

Studying Collective Behaviour Using Agent-Based Models

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Certificate of Examination

This is to certify that the dissertation titled “Studying Collective Behaviour Using Agent-Based Models” submitted by Mr. Adarsh Prabhakaran (Reg. No. MS14110) for the partial fulfilment of BS-MS dual degree programme of the Institute, has been examined by the thesis committee duly appointed by the Institute. The committee finds the work done by the candidate satisfactory and recommends that the report be accepted.

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Dated: April 25, 2019

Declaration

The work in this dissertation has been carried out by me under the guidance of Professor Somdatta Sinha at the Indian Institute of Science Education and Research Mohali.

This work has not been submitted in part or in full for a degree, a diploma, or a fellowship to any other university or institute. Whenever contributions of others are involved, every effort is made to indicate this clearly, with due acknowledgement of collaborative research and discussions. This thesis is a bonafide record of original work done by me and all sources listed within have been detailed in the bibliography.

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In my capacity as the supervisor of the candidate's project work, I certify that the above statements by the candidate are true to the best of my knowledge.

Prof. Somdatta Sinha

(Supervisor)

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Notation

ABM : Agent-based Model
GRT : Grass regrowth time
I : Infected Population
ODE : Ordinary differential equation
S : Susceptible population
SI : Susceptible infected
SIS : Susceptible infected susceptible

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Abstract

Agent-based modelling is a technique to study complex collective behaviour through a ground-up approach and is much closer to real-world modelling than other techniques that exist. In this thesis, I have attempted to show the similarities and differences in dynamics that the micro modelling approach of Agent-based modelling and the macroscopic technique of differential equation modelling show. Comparative studies have been done on Lotka-Volterra Prey-Predator systems and Epidemiological models of SI and SIS types. The observations from the Agent-based approach have been compared with the differential equation models, and information like the probability of different type of dynamics including rare events to properties emerging out of the spatial distribution of the heterogeneous agents were studied. In the case of epidemiological models, the effect of boundaries on time taken for infection spread has also been studied to understand the method of quarantining within the space during disease spread.

Chapter 1

Introduction

Coordinated behaviour of large groups of animals and the emergent properties of the same have always been looked into with curiosity. It is such behaviour, where properties which are not seen in the individuals constituting the group are seen in the aggregate which is called collective behaviour. This falls under the broad stream of complex systems.

The spatiotemporal behaviour exhibited by an interacting multi-component system (“collective”) can be studied at different scales.

- At a macroscopic scale, both space and time are continuous states, and the mean-field description is used for the system with differential equations.
- At a mesoscopic level, spatial description is discrete, and a lattice of coupled subsystems are used.
- At the microscopic level, both space and time are discrete and each subsystem’s evolution in space and time can be studied using Agent-Based Models (ABM).

The collective behaviour shown by the system can be different at these different scales of description, and individual behaviour in isolation can be different from that in a collective.

1.1 Agent-based Models

Agent-based modelling or individual-based modelling technique is a class of computational technique, which relies on dynamical interactions between autonomous, heterogeneous agents/individuals to understand the macroscopic consequences (i.e., the “collective behaviour”) of the system due to such local interactions.

It has three main components, Susceptible infected susceptible

- The agents
- The Environment: The space in which the agents interact. This can be continuous, discrete or characterised by networks.
- The Interaction Rules : Specifications on how agents interact with each other and the environment.

By modelling systems with a ground-up approach using agent-to-agent interactions, self-organization can often be observed in such models (Macal 06). New structures, behaviours, and patterns which were not explicitly programmed into the models emerge out of it which arise through the agent interactions.

In ABM the properties (Goldstone 05) of each individual can be tracked with time in contrast to other mean-field methods where everything gets averaged. ABM’s have four main properties :

- Autonomy of agents : Each agent can be completely independent, where decisions need not be taken just on the basis of calculated optimised paths and methods but can also be made through methods like reinforcement learning, adaptation etc.
- Local rules at the level of agents: The interactions in an ABM are made based on the local rules given to each agent rather than the ones given to entire populations. The effect of such local rules on the entire system can be therefore easily studied.
- Stigmergic interactions : The agents can modify the environment in which they are and also can react to the environment.

- ABM usually consists of two dimensional or three dimensional environments, and spatial properties can easily be studied.

Agent-based models have been used to study a variety of systems, from crowd behaviour (Trivedi 18) to understanding social epidemiological (El-Sayed 12) and evolutionary dynamics of influenza viruses (Roche 11), from ecology (Grimm 05) to political sciences (Huckfeldt 04). The universality of its application and the closeness to real life systems is what makes agent-based modeling apt for the study of collective behaviour.

1.2 Agent-based Modelling tools and softwares

There are multiple tools for Agent-based modelling, a few of them are mentioned below. For a complete list and a comparative study look into (Abar 17)

- NetLogo - Usually used for 2D / 3D simulations in social and natural sciences, falls in the large scaled and simple softwares category. (<https://ccl.northwestern.edu/netlogo>)
- Swarm - Simulations in complex adaptive systems, supply chain optimization traffic management etc. Falls in the extreme-scale and hard softwares group. (http://www.swarm.org/wiki/Main_Page)
- PyNetLogo - python library to link with NetLogo. (<https://pynetlogo.readthedocs.io/en/latest>)
- AgentScript Framsticks for 2D and 3D modelling, falls in the light-weight and simple category. (<http://agentscript.org>)

1.3 Outline of thesis

The thesis has been organised in the following chapters

1. Introduction

2. The differential equation models for both the prey-predator system and epidemiological systems are explained in this chapter.
3. The methodological details used to build the agent-based model for both prey-predators and epidemiological system (SI and SIS) are discussed here.
4. The observations and results obtained from the agent-based model for prey-predators are presented here.
5. The observations and results for Agent-based SI and SIS models are discussed here.

