for disease parameters, we have tested different values and observed their effect on the epidemic (Table 4.2). Although selecting the disease parameter values depend on a wide variety of

aspects, such as specific type of disease as well as different scenarios for the epidemic, we have selected parameters that provide reasonable timing and spread of infection for studying different aspects of the epidemic in EcoDemics (Table 4.2, last column).

Table 4.2. Disease parameters and range of experimented values along with their principal effect on the Epidemic; last column: values selected for further experiments in the EcoDemics.

Parameter	Experimented Range	Major Effect on Epidemic	Values Selected for Further Experiments
$p_{InitInfection}$	2% - 40%	Epidemic Spread	5%
p_{immune}	0% - 95%	Epidemic Duration	60%
p_{heal}	20% - 80%	Epidemic Spread	60%
p_{kill}	0% - 80%	Epidemic Duration	1%
minInfectedTime	5 – 50	Epidemic Peak Time	10

At the initialization stage of the simulation, the prey and predator number of individuals are set to 12000 and 500, respectively. These individuals, along with sources of food, are located randomly in the entire environment of 1000×1000 cells. An initial 750 time steps gap is used as a stabilization stage for the simulation. This allows the individuals to socialize, find mates, and group together or displace to locations with enough resources. At this stage of the simulation run, the prey and predator populations grow to around 200,000 and 30,000 respectively. Considering only the cells occupied by at least one individual, the average number of prey per cell is 4 while having an average of 2 for predators. Figure 4.3 shows spreading the infection during 8 time steps in a small part of the environment. The green and red dots are related to the cells containing at least one susceptible individual and one infected individual respectively.

The initiation of the infection occurs after the stabilization stage in the square-shaped window of the environment which has a top left coordinate of (600, 800). The window

area is 1/256 of the environment. Using infection parameters as presented in Table 4.2, susceptible prey are infected and passed through different states of the disease model.

(a) (b)

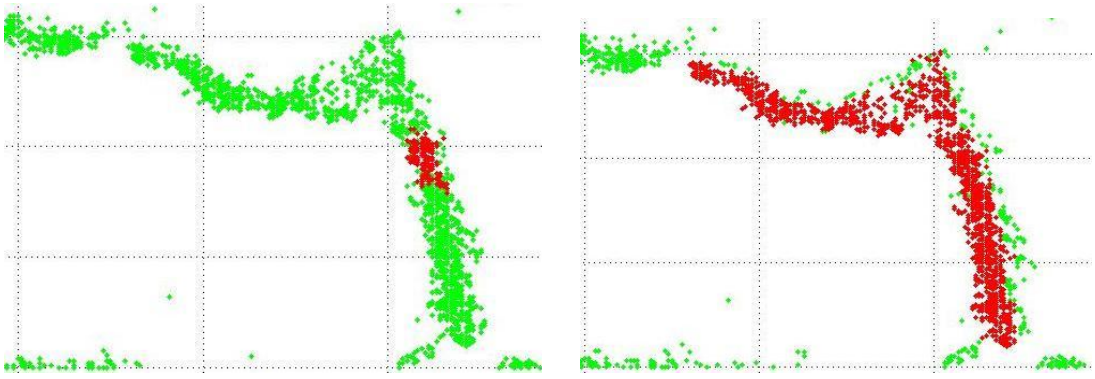

Figure 4.3. Example of spreading the disease among prey individuals in a sub-part of the environment. (a) Susceptible and infected cells at the initial stages of the disease. (b) Susceptible and infected cells after 8 time steps.

4.3.2 Pattern of spread in the EcoDemics and the Neutral model

To understand the effect of the behaviour of individuals and their spatial distribution in disease spread, we have focused on the comparison between the patterns of spread in the EcoDemics and in the Neutral model. Figure 4.4 (a) shows the pattern of spread in the EcoDemics. This figure shows an area representing 10% of the virtual world. The white dots represent predator cells (cells with at least one predator), green dots susceptible cells and red dots represent infected cells. Prey and predator individuals have migrated and formed a spiral wave pattern. This pattern is in direct agreement with many previous predator-prey models: both simulation results and mathematical theory predict that organisms are more likely to disperse in spiral waves [102] [90]. Also spirals have been shown to potentially play a very important role in ecological systems [101]. This phenomenon in the EcoDemics is due to many short term or long term factors such as socialization, force of predation and speciation. These types of phenomenon that arise from the behavioural model of the agents, occur during hundreds of generations through the course of evolution.

The spread of epidemic in the Neutral model is shown in Figure 4.4 (b). Although the same stabilization state (the initial 750 time steps) is used in this model, the spread of the individuals in the virtual world remained random. As it can be seen from this image, spatial distribution is different in the Neutral model due to the removal of the behaviour component of the model that influences the actions taken, and therefore the spatial distribution of individuals. The spatial spread of the infection, as a result of lack of density patches, is noticeably less than that of EcoDemics. The infection curves corresponding to the two aforementioned models are presented in the next section.

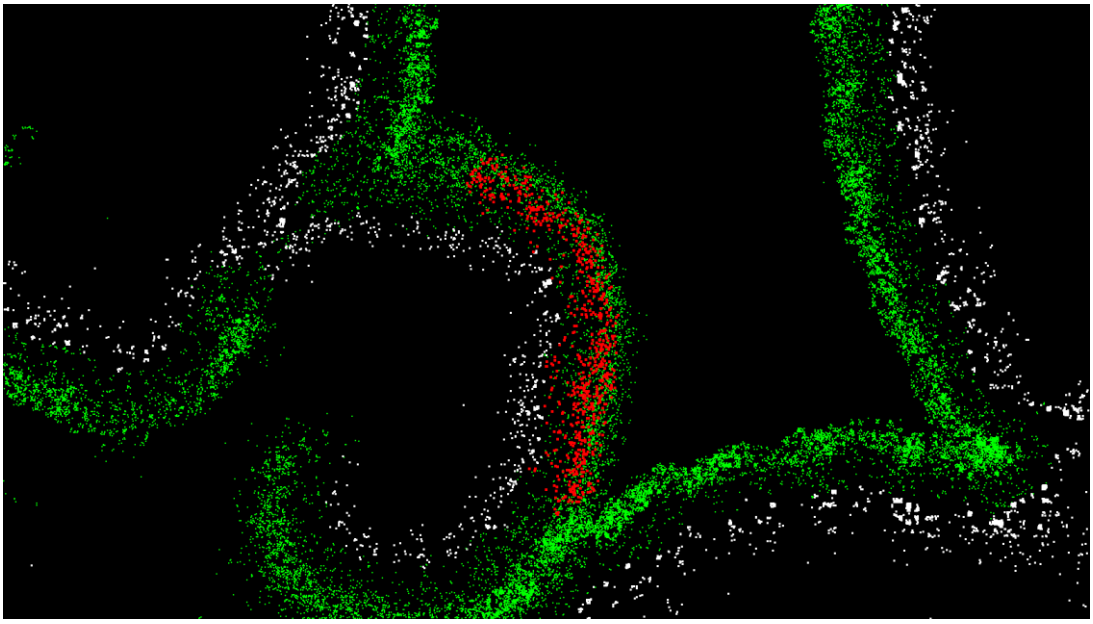

Figure 4.4 (a) Patterns of spread in EcoDemics. The white dots represent predator cells, green dots susceptible cells and red dots represent infected cells.

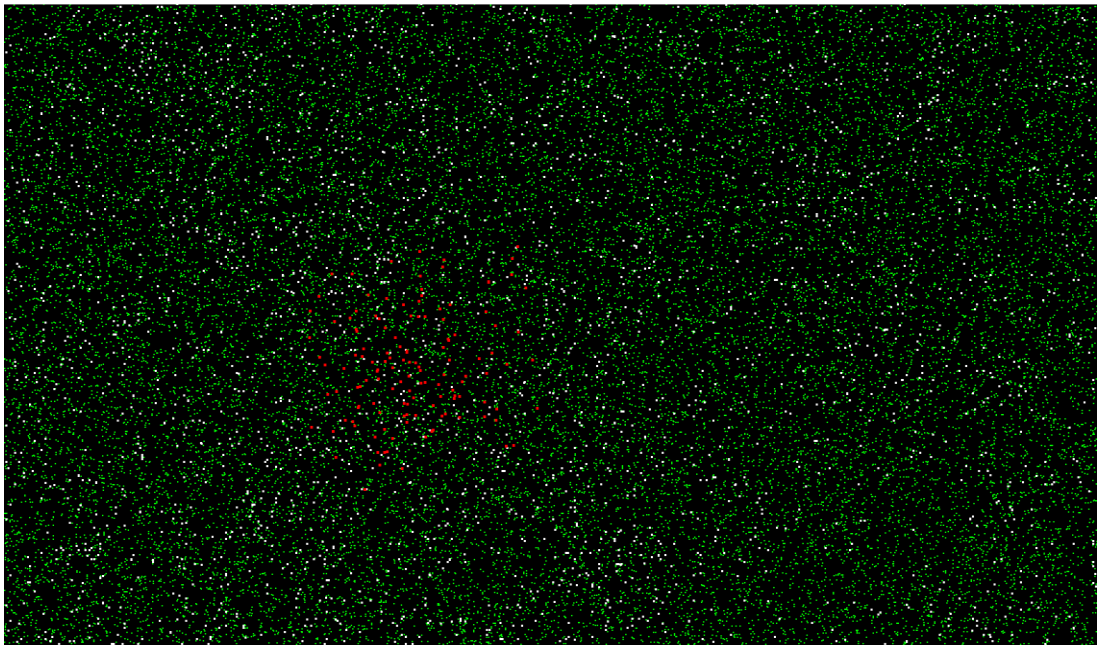

Figure 4.4 (b) Patterns of spread in Neutral model (bottom figure). The white dots represent predator cells, green dots susceptible cells and red dots represent infected cells.

4.3.3 General Infection Curve and Numeric Comparisons

4.3.3.1 The EcoDemics Infection Curve

Figure 4.5 illustrates the epidemic curve corresponding to the EcoDemics model. This figure shows the mean of 10 independent runs of the simulation. The time steps provided here are given after the outbreak of the disease and not from the beginning of the simulation; in other words, the figure does not include the stabilization stage of the simulation during which the disease is inactive. The number of infected individuals in the population at the first occurrence of the disease is about 124 on average, and reaches an average peak of 1222 just before 10 time steps. The average outbreak length is 136 time steps in average. The standard deviations of the number of infected individuals at each time step for 10 different runs ranged between 1 and 347. These two extreme values correspond to the time steps 133 and 67 respectively.