Chapter 2

Differential Equation models

2.1 Prey-predator systems

The famous prey-predator equations, also known as the Lotka-Volterra equations are based on the following assumptions (Segel 88),

- Prey growth is unlimited if the predators do not keep them under control.
- Predators depend on the presence of their prey to survive.
- The Rate of predation depends on the likelihood that a prey is encountered by a predator.
- The predator population growth rate is proportional to food intake (rate of predation).

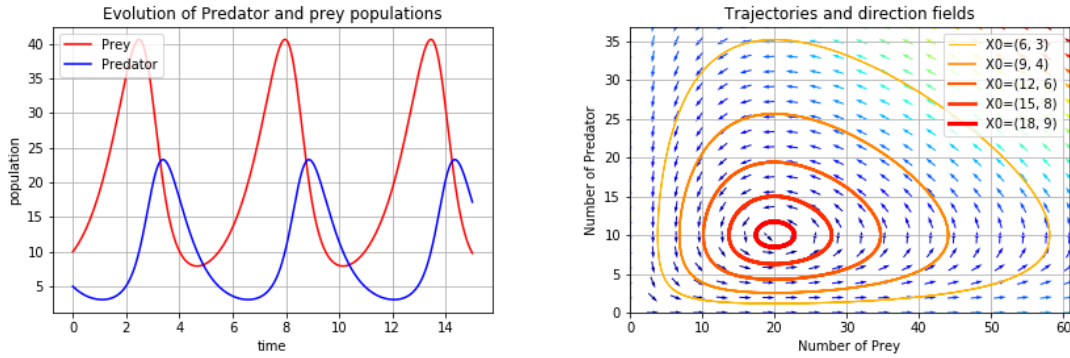
If x is the prey population and y is the predator population, then the Lotka-Volterra model is given by (Volterra 26) (Lotka 20):

$$\frac{dx}{dt} = \alpha x - \beta xy \qquad \frac{dy}{dt} = -\gamma y + \delta xy \qquad (2.1)$$

$\alpha =$ Prey growth rate (without predation)		$\gamma =$ Predator death rate
$\beta =$ Prey death rate (with predation)		$\delta =$ Predator growth rate

The equations 2.1 have two steady states,

$$(x_1, y_1) = (0, 0) \qquad \text{and} \qquad (x_2, y_2) = \left(\frac{\gamma}{\delta}, \frac{\alpha}{\beta}\right)$$



(a) Population size with time.

(b) Phase plot for different initial conditions.

(source : <https://scipy-cookbook.readthedocs.io>)

$$\alpha = 1, \beta = 0.1, \gamma = 1.5, \delta = 0.75$$

Figure 2.1: Population dynamics and behaviour of the prey-predator model

This system shows neutral stability and oscillations around the coexisting positive steady state. Thus the Prey-Predator model always shows oscillations around the positive steady state, but the amplitude depends on initial values of the Prey and Predator populations.

This dynamics is completely suppressed if the prey growth is limited by the environment's carrying capacity. The coexisting positive steady state shows stable dynamics. In this case of limited resources, the equations change and the dynamics become stable (Segel 88).

2.2 Epidemiological models

Epidemiological models are used to study propagation of infection in a population, by subdividing the whole population into different compartments - S (susceptible), E (exposed), I (infected), and R (recovered) based on their infection status (Mandal 11).

2.2.1 SI Model

The SI model is one of the simplest mathematical model for the spread of infection. According to the model,

- Each individual in the population can be either infected or susceptible to an infection.
- Once an individual is infected, he/she remains infected.
- There is no birth or death. Total population is constant.

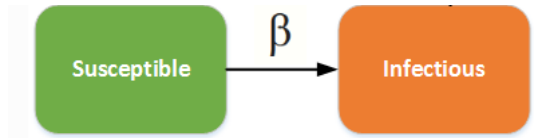


Figure 2.2: SI Model

β is the rate of transfer from the Susceptible compartment to the Infectious compartment.

The SI model equations are :

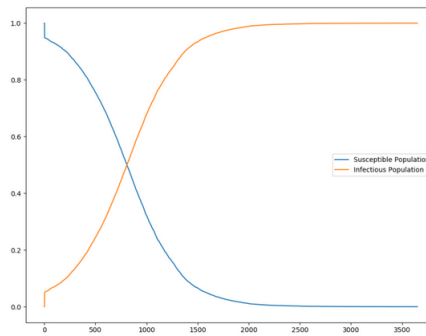
$$\frac{dI}{dt} = \frac{\beta SI}{N} \qquad \frac{dS}{dt} = -\frac{\beta SI}{N} \qquad (2.2)$$

I = Number in Infected state

S = Number in Susceptible state

N = Total Population (I + S)

β = Rate of infection



(source : <https://instituteofdiseasemodeling.github.io>)

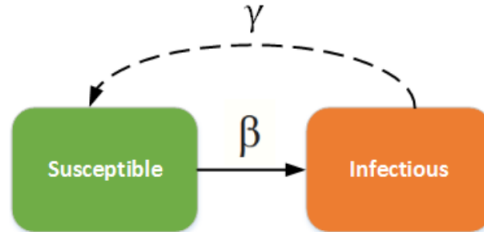
Initial condition: $S_0 = 99$ and $I_0 = 1$, and $N = 100$, Y axis is scaled by N.

Figure 2.3: Time-series for SI Model

As can be seen in Figure 2.3, the entire population goes into infected state in the SI model.

2.2.2 SIS Model

The SIS model has similar properties to that of SI model. Again, there are two states in which any individual can be - Susceptible to an infection or Infected.



β = rate of transfer from the Susceptible compartment to the Infectious compartment and γ vice versa (dotted line)

Figure 2.4: SIS Model, the dotted line shows transfer from infected compartment to susceptible compartment

The SIS model equations are :

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I \qquad \frac{dS}{dt} = -\frac{\beta SI}{N} + \gamma I \qquad (2.3)$$

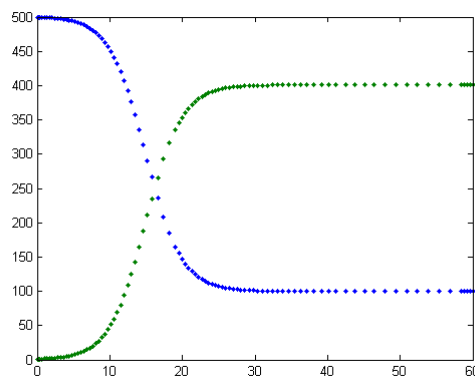
I = Number in Infected state

S = Number in Susceptible state

N = Total Population (I + S)

β = Rate of infection

γ = Rate of transfer from infected state to susceptible state.



(source : <https://en.wikipedia.org>)

Figure 2.5: Time series for SIS model.

$$\beta = 0.001 ; \gamma = 0.1 \quad S_0 = 499 ; I_0 = 1$$

The SIS Model gives a provision of going back to the susceptible state once an individual has been infected. This ensures that not everyone is infected and there is coexistence between the infected and the susceptible individuals in this model as can be seen in Figure 2.5.

Thus both SI and SIS models show stable dynamics around the positive steady state irrespective of initial values of S or I. In the SI model all in population gets infected, and in the SIS model co-existence of S and I occurs.

Chapter 3

Methods

The Differential Equation models were simulated using Python tool box and the ODE integrator was used. The agent-based models corresponding to the prey-predator system and epidemiological systems was modelled using NetLogo (Wilensky 99), a multi-agent programmable modelling environment.

For parameter sweeping, the behaviorspace tool in NetLogo was used, which allowed simulations with different parameters to be run in parallel thus reducing the simulation run time significantly. All the data analysis was done using python and its associated libraries.

3.1 Prey-predator System

The model consisted of three agents -

- The Prey - Sheep
- The Predator - Wolves
- The Resource - Grass

A certain number of these two types of agents were allocated randomly (unless specified) in the patches. The environment was a mesh of 41 x 41 patches with the option of having a closed or open boundary or without resource (grass). The agents interacted with each other and with the environment through the behavioural rules. Multiple

sets of rules for movement, reproduction and death were made and are given in the following section. All the sheep and wolves were identical. Each agent had a variable associated with it which denoted its energy. Energy got used up when the agent moved and got added when it fed.

A basic model was available in the NetLogo models library (Wilensky 97) which was helpful to understand prey-predator systems, but the parameters that were taken into consideration varied and therefore the observed behaviours as well.

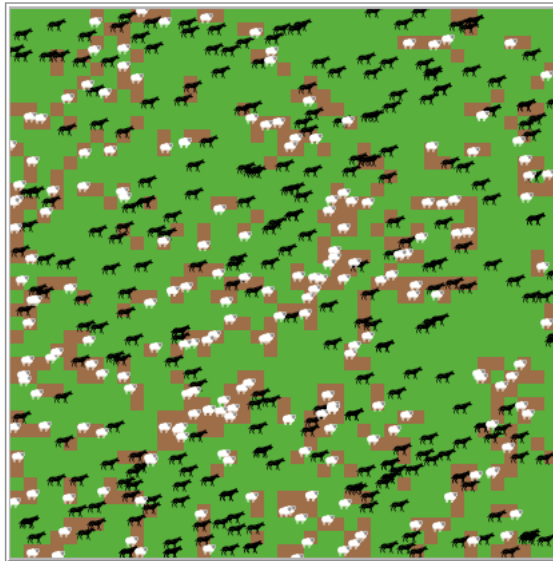


Figure 3.1: A typical description of the prey-predator agent-based model. Wolves are in black, sheep in white, the grass is green, and patches without grass are brown.

3.1.1 Parameters

The parameters in the model are given below. The effect of the parameters given in italics was studied by keeping the others constant.