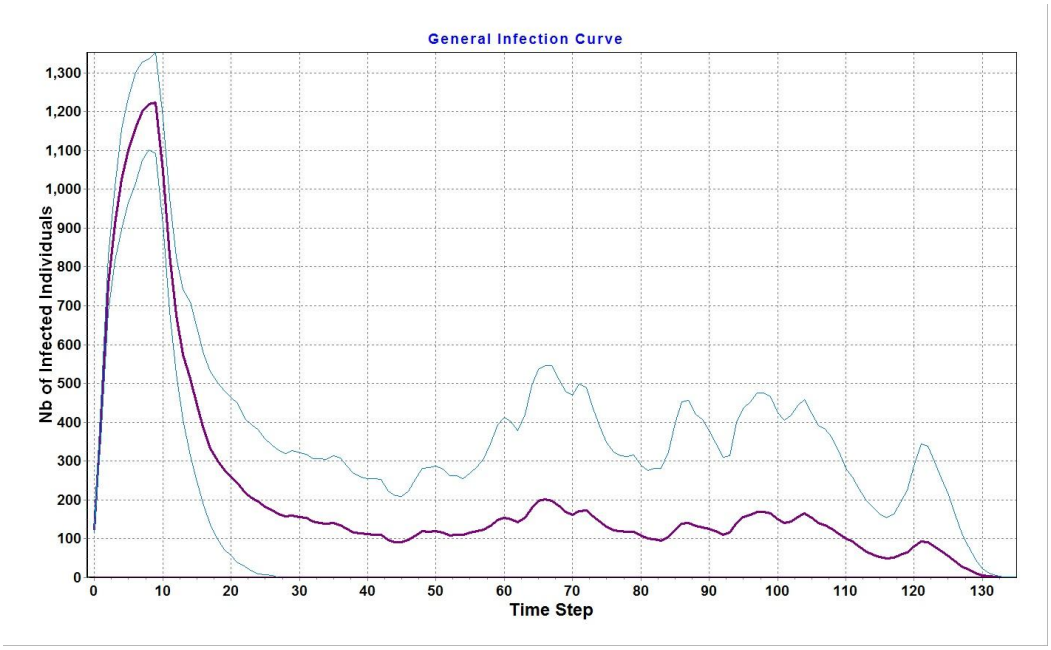

Figure 4.5. Average Epidemic spread curve in EcoDemics. The bold line represents the mean curve and the top and bottom lines represent one standard deviation.

4.3.3.2 The Neutral model Infection Curve

Figure 4.6 illustrates the epidemic curve corresponding to the Neutral model. The figure shows the average of 10 independent runs of the simulation. The time steps provided in this figure are given starting at the outbreak of the disease, which occurs after the stabilization step of the simulation. The average number of infected individuals reaches a peak of 170 at time step 9 and the average outbreak length is 52 time steps.

Although the neutral version of the simulation is initiated with the same parameters, number of individuals, and stabilization time (initial 750 time steps), the infection curve shows differences both for numerical value and shape in comparison to the EcoDemics curve. The extended discussion is presented in the comparison section.

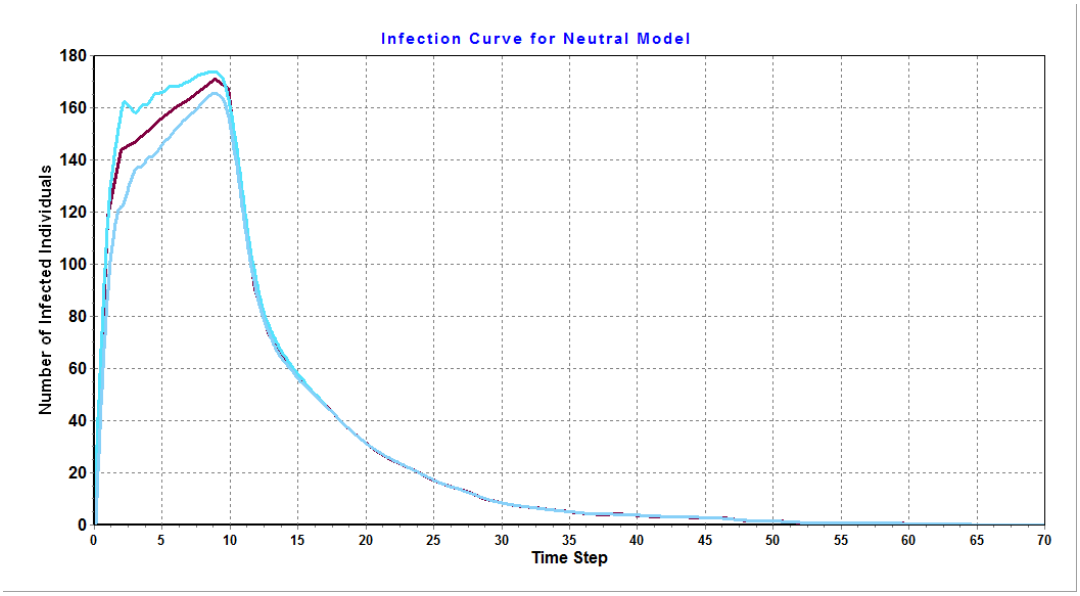

Figure 4.6. Average epidemic spread curve for the Neutral model. The bold line represents the mean curve and the top and bottom lines represent one standard deviation.

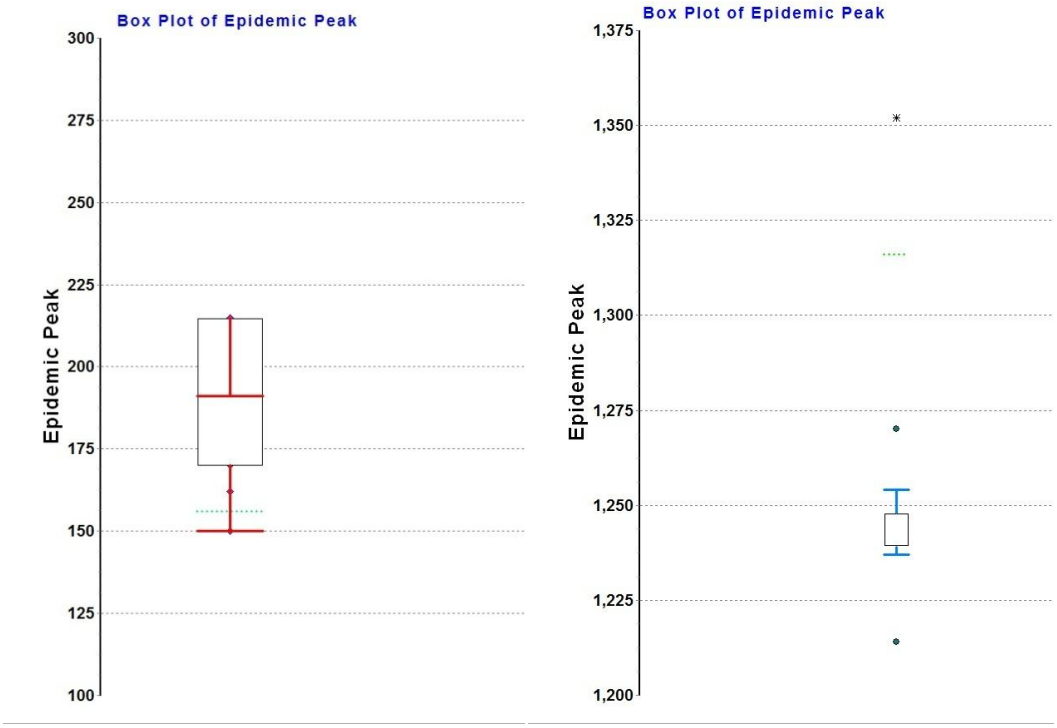

Figure 4.7 (a) Comparison of epidemiological signatures regarding epidemic peak. Blue boxplots show the distribution for EcoDemics and red boxplots show the corresponding distribution for the Neutral model.

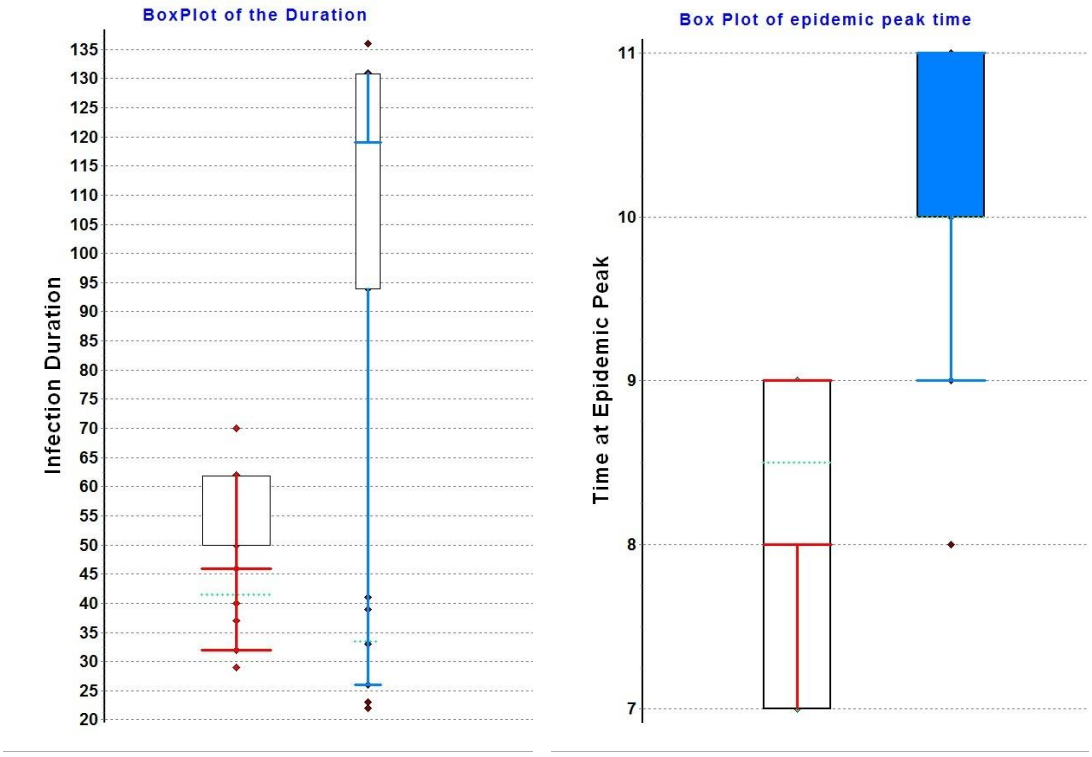

Figure 4.7 (b) Comparison of epidemiological signatures regarding epidemic duration and peak time. Blue boxplots show the distribution for EcoDemics and red boxplots show the corresponding distribution for the Neutral model.

4.3.3.2 Epidemiological signature comparisons

In this section we compare the epidemic peak, epidemic peak time and epidemic duration for the EcoDemics and the Neutral model. For both approaches, Figure 4.7 (a), (b) shows the boxplots for 10 independent runs of each simulation. The signatures of the EcoDemics model are shown by blue boxplots, while the signatures for the Neutral model are represented by red boxplots. These boxplots highlight the differences between the two models, especially in epidemic peak, for which the Neutral model shows a much lower value. Although both models have the same number of individuals at the initiation of the infection, and the same parameters have been used for the infection function, the size of epidemic is significantly different. This emphasizes the role of the population distribution in epidemic size.

4.3.3.3 Mathematical SIR model infection curve

The SIR model has a long history in modeling epidemics. We present the mathematical SIR model results using Mathematica [58], based on the same parameters that we have used in the previous section (duration of Infection = 10, initially immunized = 0.6, contact number = 20, initially infected = 0.05 - see Figure 4.8). The mathematical SIR model includes the unrealistic assumption that all individuals are equally susceptible to disease; therefore, parameters such as age and geographical dispersal are not taken into account.