- *Initial number of sheep (randomly allocated in the environment).*
- *Initial number of wolves (randomly allocated to the patches unoccupied by sheep).*
- *Grass regrowth time (time-steps taken by the grass to grow back once it has been eaten by the sheep).*
- Energy from sheep and Energy from grass.
- Wolf reproduction and Sheep reproduction rates.

According to the model, the population of the sheep depended on both grass and the population of wolves (predation), while the population of wolves depended only on the population of sheep.

Chain of Events

At each time-step,

- The Sheep ate the grass in its patch, increasing its energy.
- Wolf ate the sheep in its patch, increasing its energy.
- Both sheep and wolves reproduced.
- The wolves and sheep tried to move.
- Death condition was checked.
- Grass-regrowth condition was checked.

3.1.2 Behavioural Rules

The rules for interaction were made such that the maximum number of agents in a particular patch was limited to 2. This was done to avoid overcrowding and to stop the exponential increase of population when left unchecked.

Rules for Movement

- The Sheep moved randomly into an empty patch in its Moore neighbourhood (one of the eight immediate neighbouring patches).
- The Wolf moved randomly into a patch in its Moore neighbourhood which had no other wolf but could have a sheep.
- Each movement step consumed one unit of energy for both the sheep and the wolf.

Rules for Reproduction

- A variable number of sheep and wolves were chosen who did not share their patch with any other agent. This variable number depended on the sheep / wolf reproduction rate parameter. All the chosen ones, reproduced in that time step to give one offspring in the same patch.
- The energy of the parent sheep / wolf was distributed equally (halved) between itself and the offspring.

Rules for Death

- Sheep got killed due to predation by the wolves. Each wolf could eat one sheep in a particular time-step provided that the sheep was in the same patch as the wolf.
- If the energy parameter of one of the sheep or wolves was less than 1, then that particular sheep or wolf died.
- After reproduction, if one of the two agents in the same patch did not move out, the one with lower energy died.

3.2 Epidemiological Model

There were two epidemiological models built using ABM-

- SI Model (Susceptible - Infected)
- SIS Model (Susceptible - Infected - Susceptible)

Except for an additional parameter (susceptible time) in the case of SIS Model, both the models had a similar structure. The models consisted of three agents again -

- The Infected host (I)
- The Susceptible host (S)
- The Boundary walls (additions in the environment used in few simulations)

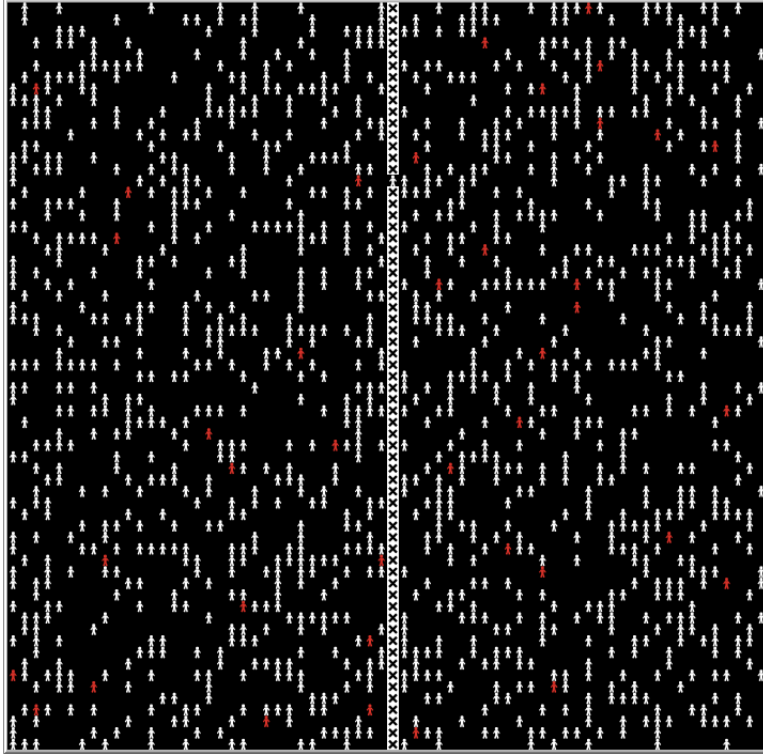


Figure 3.2: A description of the SI agent-based model with boundary. Susceptible hosts are in white, the infected ones are in red, and the black crosses on the white background in the middle is the boundary wall.

The environment was a mesh of 65 x 65 patches with the option of having a closed or open boundary. A certain number of S and I agents were initially allocated randomly to patches. This model did not support death or reproduction, so the total population was constant at all points in time.

3.2.1 Parameters

The effect of all the available parameters in the epidemiological model was studied. As mentioned above, the SIS model had an additional parameter (this is given in italics). The parameters were,

- Initial infected hosts - The number of infected hosts in the environment when the simulation started.
- Total population - The sum of infected and susceptible hosts in the environment.
- *Susceptible time* - *The time required by an infected host to change into a susceptible host again in the SIS model.*

3.2.2 Behavioural Rules

The rules for interaction had been made such that the maximum number of agents in a particular patch was again limited to 2. This was done to avoid overcrowding in a particular patch.

Rule for infection spread

A susceptible host got infected when he or she was in a patch with an infected host.

Rules for Movement

- The susceptible hosts moved randomly into an empty patch in its Moore neighbourhood.
- The infected hosts moved randomly into a patch in its Moore neighbourhood which had no other infected host but might have a susceptible host.