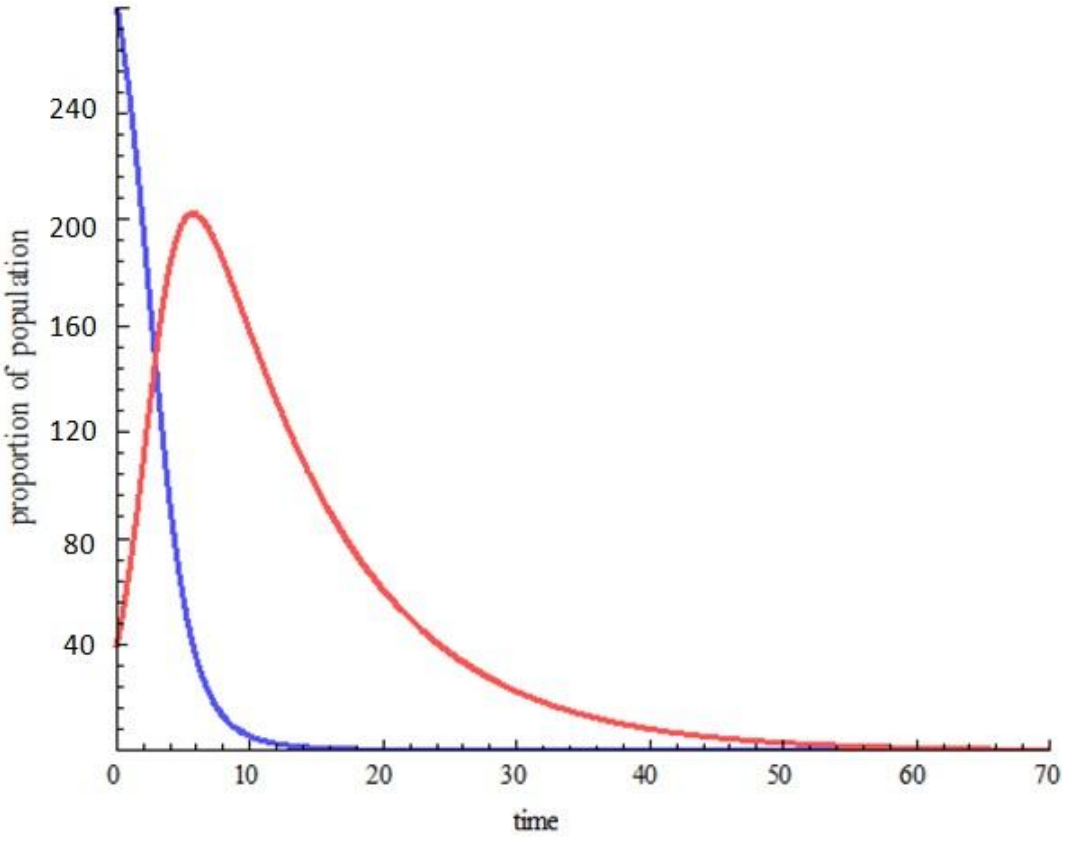

Figure 4.8. The Mathematica SIR model with parameters: duration of infection = 10, initially immunized = 0.6, contact number = 20, initially infected = 0.05. Red and blue curves represent the infected and susceptible individuals respectively.

4.3.3.4 Comparison and analysis

In this section we have compared the results of the EcoDemics model with the mathematical SIR model and related field data. In order to make fair comparisons of the

curves that are not all in the same range of value, we define epidemic size and duration ratio as follows

$$\text{Epidemic Size Ratio} = \frac{\text{Epidemic Peak Size}}{\text{Average Nb of Infected Indiv.}} \qquad (4.2)$$

$$\text{Epidemic Duration Ratio} = \frac{\text{Width of the curve at } \frac{1}{3} \text{ of the Epidemic Peak}}{\text{Average Epidemic Duration}} \qquad (4.3)$$

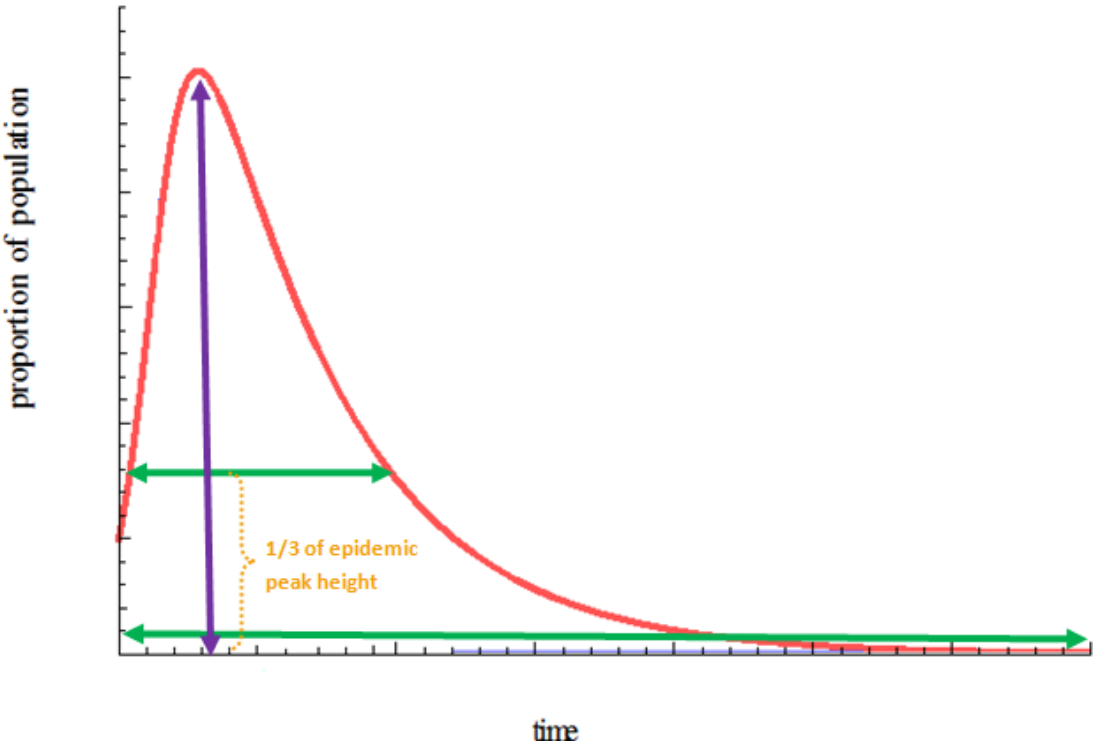

Figure 4.9. Epidemic duration ratio for an epidemic curve. Vertical arrow represents the epidemic peak size, upper green arrow represents the width of the distribution at 1/3 of the epidemic peak, and the lower green arrow represents the average epidemic duration. Epidemic size ratio can be computed by the ratio of the two green arrows.

Equation (4.2), describes the ratio of the total number of infected individuals at the epidemic peak to the mean number of infected individuals, during the whole period of the epidemic. Equation (4.3) is the ratio of the width of the epidemic curveat 1/3 of the epidemic peak height to the average duration of the epidemic. Figure 4.9 clarifies this

equation in which the epidemic size ratio can be computed by the ratio of the two green arrows.

These ratios for EcoDemics, the Neutral model, and the SIR model are given in Table 4.3. Unlike mathematical SIR model which is a deterministic system, random and chaotic features influence the dynamics in EcoDemics and Neutral model. The differences between EcoDemics and Neutral model in the epidemic size and duration ratios are statistically analysed with Welch's t-test ($t=34.46$, $d.f.=9$, $p=0.99$ for epidemic size, and $t=1.95$, $d.f.=10$, $p=0.90$ for epidemic duration) showing that the values observed in the two situations are significantly different. Although the Neutral model is a simplification of EcoDemics with the same initial parameters, the numerical results confirm the similarity between the Neutral model and its counterpart in the mathematical SIR model. This similarity between a completely random population and the mathematical SIR model demonstrates the inaccuracies caused by the random mixing assumption of the mathematical SIR based epidemic modeling. Both models fall short in capturing real life distributions and behaviours that affect the results of epidemic modeling.

To further confirm the EcoDemics results we compare it to a real epidemic field data in the next section.

Table 4.3. Numeric comparison of epidemic size and duration ratio

	Epidemic Size Ratio	Ep. Size Ratio Standard Deviation	Epidemic Duration Ratio	Ep. Dur. Ratio Standard Deviation
EcoDemics	5.9	0.06	0.1	0.04
Neutral Model	3.5	0.001	0.2	0.08
SIR Model	4	---	0.3	---

4.3.4 Field data

The inclusion of the behavioural component of the model to the population and the spatial distribution of the individuals in the virtual world, explained in Section 2, leads to a heterogeneous model as opposed to the assumptions of classical mathematical SIR model. We wished to see which one comes closer to reality. For this purpose, we compare the EcoDemics epidemic curve with the field data of a real epidemic.

Figure 4.10 shows the number of raccoons and cats reported rabid at different epizootic temporal stages in different parts of USA. The patterns of a real epidemic clearly do not follow the mathematical SIR model since complex heterogeneous features are involved in the real ecosystems that affect the real epidemics. The fluctuations and 'residual infections' (tail of the epidemic) are very common in real infections; for instance, it has also been observed in FMD outbreaks in several parts of UK [93], and SARS outbreaks in Hong Kong, Vietnam, Singapore, and Canada [114]. The fluctuations and irregularity found in the field data curve is also found in EcoDemics but is missing from the SIR model and the Neutral model. Often, as an epidemic spreads, the leading front is irregular, reflecting spatial variation in local transmission rates [18], [107]. By including the complex behavior of the agents in EcoDemics and having the parameters of spatial distributions to influence the epidemic spread, we observed patterns similar to those of real epidemics (see figure 4.5 and 4.10).

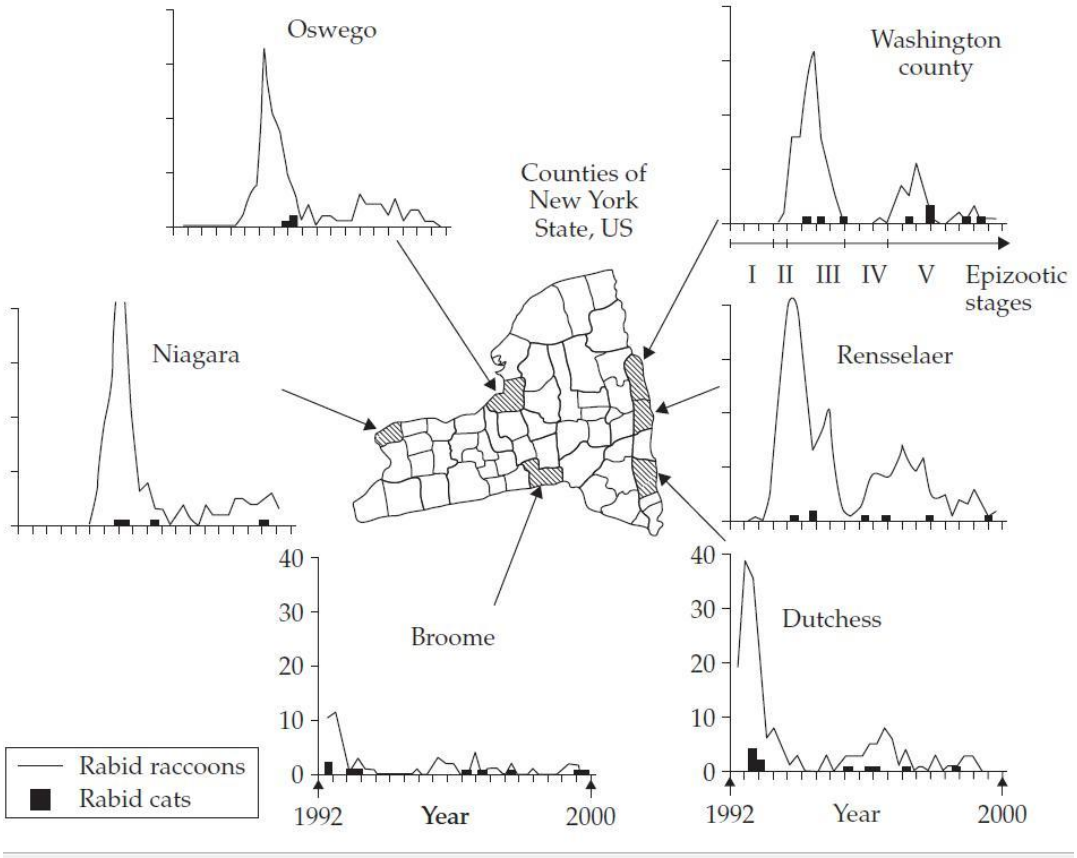

Figure 4.10. Number of raccoons and cats reported rabid at different epizootic temporal stages in Oswego, Washington, Rensselaer, Dutchess, Broome, and Niagara counties [19].

The spatial variation of the individual plays a great role in the epidemic spread as the density of regions affects the magnitude of the disease spread. In a real ecosystem, some individuals are grouped within densely populated regions and others in disconnected ones. Species population sizes and densities play a major role in the spreading of disease. The predators also force the escape of prey, which affects the movement of prey from one place to another. The behavioral model, which accounts for predator-prey interactions along with the prey's spatial distribution in the virtual world, produces a more realistic epidemic spread in the EcoDemics model.

4.4 Conclusions

As it has been discussed in chapter III, the individual-based evolving predator-prey ecosystem simulation, EcoSim, first introduced by Gras, et al [44] has been designed to simulate agents' behavior in a dynamic, evolving ecosystem. In this framework, each

agent behavior is modeled by a fuzzy cognitive map (FCM), allowing the evolution of the agent behavior through the epochs of the simulation. This chapter introduced the extension of this complex simulation to model the spread of epidemics.

We presented EcoDemics, a simulated predator-prey ecosystem for modeling the spread of directly transmitted diseases. We were able to represent epidemic spread among prey individuals based on a probabilistic timely controlled model that follows the general behavior of classical SIR model. The strength of this model comes from integrating SIR disease spread in a dynamic heterogeneous ecosystem simulation in which spatial distribution and interactions of the individuals emerge naturally as a consequence of including a complex behavioural model. The simplified assumptions like constant population size in classical mathematical SIR model or fixed structure in network-based models have been avoided by modelling births and deaths as well as mobility patterns. Also, the age structure has been included in the model since, for some infectious diseases, the age characteristic has a significant influence on the dynamics of the epidemic in the population. Again, unlike mathematical models that assume individuals to be uniformly distributed, individuals in EcoDemics are capable of socializing to form groups based on many environmental conditions such as predator pressure or sources of food. Comparing EcoDemics, the Neutral model, the classical mathematical SIR model and a field data about rabies spread, we have shown that the heterogeneity in the ecosystem influenced by a behavioral model plays a significant role in the epidemic spread in prey individuals, as the density of regions affect the magnitude of the disease spread.

This study highlights the significance of heterogeneous ecosystem in modelling disease progression compared to random mixing ecosystems. The unique values of our approach rely on the fact that we did not design a system dedicated to disease spread modeling and that the heterogeneity of the predator-prey population emerged from the ecosystem itself. This overcomes the extremely difficult task of gathering population properties of animals in an ecosystem. Analysing all of the EcoSim's features that can contribute to disease spread in the EcoDemics model such as genomic representation and evolution is beyond the scope of this study; however, the built in framework in EcoDemics provides us with the opportunity to utilize these attributes for future studies.

Chapter 5

Analyzing Vaccination Control and Herd Immunity Threshold in EcoDemics

As presented in the previous chapter, EcoDemics gave us a rich ground, with more depth and details to study epidemic outbreaks. In this chapter we are interested in analyzing vaccination strategy to control the spread of the infection. In the next section a short background of mitigation strategies will be presented. Section 5.2 is dedicated to the vaccination and herd immunity explanation. The experiments and results will be discussed afterwards. We then conclude this chapter in the final section.

5.1 Introduction

During the last few decades, several models have been developed to explore mitigation strategies in disease models. Tsunoda, et al. simulated the spread of influenza for exploring the most efficient mass vaccination strategies to prevent an epidemic [110]. In another study, the role of travel restrictions in delaying and ending the H1N1 pandemic has been explored [8]. A large-scale epidemic simulation was used in [31] to examine intervention options in an influenza outbreak. Keeling, et al. modeled vaccination strategies against foot-and-mouth disease [66]. The roles of individual imitation behavior and population structure in vaccination were explored in [35] to control infectious diseases. In these models, however, many details of the progression of infection and individual behaviors are neglected. Additionally, either unrealistic mixed-populations have been assumed or the number of different subpopulation types is small. Pourbohloul et al. used contact network epidemiology to predict several control policies for a mildly contagious disease [95].

Due to the high mitigation capacity and significance of the immunization intervention in the literature of epidemiology, we explore vaccination technique with various scenarios.

5.2 Vaccination and herd immunity threshold

We assume no initial immunity to the infection for individuals in the disease model and full immunity for those susceptible individuals being vaccinated.

5.2.1 Variation in time delay

Intervention timing has received a great deal of interest in many disease mitigation studies including mathematical models [36], [69], and simulations that use real epidemic data to parameterize their model [31]. For this reason, we explore the effect of immunization delay in the first experiment. We apply the vaccination with various time delays from the initiation of the infection and observe the difference in the magnitude of infection.

5.2.2 Variation in proportion of population and herd immunity

In another experiment we study the effect of vaccinating various population percentages. In this case, vaccination starts immediately after the initiation of the disease and is performed in 3 different phases. Each phase consists of 3 steps in which the number of vaccinated individuals are the same. In the first phase, the number of vaccinated individuals in each step is high to accelerate the mitigation process. We call this number Vaccination Capacity (VC). In the second and third phase, the number of vaccinated individuals in each step decreased to 2/3 and 1/3 of VC, respectively. Therefore, to ascertain the immunization of the chosen total percentage, VP, of the population during the whole 3 phases of vaccination, maximum vaccination capacity is defined as follows:

$$\mathrm{VC} = \mathrm{VP} * \mathrm{S}/6 \qquad (5.1)$$

where VC is maximum vaccination capacity in a step, VP is total vaccination percentage of the population, and S is the number of susceptible agents. This process guaranties that the total number of individuals vaccinated during the 9 steps that cover the 3 phases is equal to VP * S.

There is an important theory in epidemiology known as *herd immunity* which proposes that, all the individuals can be protected against a contagious disease by the vaccination of a fraction of a population [63]. The minimum proportion of vaccinated individuals in a

population for which a contagious disease is eradicated is the *herd immunity threshold*. This value depends on the type of the infection and population parameters, such as individual interactions and spatial distribution [32]. We are interested in investigating this principle in EcoDemics. This will be explored by varying the VP value and observe the epidemic trend over time in the next section.

5.3 Implementation, results, and analysis

The simulation is implemented in C++ and all experiments are performed on Sharcnet [105] using the Linux XC cluster. At the beginning stage of the simulation, the prey and predator populations are set to 12000 and 500 respectively. Initiation of the infection occurs after the stabilization stage that is, after 750 time steps of the simulation. At this stage of the simulation run, the prey and predator populations grow to 178340 and 29656 respectively. Due to the large number of parameters in our EcoDemics, numerous scenarios can be defined and experimented on. Different range of values for the disease parameters along with their principal effect on the epidemic have been studied in EcoDemics (previous chapter). For this experiment we chose one set of parameters but many such sets have been tested and led to the same results. Using probability of $p_{InitInfection}$ = 0.05, only 5% of the susceptible prey in the initial window are set to be infected during the initial infection stage. The infected individual goes through different states based on the parameters and probabilities of the disease model. We define the infection model with the following specifications: susceptible individuals become infected with the disease based on the probability function (1) with α = -0.2 and β = 2 for high risk individuals, and α = -0.15 and β = 4 for low risk individuals, infected individuals may recover from the disease after a minimum of 10 time steps (minInfected) and with the probability (p_{heal}) of 60% and the recovered individual is naturally immune. The killing rate of 1% is also assigned to this infection model according to p_{kill}.

5.3.1 Variation in time delay

In order to study the effect of timing in vaccination, we applied various time delays to the vaccination from the initiation of the infection, and then observe the corresponding values of the total number of infections. We vaccinated 90% of the population in delays ranging from 1 to 8 time steps after the initiation of the infection. We computed the

average of 10 different independent runs of the simulation. Our results show that with the early initiation of the vaccination, which correspond to an intervention delay of 1, the number of infections would be around 900, 5% of the population; however, having an intervention delay of 3, would increase the number of infections to 2500, 14% of the population. In other words, an intervention delay corresponding to 25% of the maximum delay increases the magnitude of infection in the population by a factor of 2.7 (Figure 5.1). This result follows the process of the studies presented in [69]. They presented similar curves considering 8 time steps for intervention delays, one time step being a week of delay. In this study final attack rates in a worst case epidemic increased by a factor of 3.2 in a delay of only 25% of the maximum intervention delay which is very similar to our results.

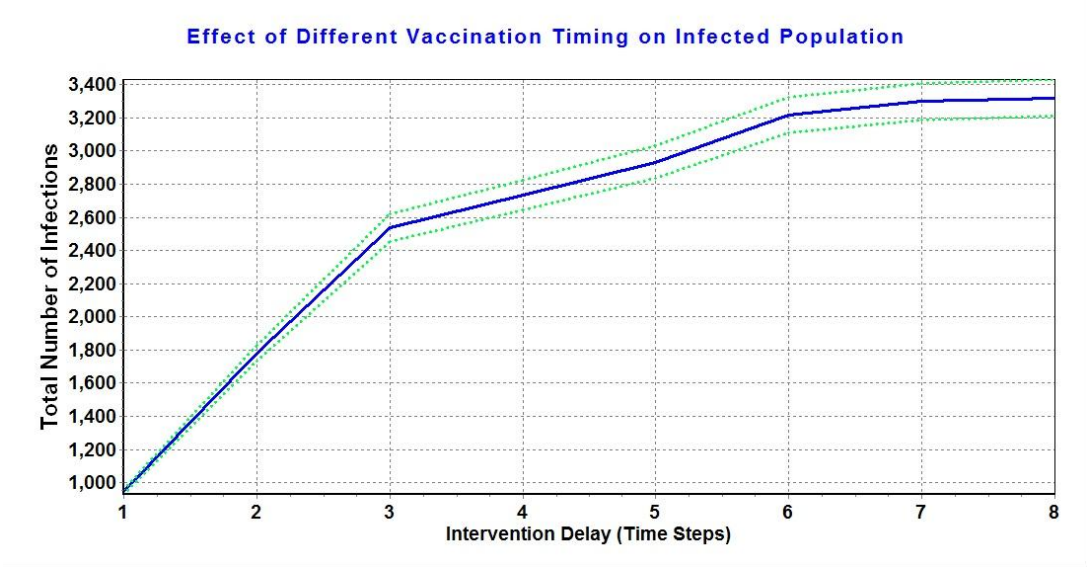

Figure 5.1. Effect of varying the vaccination delay on the total number of infections. Dotted lines represent one standard deviation.