At each time-step,

- The susceptible hosts moved.
- The infected hosts moved.
- Infection got spread when an infected host interacted with a susceptible host.

Both the prey-predator and epidemiological models were studied for multiple parameters and the effect of these parameters on the behaviour was observed. Each realization of the models were simulated 50 times to study the effects of spatial variations in agent distributions. The results of the same are given in Chapters 4 and 5.

Chapter 4

Modelling prey-predator systems

The results of the agent-based model of prey-predator systems are given in the following sections.

4.1 Prey-Predator Model

The ratio of the number of predators to preys in the population was varied by keeping all the other parameters constant. This was then studied for different values of Grass Regrowth Time (GRT) to analyse the effect of resource availability on the dynamics of the system. The value of the parameters, other than GRT and initial population values, were as follows -

$$\begin{array}{l|l} \text{Wolf Reproduction} = 5\% & \text{Energy from Sheep (EFS)} = 10 \\ \text{Sheep Reproduction} = 5\% & \text{Energy from Grass (EFG)} = 10 \end{array}$$

4.1.1 Unlimited Resource for prey ($GRT = 0$)

For unlimited resources, the sheep could grow indefinitely unless predated by wolves. The ratio of the predator population to prey population was varied by keeping all the other parameters constant. All the simulations were carried out for 50,000 time-steps or till one of the species (sheep or wolf) got extinct. The plots summarising the 50 replicates (with different random distributions of sheep and wolves in the environment)

for each ratio are given in Figure 4.1.