5.3.2 Variation in percentage of population vaccinated

To study the importance of the number of individuals vaccinated, different proportions of the population are vaccinated. For this purpose, the value of VP is varied from 10% to 90% of the population. The average numbers of infected individuals and epidemic duration for 10 runs using the same VC value are computed. Figure 5.2 shows the effect of different vaccination rates on the total infected population. Similarly, Figure 5.3 shows

the effect of different vaccination rates on the total duration of the infection. These results are similar to other vaccination models such as [66], which used the 2001 real cattle epidemic as a template (see Appendix 2). As shown in the Figure 5.2, the infection has a maximum value of almost 355,000 individuals, which is a cumulative value over more than 100 time steps, while the number of vaccinated individuals is around 10,000, which represents approximately 10% of the population. However, the number of infections decreases drastically to less than 10,000 agents when the number of vaccinated individuals is more than 60% of the population and even decreases to 2000 infections when 90% of the population is vaccinated. The comparison of actual infections with the study that used a real cattle epidemic [66] is not applicable, as it considered the number of infected farms instead of the infected population; however, the obtained curves have the same trend: the average size of epidemic declines rapidly with the vaccination rate at each time step, reaching a lower plateau that corresponds to a disease eradication threshold [66].

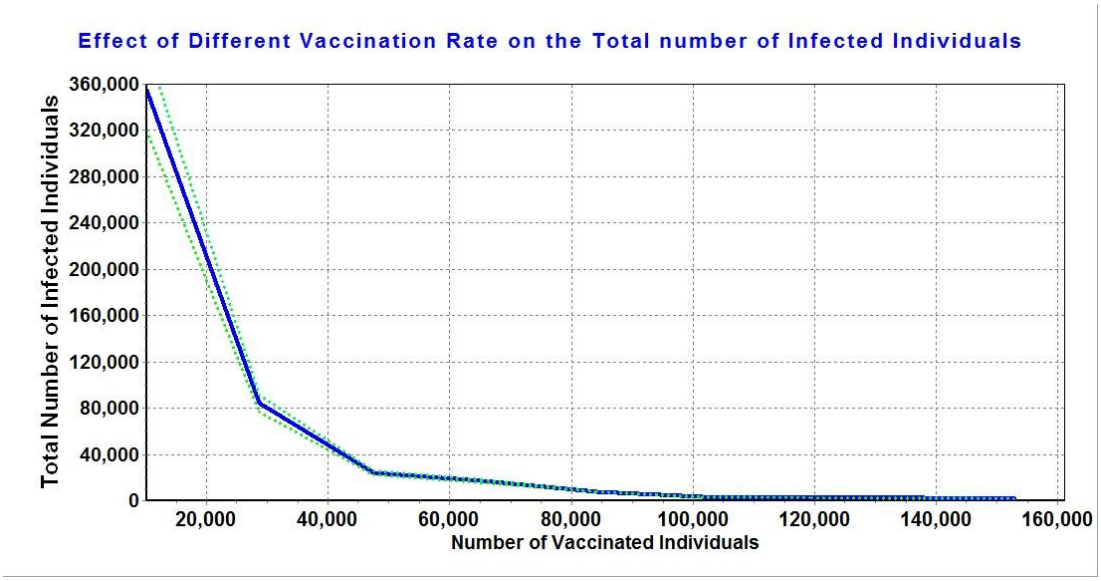

Figure 5.2. Effect of varying the number of vaccinated individuals on total infected population. The total number of vaccinated individuals is in abscissa and the cumulative total number of infected individual during the whole epidemic duration is in ordinate. Highest and lowest values in infected population correspond to the lowest (10%) and highest (90%) VP values respectively. Dotted lines represent one standard deviation.

In Figure 5.3, it can be seen that the epidemic lasts for an average period of 466 time steps with 10% vaccination; however, the duration is substantially reduced to less than 22

time steps while the vaccination percentage is more than 70% of the population. Similarly, this trend matches the reactive vaccination for cattle [66] which started with 400 days for the lowest vaccination rate, versus 466 time steps in our study, and achieved the herd immunity threshold in around 25 days, versus 22 time steps in our study.

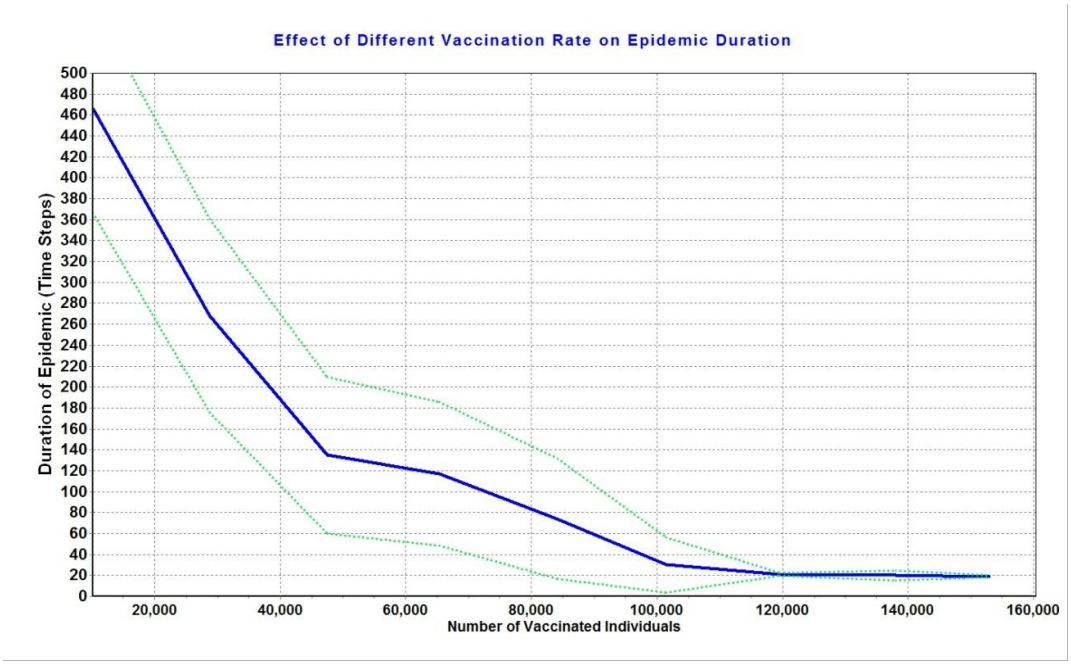

Figure 5.3. Effect of varying the number of vaccinated individuals on the infection duration. The total number of vaccinated individuals is in abscissa and the duration of the epidemic is in ordinate. Highest and lowest values in epidemic duration correspond to the lowest (10%) and highest (90%) VP values respectively. Dotted lines represent one standard deviation.

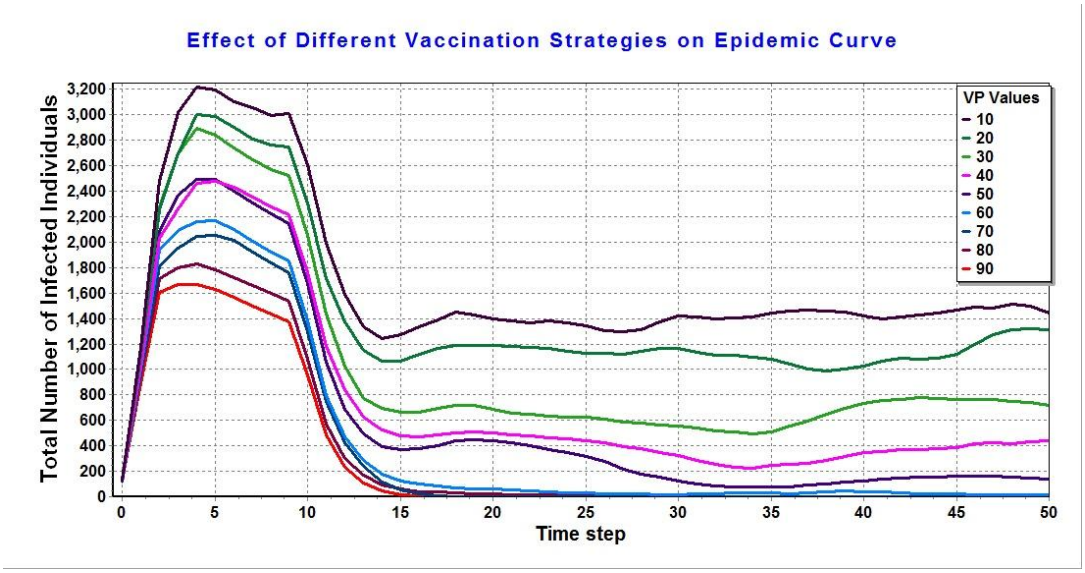

Figure 5.4. Effect of varying the percentage of vaccinated individuals on the epidemic curve. Each curve is the average of 10 independent runs for the corresponding VP value.

Figure 5.4 depicts epidemic curves for different VP values. The curves with the highest and lowest peak represent the VP values of 10% and 90% respectively, and each curve is the average for 10 independent runs. Only the first 50 time steps of the infection are depicted, as they are the most characteristic part of the epidemic patterns. For the VP of 60%, 70%, 80% and 90%, which are the four lowest curves, the epidemic was significantly mitigated and finally eradicated. For the lower VP values, although the trend of the epidemic over the first 15 time steps is similar to the 4 aforementioned curves, the vaccination strategy was unable to fully suppress the infection at the desired time and we observed jumps of infection after the global decline. This phenomenon suggests an immunity threshold to ensure the eradication of the epidemic over an acceptable duration. For this study the vaccination percentage of the total population needs to be equal or above a threshold of 60% to stop the disease diffusion. In qualitative context, this result is validated by the study about the herd immunity: high levels of herd immunity in cattle can prevent the long tail of the epidemic and is necessary to inhibit stochastic jumps of infection for a given special transmission kernel [66]. This correspondence only applies to the threshold for eradication of infection by vaccination: lower levels of vaccination can generate complex, nonlinear, spatio-temporal disease dynamics [66]. As mentioned earlier, we observed this nonlinear complex behaviour in lower VP values that are unable to eradicate the disease.

The above results show that our system, which includes much more complex mechanisms than the others, like the ability to model concepts such as complex individual behaviours, multi-level food chains, reproduction, evolution or speciation, produces results similar to the ones observed in systems dedicated to epidemic modeling. This is a significant result for the evaluation of EcoDemics' potential as a platform for studying open complex problems in epidemiology that are unable to be tackled in simpler simulations.

5.4 Conclusions

We simulated vaccination strategies in EcoDemics to model the mitigation of epidemics. We explored the effect of this technique with various timing and population percentage parameters. Our experiments revealed that there is a threshold value for the parameter setting the percentage of the population that is vaccinated. This is the same result observed in the herd immunity study (for more details see also Appendix 2): lower levels of vaccination can generate complex, nonlinear, spatio-temporal disease dynamics [66]. We observed that with a value greater than 60%, the pattern of the disease spread changes abruptly. However, these measures may not be appropriate to apply directly as quantitative values, as extensive disease specific parameters need to be adjusted depending on the different situations [50] [66] [53]. Nevertheless, this study highlighted the importance of effective vaccination policies in mitigating the infection and confirms the fundamental role of increasing individual's immunity over a relatively wide area to inhibit stochastic jumps of infection [66].

5.5 Appendix 2

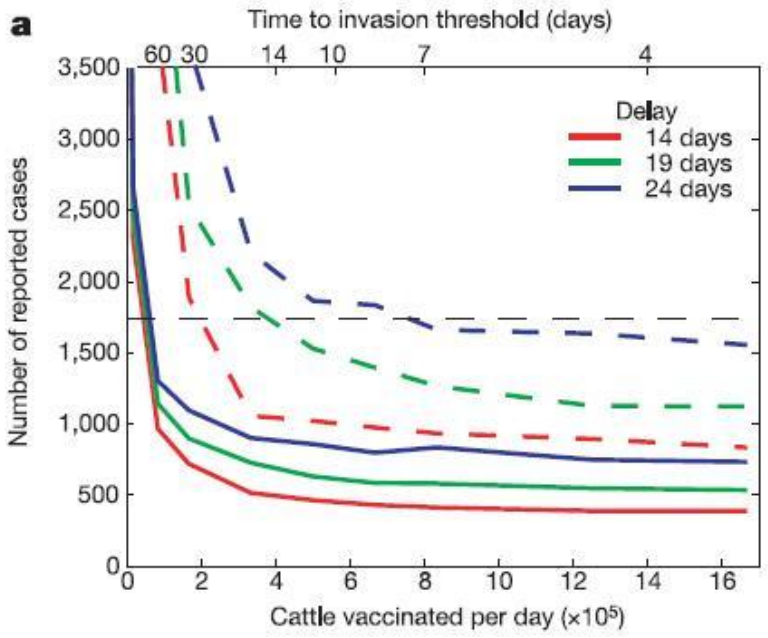

Figure 5.5: Effect of varying the number of vaccinated cattle on total infected population using the 2001 epidemic of Great Britain as a template [66].

Figure 5.5 shows how an epidemic can be controlled by the rapid vaccination of cattle during the early stages, using the 2001 epidemic of Great Britain as a template. Throughout, the vaccination is only performed on cattle and assumed to be at 90% efficacy. Expected number of farms reporting infection against the number of cattle vaccinated per day (bottom axis) or the corresponding time to achieve the disease eradication threshold of about 5.5 million cattle (top axis). Solid and dashed lines show the result when different culling is performed. Solid lines depict the average size of the simulated epidemic, which declines rapidly with daily vaccination rate, reaching a lower plateau at a rate of around 300,000 cattle per day. This rate allows achieving the vaccination threshold in about 25 days. Similarly, Figure 5.6 represents the expected duration of the epidemic by varying the number of vaccinated cattle [66].

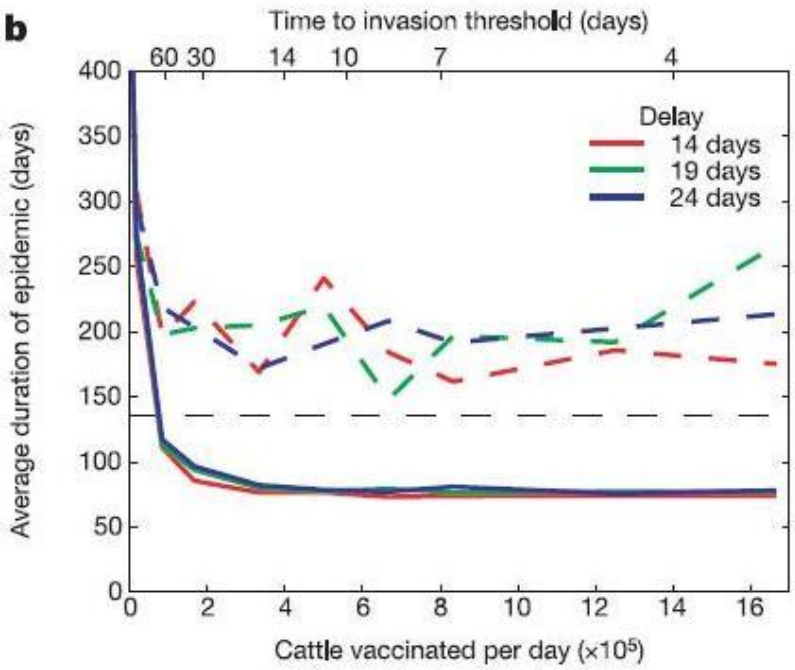

Figure 5.6 : Effect of varying the number of vaccinated cattle on the epidemic duration using the 2001epidemic of Great Britain as a template [66].

Chapter 6

Prey Infection and Effect of Predators

As presented in the previous chapters, EcoDemics framework provides us with the opportunity to realistically model disease in a predator-prey ecosystem and analyze strategies to control the spread of the infection. Having infection in prey individuals, the main focus of this chapter is to study the effect of predation on infection dynamics in the EcoDemics. Section 6.1 describes the background of predator-prey studies that have a pathogen in prey species. Section 6.2 is dedicated to the effect of predators in the system. The experiments and results will be discussed afterwards. We then conclude this chapter in the final section.

6.1 Introduction

To date, the effect of infection of prey species by a pathogen on predator-prey dynamics has been investigated in a variety of studies primarily employing numerical simulations ([7], [23], [48], [52], [62], [89], [91], [100], [117]). A key result of these studies, viz., that infected prey are more vulnerable to predation than uninfected prey tend to agree with empirical findings. Arthurs et al. found that locusts infected with a fungal pathogen are more vulnerable to predation due to reduced mobility and hence capability of escape [5]. Hudson et al. found following post mortem examinations that worm burdens in grouse killed by predation were significantly lower than worm burdens in grouse that died due to the parasite [60]. Further, Krumm et al., report that mountain lions prey on prion-infected mule deer more than on uninfected deer [75]. Johnson et al., claim also that yellow perch and bluegill fish demonstrated selective preference for Daphnia with chytrid infection vs. uninfected Daphnia suggesting that chytrid infection in Daphnia is a predictor of predation risk [64]. As a result of vulnerability to predation, field biologists found that predation in low-density populations is usually high enough to eliminate outbreaks [28], [92], [73].

A number of additional related results regarding host-pathogen dynamics in the presence of predators have been obtained using numerical simulations. First, introduction of

predation reduces the virus production and prey infected population[37]. Further, selective predation on infected prey may lead to an eradication of the disease in the prey population which could avoid extinction of the prey species[52], and [106]. A possible reason for eradication of the disease in the prey community is not simply a reduction in the number of infected prey due to morbidity and predation, but also selection pressure due to predation resulting in a higher number of immune prey individuals [100]. Moreover, in one numerical simulation study, it was found that predators have a tendency to switch to susceptible prey when the numbers of infected prey have been depleted [89]. The results of a numerical simulation study piloted by Bairagi et al., 2007 also suggest that predators, prey and prey-pathogens cannot co-exist in a stable state of equilibrium [7].

However, limitations of the numerical studies investigating predator-prey-pathogen dynamics are the unrealistic assumptions they rest on along with a limited number of parameters. For example, the numerical models developed by Haque et al. [48], Mukhopodhyay et al. [89], and Xiao et al. [117], assume that only susceptible prey reproduce and that infected prey do not recover nor develop immunity to the disease. A more realistic assumption is that prey sometimes recover (depending on the virulence of the disease) and acquire immunity to the disease, which is consistent with the SIR (susceptible-infected-recovered) epidemiological model. These limitations can be overcome by using our individual behavior based simulation that employs an SIR disease model. As explained in Chapter 4, EcoDemics is able to model births and deaths of individuals, as opposed to merely global functions in numerical simulations, along with being able to link the death of individuals to concrete reasons such as lack of energy, disease, or capture by a predator. Also, in an EcoDemics simulation, prey individuals that are immune due to their genetic make-up (innate immunity) will be naturally selected implying that it could be easy to model the transmission of their immunity to future generations. However, this feature of inter-generational immunity is beyond the scope of this study. Although there are a number of recent studies in the literature using individual-based approaches to investigate the effect of disease in populations using the SIR model (for example [14],[17],[3]), this is the first such study to focus on the effect of predators in prey infection dynamics.

An important virtue of an individual-based simulation approach is that the larger number of parameters along with the modeling of complex individual behaviors give rise to a larger number of scenarios that can be investigated. Additionally, because the global complexity of the simulations is linear, the experiments can be done in an acceptable time. A key basis of any empirically adequate simulation is that it agrees with corroborated and replicated empirical findings. Thus, the simulations used in this chapter rest on the assumption that infected prey will be less capable of escaping predators than susceptible prey thereby making them more vulnerable to predation in agreement with the empirical studies cited above. This assumption is met by varying the mobility of infected prey at various levels depending on the virulence of the pathogen.

The purpose of this chapter is to fill the current lacuna of individual-based studies regarding predator-prey-pathogen systems with the goal of testing some of the hypotheses corroborated by the numerical studies based on realistic, paramater-rich EcoDemics integrating an SIR disease model. These hypotheses include the claim that predator selection of infected prey may lead to eradication of the disease in the prey population or result in predator-switching to susceptible prey. An additional hypothesis to be tested using EcoDemics is that a predator-prey-pathogen system does not attain a stable equilibrium. The findings obtained regarding these hypotheses will be compared with results obtained in both numerical and empirical studies.

6.2 Predator effect

This section defines scenarios to study the effect of predators in pathogen dynamics. As explained in Chapter 4, depending on the infection and type of the test, different values can be used for EcoDemics' parameters. The values used for the experiments in this section are shown in table 6.1. All of the values are close to those experimented in Chapter 4, except that the infected population does not become immune. This is due to the fact that immunity has a major effect on disease duration; and therefore zero immunity provides the EcoDemics with a very long infectious period which is suitable to observe the effect of different scenarios experimented in this chapter.

Table 6.1. Disease parameters used for the experiments.