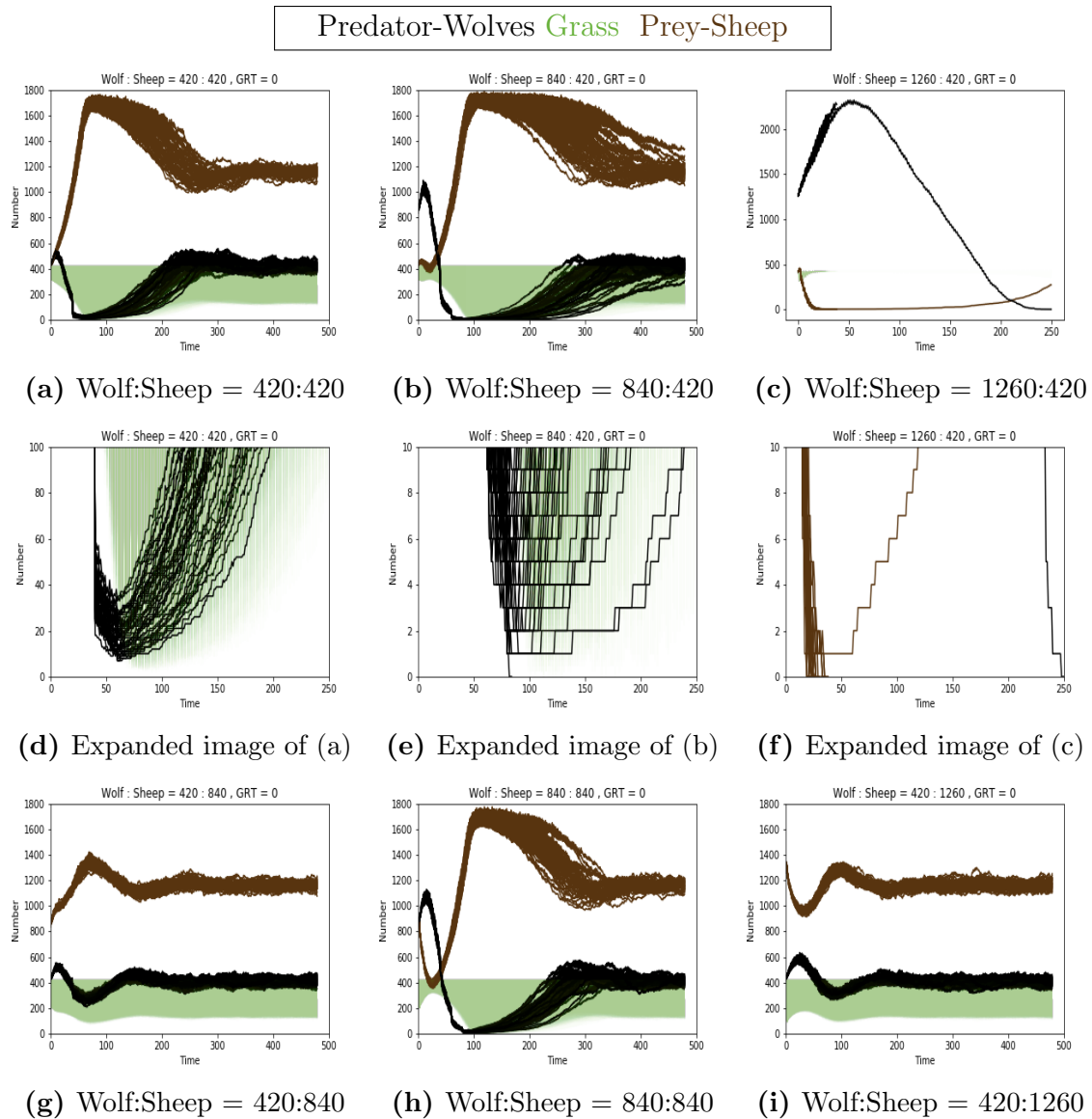


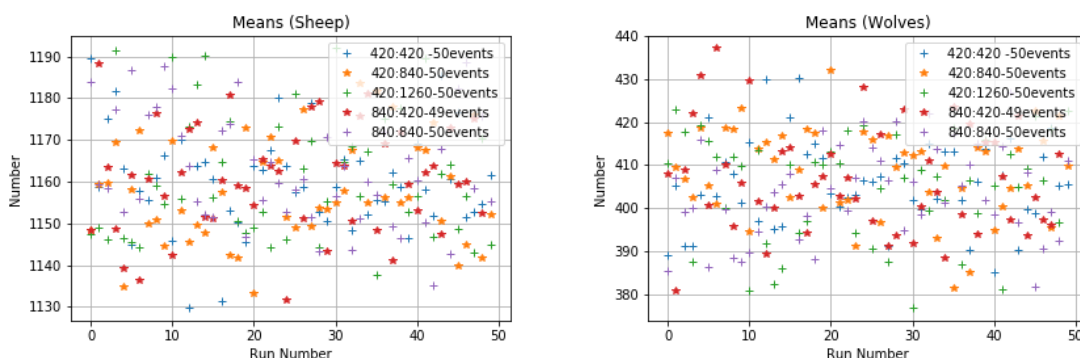
Figure 4.1: Plots for different ratios of initial number of Predator to prey (initial 500 time steps of the 50,000 time steps are shown) when $GRT = 0$.

When the GRT was set at 0, it was observed that in all the cases when the initial number of prey (sheep) population was higher or equal to that of the predator population (wolves) both the species coexisted (as can be seen in Figure 4.1(a), 4.1(g), 4.1(h) and 4.1(i)). It can be observed that the wolf population almost went into extinction (the dip in the plot) in Figure 4.1(a) and 4.1(h), but since the population of the prey shot up due to reduction in predators, the wolf population recovered even after reaching very low values due to the abundance of food, and hence both species co-existed.

In Figure 4.1(b), similar to Figure 4.1(a), the wolf population was on the verge of

extinction and in 1/50 simulations the wolf population went extinct.

Even though all the simulations resulted in extinction in Figure 4.1(c), the manner in which they went extinct showed some remarkable differences. The predator population kept going up even when the prey population dived down. In 49/50 simulations the prey population went extinct before 50 time-steps, but in one rare case i.e., in 1/50 simulations the prey population survived complete extinction; the prey population went down to the lowest value of 1 and then it successfully avoided predation just because of the spatial orientation of the prey. The rare event in this particular case was decided by the manner and the time taken by one of the species which became extinct.



(a) Distribution of means for the prey. (b) Distribution of means for the predator.

Figure 4.2: Plot showing the mean value of steady state (averaged over all the runs which lead to coexistence) when $GRT = 0$.

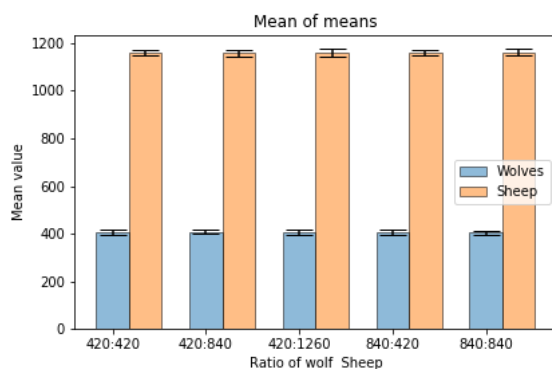


Figure 4.3: Bar plot showing the values of steady state averaged over 50 simulations when $GRT = 0$.

In Figure 4.1 we can see that whenever the system led to coexistence between the two species, it approached a steady state. This value was calculated for each run by

averaging the population number in the last 500 time steps and plotted in Figure 4.2. The number of events mentioned in the legend of Figure 4.2 denote the number of times that particular set of parameters led to coexistence.

From Figure 4.3 it can be seen that the steady state value whenever it existed, it remained the same for different ratios of initial population of predator to prey when the GRT is 0.