Parameter	$p_{InitInfection}$	p_{immune}	p_{heal}	p_{kill}	*minInfectedTime*
Value	2%	0%	60%	2%	10

Recalling from Chapter 3, several actions have been modeled for prey and predators in EcoDemics. Predator actions include searching for food, hunting, socializing, exploring, resting, eating, and breeding. For the purpose of observing the effect of predation on disease dynamics in prey, two different sets of scenarios have been studied. In scenario 1, infection dynamics before and after adding predators to the system have been tested. The second set of scenarios is related to the attack rate of predators, in which three main scenarios were studied. For each scenario different attack rates of the predators have been simulated by removing some of the actions that predators can perform; in other words, by removing some of the non-predation actions that a predator can take, the possibility of hunting action, and therefore the attack rate has been increased. Among the 7 possible actions of predators, we chose to remove socialization, and/or exploration actions that only marginally disturb the normal behavior of the predators. On an average normal run of the EcoDemics, at each time step 9% of the predators perform socialization, and 1% perform exploration. The scenarios are as follows:

Scenario 2A: The socialization action is removed from the possible actions of predator (predator attack rate 1).

Scenario 2B: The exploration action is removed from the possible actions of predator (predator attack rate 2).

Scenario 2C: Both the socialization and exploration actions are removed from the possible actions of predator (predator attack rate 3).

It is assumed that the infectious disease reduces the capability of movement in prey individuals which agrees with empirical findings [5], and [75]. Therefore for each scenario, different levels of mobility in prey have been studied as well. This is simulated

by decreasing the mobility of the infected prey to 75%, 50%, and 25% of its original movement ability. For each of these experiments the average of 10 independent runs has been taken into account.

6.3 Implementation, results, and analysis

The simulation is implemented in C++ and all experiments are performed on Sharcnet using the Linux XC cluster. Although complex behaviors have been modeled in the simulation, its global complexity is still linear and the experiments are done in an acceptable time.

For all the scenarios, the simulation is given a 2500 initial time steps for stabilization of the ecosystem (not shown in the figures). After that the infection is introduced into the ecosystem in which 2% of the prey population was initially infected.

Figure 6.1 shows the number of infected population for scenario 1. In this figure, the upper line (red) shows the infected prey population without having predators in the ecosystem. The lower line (blue) shows the infected prey population when the predators were present in the ecosystem. The overall ratio of infected prey individuals during 1500 time steps for the first and second cases were 0.26 and 0.14 respectively. Therefore the overall infection percentage while having the predators in the system has been reduced to almost half. This is an interesting result considering the fact that we have done nothing to force the predators to select infected prey; therefore the lower rate of infection in the presence of the predators emerged directly from the behavioral model of prey and predators and the disease properties which accounts for lower physical capacity (0.25 of its normal mobility) of the infected prey. This result is in accordance with the numerical simulations ([7], [23], [48], [52], [89], [91], [100], [117], and [37]), and empirical findings ([5], [60], [75], and [64]).

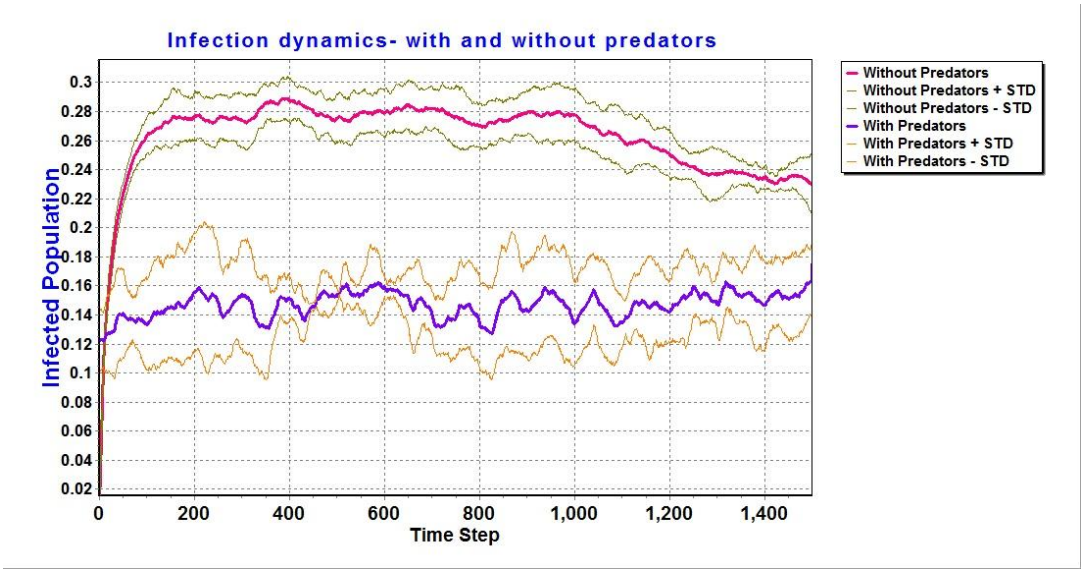

Figure 6.1. Prey infection dynamics in the presence and absence of predators related to scenario 1.The thinner curves show the standard deviations.

Infected population for scenarios 2A, 2B, and 2C are shown in figures 6.2, 6.3, 6.4 respectively. As shown in these figures, the infected population for all the mobility values decreased drastically. Interestingly, the infection was eradicated for the scenarios with the infected prey mobility reduced to 25%, 50%, and 75%. The eradication of the disease was observed for all the 2A, 2B, and 2C scenarios except for those scenarios that the disease does not affect the mobility of the prey (see the upper curve referred to as movement 1 in figures 6.2, 6.3, and 6.4). For these scenarios where the disease was not eradicated, the average infected populations during 2500 time steps were around 9-10% of the total population. This result suggests that the higher an infection affects the mobility of the prey, the higher the chance of the predation on infected prey, and eventually the fastest eradication of the disease. This dependency between the reduced mobility of the infected prey and the time step at which the infection was eliminated, is shown in table 6.5. The disease elimination time was assumed to be at the time step in which the infected population was less than 0.2% of the total population. As it can be seen in this table, the shortest eradication time for each of the scenarios 2A, 2B, and 2C was observed in the case where the mobility of the prey was as low as 25% of its original mobility; whereas the longest eradication time corresponds to the scenarios where the mobility of the prey was 75% of its original. In other words, the lower the mobility of the

infected prey, the lower the disease elimination time step. This result is in concordance with the findings presented in [37], [25], and [111], that shown that infective mobility has a significant impact on elimination of the infection. The time step at which eradication occurred was also different based on the attack rate of the predators. For scenario 2A (predator attack rate 1), the average time step at which the disease was eliminated was time step 1893, whereas for scenario 2B (predator attack rate 2) it was 2149. Therefore, removing the socialization action from the possible actions of the predators had more effect on predation rate than removing exploration. This is as we expected because predators normally take socialization action more than they take exploration. Removing both of the socialization and exploration actions for predators in scenario 2C (predator attack rate 3), resulted in the average elimination time step of 1796. In other words, the disease eradication occurred faster when predators are more hostile as a result of removing their socialization and exploration actions. For the infectious scenarios with severe movement inabilities, the predation on infected prey will lead to elimination of the pathogen. Predators are often responsible for infections going extinct assuming that it is easier for a predator to hunt an infected individual [106]. This result is also in accordance with the numerical studies presented in [52], and [100]; and field studies in [28], [92], and [73]. Moreover, this is an individual-based demonstration of the fact that predator, prey and prey-pathogens cannot co-exist in a stable state of equilibrium [7].

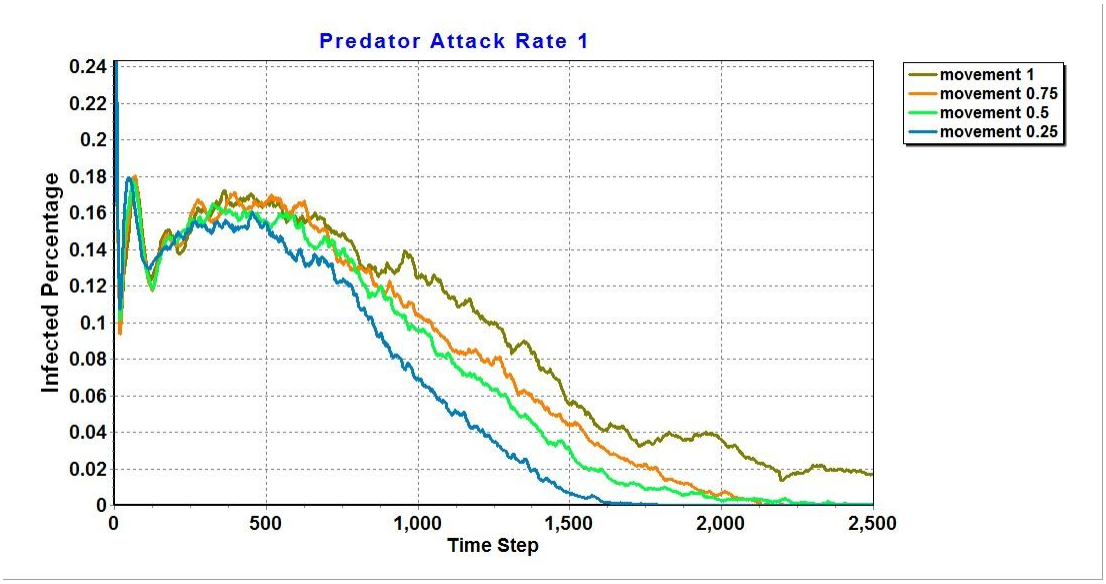

Figure 6.2. Infection dynamics for prey with different levels of mobility related to scenario 2A.

Table 6.2. Two tailed P-value for scenario 2A: the average value for each of the time series in scenario 2A was computed and the P-value is calculated for each pair of samples (ratios 0.25 and 0.5; ratios 0.25 and 0.75; ratios 0.25 and 1; ratios 0.5 and 0.75, ratios 0.5 and 1; ratios 0.75 and 1).

Infected Movement Ratio	0.25	0.5	0.75	1
0.25	…	0.000004	Less than 0.000001	Less than 0.000001
0.5	0.000004	…	0.000538	Less than 0.000001
0.75	Less than 0.000001	0.000538	…	0.000021
1	Less than 0.000001	Less than 0.000001	0.000021	…

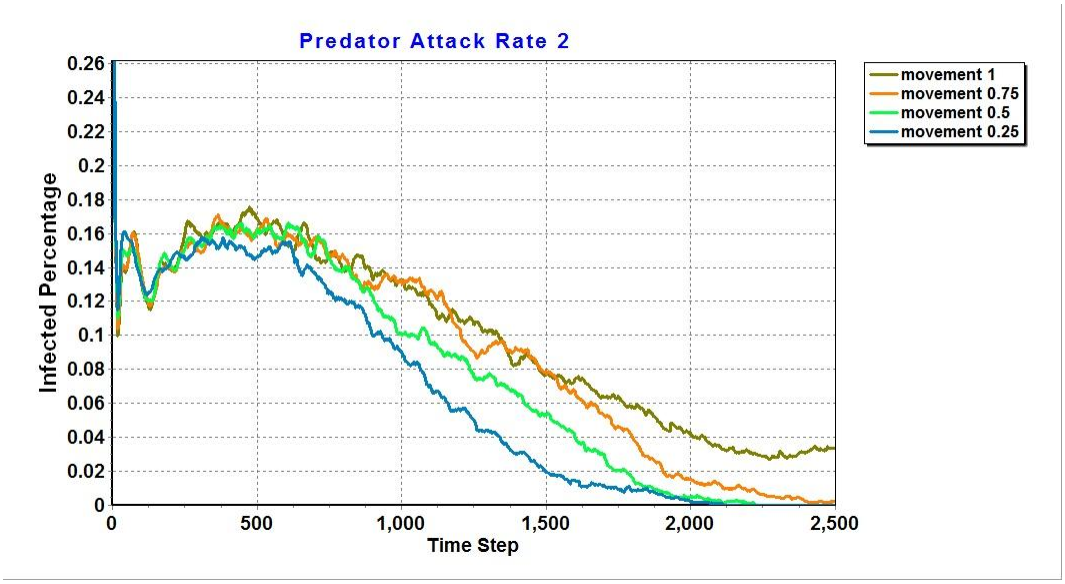

Figure 6.3. Infection dynamics for prey with different levels of mobility related to scenario 2B.