4.1.2 Limited Resources for prey ($GRT = 5$)

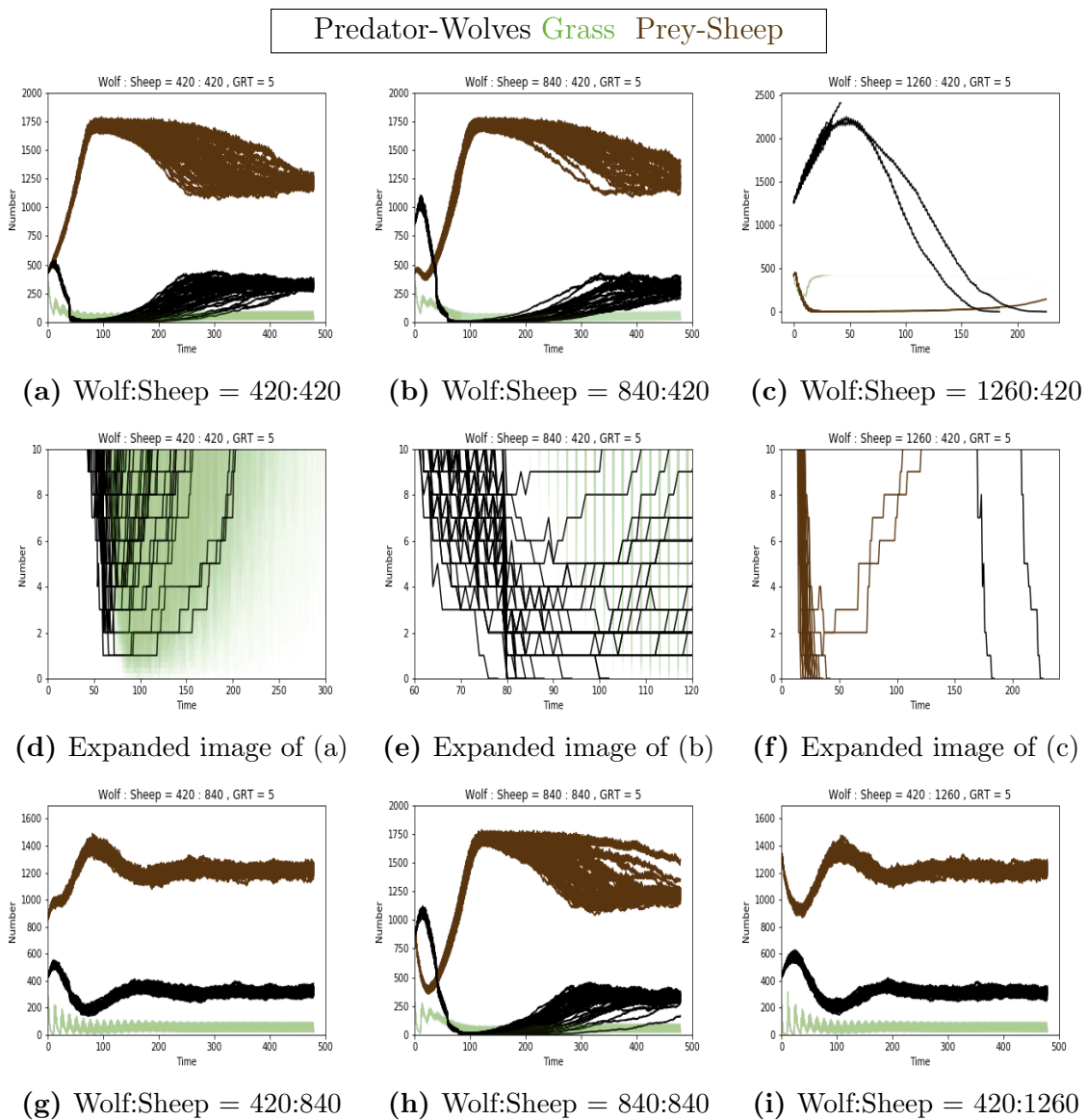
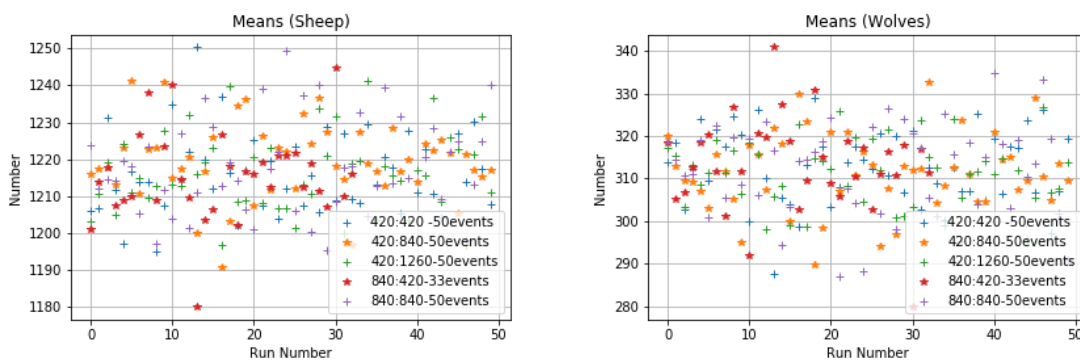


Figure 4.4: Plots for different ratios of initial number of Predator to Prey (initial 500 time steps of the 50,000 time steps are shown) when $GRT = 5$.

Similar to Section 4.1.1, the plots representing the population dynamics for different ratios of predator population to prey population when the grass regrowth time was kept at 5, are shown in Fig.4.4 below. All simulations were done for 50,000 time-steps or till one of the species (sheep or wolf) went extinct and were sampled 50 times.

Figure 4.4 (a) shows that even when GRT value is set at 5, both the species coexist just like the case in GRT 0 for the population ratio 420:420 (W:S). But in Figure 4.4 (b), the number of times the wolf population went extinct increased (17/50 runs the species went extinct when GRT is 5) from that of GRT 0.

In all the three remaining cases in Figure 4.4, ie, (g), (h), (i) both the species coexisted. Even though (h) went through a dip which was really close to zero, but the spatial orientation of the prey and the predator helped it to survive in each of the 50 runs.



(a) Distribution of means for the prey. (b) Distribution of means for the predator.