Table 6.3. Two tailed P-value for scenario 2B.

Infected Movement Ratio	0.25	0.5	0.75	1
0.25	…	0.000004	Less than 0.000001	Less than 0.000001
0.5	0.000004	…	0.000002	Less than 0.000001
0.75	Less than 0.000001	0.000002	…	0.000219
1	Less than 0.000001	Less than 0.000001	0.000219	…

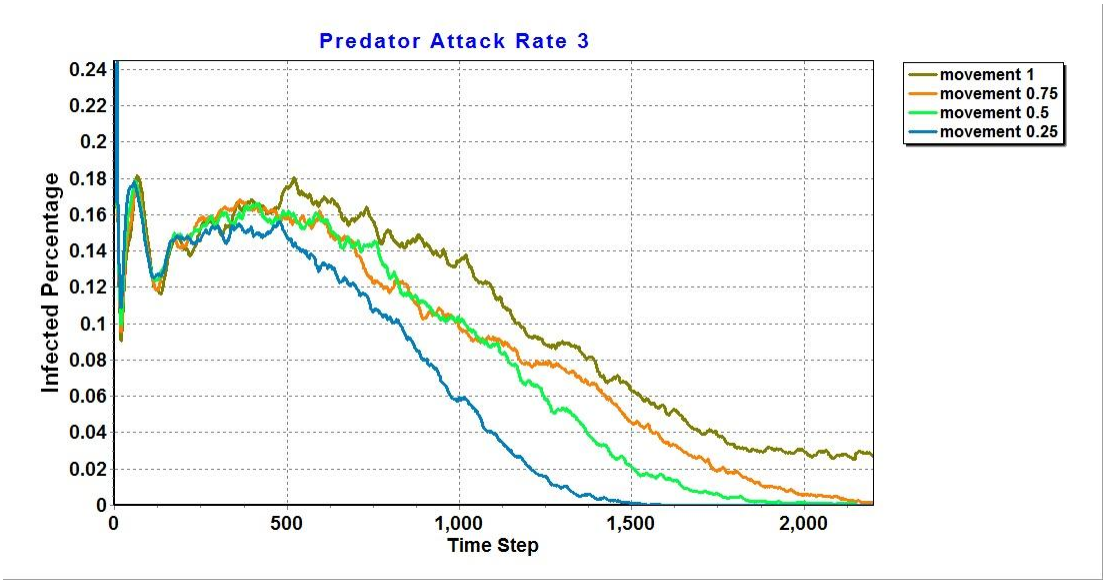

Figure 6.4. Infection dynamics for prey with different levels of mobility related to scenario 2C.

Table 6.4. Two tailed P-value for scenario 2C.

Infected Movement Ratio	0.25	0.5	0.75	1
0.25	…	Less than 0.000001	Less than 0.000001	Less than 0.000001
0.5	Less than 0.000001	…	0.002913	Less than 0.000001
0.75	Less than 0.000001	0.002913	…	0.000001
1	Less than 0.000001	Less than 0.000001	0.000001	…

It can be seen that for all scenarios, predation on the infected prey will cause the infected population percentage to reduce. For each scenario, the differences between infected population percentages are statistically analyzed with Welch's t-test. The t-test is applied on the averages and standard deviations of all the values of each time series, and the resulting two tailed P-values are shown in tables 6.2, 6.3, and 6.4. By conventional criteria all the values observed in the four situations are considered to be significantly different.

Table 6.5. Disease eradication time step for scenarios 2A, 2B, and 2C with the infected prey mobility reduced to 0.25, 0.5, and 0.75 of its original movement. Standard deviations are given after slashes.

Infected Movement Ratio	Scenario 2A	Scenario 2B	Scenario 2C
0.25	1600 / 126	1983 / 166	1432 / 96
0.5	1996 / 184	2073 / 115	1831 / 187
0.75	2083 / 129	2392 / 169	2125 / 160

6.4 Conclusions

Studying dynamics of the infections in ecosystems and factors regulating the epidemics is of high importance. A variety of mathematical simulations have been studied to explore different aspects of predator-prey-pathogen systems. Although the use of individual-based methods has become very popular in modelling the biological systems, there is a lack of study considering predator-prey-pathogen systems to test predator effects in pathogen dynamics. Understanding the role of predators generating variation in pathogen dynamic has important implications for the management of natural and agricultural ecosystems. To the best of our knowledge, this is the first individual-based study exploring the effect of predators on prey infection dynamics in a predator-prey ecosystem simulation. We tested some of the hypotheses corroborated by the numerical studies using the EcoDemics simulation. We monitored the prey infection dynamics in the presence and absence of the predators. The overall infection percentage in the presence of predators in the system has been reduced significantly. This result which emerged directly from the behavioral model of the ecosystem, agrees with numerical and empirical findings cited earlier. The values observed in the various studied situations are proved to be significantly different by using the Welch's t-test. Our results revealed that predator selection of infected prey will lead to eradication of the disease in the prey population when the pathogen reduces the mobility of the prey. Moreover, we showed that the duration of the infection decrease with the reduced mobility of the prey. This is in concordance with the findings presented in [52], [7], [106], and [100].

We also defined scenarios to test the effect of predator attack rates on prey infection dynamics. In these scenarios, the elimination of the infection occurred faster when predators have a higher attack rate as a result of removing their socialization and exploration actions.

Our study offers a significant first step in individual-based methods to explore the role of predators in prey infection dynamics. The large number of parameters along with the realistic behavioral model incorporated into the EcoDemics, provides us with the opportunity to define numerous scenarios and experiments for future studies in predator-prey-pathogen systems.

Chapter 7
Conclusion and Future Work

We presented EcoDemics which integrates a disease model with EcoSim [44], for studying epidemic spread in a predator-prey ecosystem simulation. We explained EcoSim using the updated 7-points Overview-Design concepts-Details (ODD) standard protocol [45], and [46] for describing the individual-based models. We then introduced EcoDemics the extension of this complex simulation to model the spread of epidemics. The epidemic spread among prey individuals was represented based on a probabilistic timely controlled model that follows the general behavior of classical SIR model. This study highlighted the significance of heterogeneous ecosystem in modelling disease progression compared to random mixing ecosystems. The unique values of our approach rely on the fact that we did not design a system dedicated to disease spread modeling and that the heterogeneity of the predator-prey population emerged from the ecosystem itself. This overcomes the extremely difficult task of gathering population properties of animals in an ecosystem.

On the other hand, similar to any other modeling simulation, our approach has some limitations as well. Large number of parameters that do not necessarily contribute to disease dynamics, and massive data size that is produced through the epochs of the simulation are important drawbacks of our model. It is also hard to make precise estimates, and to verify a specific contributing factor for the epidemiological results. This is due to the fact that unlike classical mathematical models, individual-based models are intractable leading to more complex sensitivity analysis [10]. A comparison between different disease modeling approaches that were explained in Chapter 2, are provided in Table 7.1 below. The question of which model is the best, depends on the epidemic type, population properties, and the objective of modeling the epidemic spread. For many studies, there is a single population under consideration. If the population is close to homogeneous, the classical mathematical model is a reasonable choice. If the population is heterogeneous, but falls into a few specific classes of networks, the network models

can perform quite well [10]. If, however, the environment is dynamic or the population of individuals are evolving, individual-based models are the better choice.

Table 7.1. Summary of disease modeling types and their specifications for epidemic spread

Disease Modeling Type	Tractability	Heterogeneity	Attention to Details	Dynamic Environment	Reasonable data size
Classic Mathematical	☑	☒	☒	☒	☑
Network	☒	☑	☑	☒	☑
Individual-based	☒	☑	☑	☑	☒

In order to model the mitigation of epidemics, we simulated vaccination strategies in EcoDemics. We explored the effect of vaccination with various timing and population percentage parameters. Our experiments revealed that there is a threshold value for the parameter setting the percentage of the population that is vaccinated. We observed that with a value greater this threshold, the pattern of the disease spread changes abruptly. This study emphasized the importance of effective vaccination policies in mitigating the infection and confirms the fundamental role of increasing individual's immunity over a relatively wide area to inhibit stochastic jumps of infection.

Our study also points to the significance of predation effects in the dynamics of the infectious diseases, which has important implications for the management of natural and agricultural ecosystems. To the best of our knowledge, this is the first individual-based study exploring the effect of predators on prey infection dynamics in a predator-prey ecosystem simulation. We observed that the overall infection percentage in the presence of predators in the system has been reduced significantly. Our results also revealed that predator selection of infected prey will lead to eradication of the disease in the prey population when the pathogen reduces the mobility of the prey. Moreover, the duration of the infection decrease with the reduced mobility of the prey. We also defined scenarios to test the effect of predator attack rates on prey infection dynamics. In these scenarios, the elimination of the infection occurred faster when predators have a higher attack rate.

Our study offers a significant first step in artificial life simulations to explore the role of different aspects of the ecosystem in infection dynamics. The large number of parameters along with the realistic behavioral model incorporated into EcoDemics, provides us with the opportunity to define numerous scenarios and experiments for future studies in predator-prey-pathogen systems.

As the individuals in our system search for mates and breed, sexually transmitted diseases can easily be integrated. This will allow for studying the specific properties of sexually transmitted disease in large multi-species populations.

Similar to modelling epidemic spread in prey population, we will be able to study disease spread in predator population as well. Analysing the dynamics of the disease having a pathogen infecting both prey and predator species is an interesting topic to investigate. If a predator contracts the disease by hunting an infected prey, pathogen dynamics would be different from the one observed in the previous chapter. These kinds of studies are important for maintaining and management of natural ecosystems.The way a disease impacts the genome through the course of evolution is also an interesting question to investigate. Several biological and ecological studies have tried to argue these types of impacts in the evolution of individuals and the necessity of their recognition and interpretation for both public health [39], and the population of the ecosystem [12]. As our system integrates the notions of genome, transmission of genome and evolution; we will have the ability to analyze how individuals try to adapt and overcome a disease spread through evolution. Several thousands of time steps are required to observe evolution in EcoDemics; therefore, we will need to define a disease model that stays in the population for very long period of time. This can be done by minimizing the immunity parameter of the disease, similar to the approach followed in the predator effect study.

Co-evolution of diseases and hosts could also be represented. We will be able to track and analyze the way that one affects the other and influences its evolution over long periods of time.

The feasibility to study the effect of disease spread on different ecological and biological phenomena such as species formation, individuals behavior, predation, evolution and co-evolution are what differentiate our model from the others.

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