Figure 4.5: Plot showing the mean value of steady state (averaged over all the runs which lead to coexistence) when $GRT = 5$.

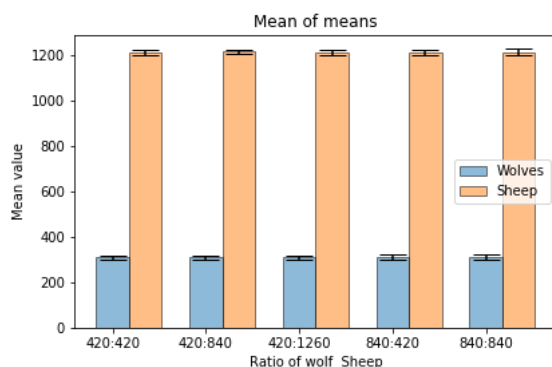


Figure 4.6: Bar plot showing the values of steady state averaged over 50 simulations when $GRT = 5$.

The steady state value was calculated for each run and this is shown in Figure 4.5.

This was then averaged over 50 samples for each set of parameters and they were plotted (see Figure 4.6) for both the sheep population and the wolf population.

As observed in the case of $GRT = 0$, the steady state value of sheep increased and the wolves decreased for $GRT=5$ when the ratio of population of wolf to sheep was changed.

4.1.3 Very limited Resources for prey ($GRT = 10$)

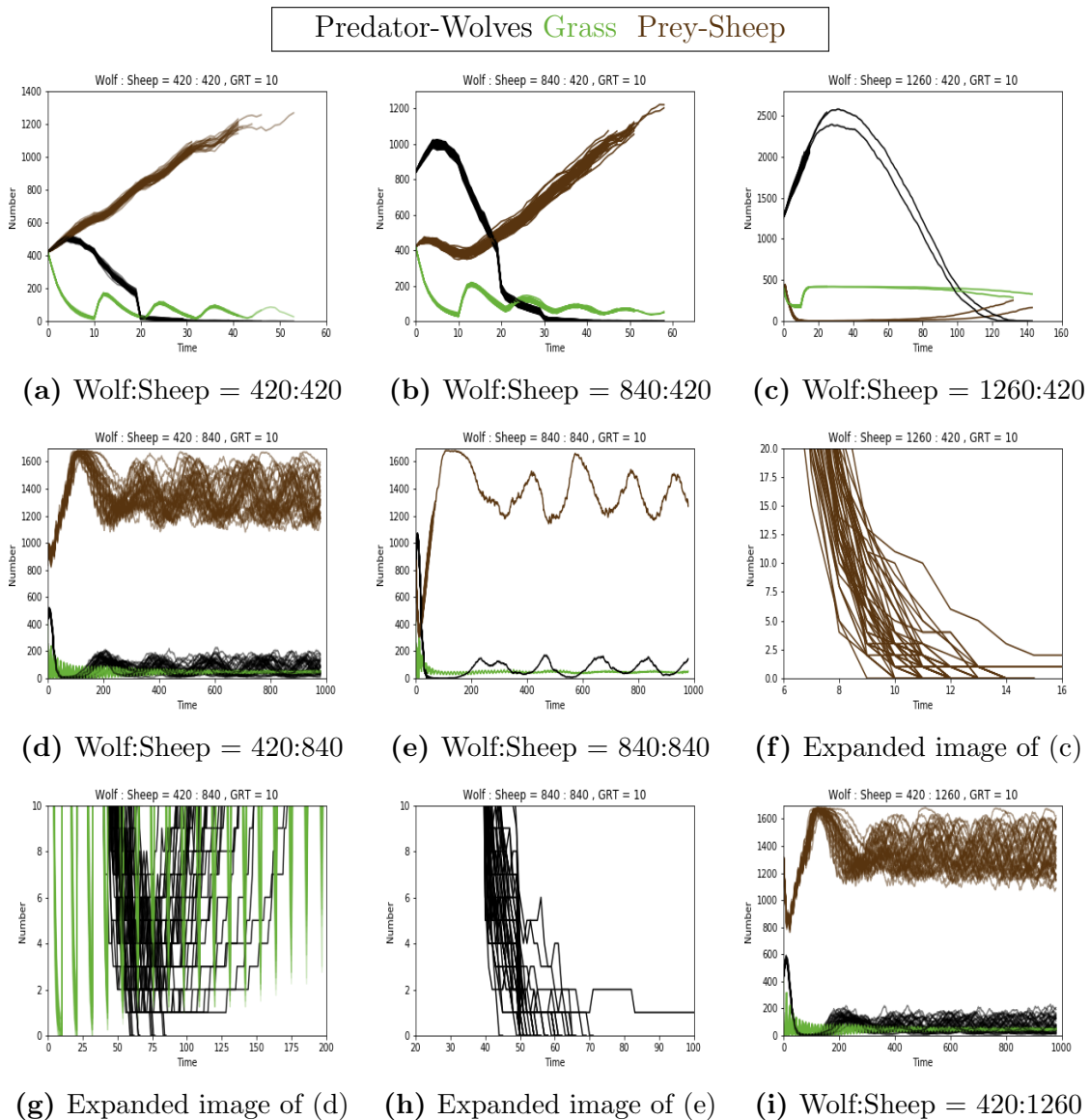
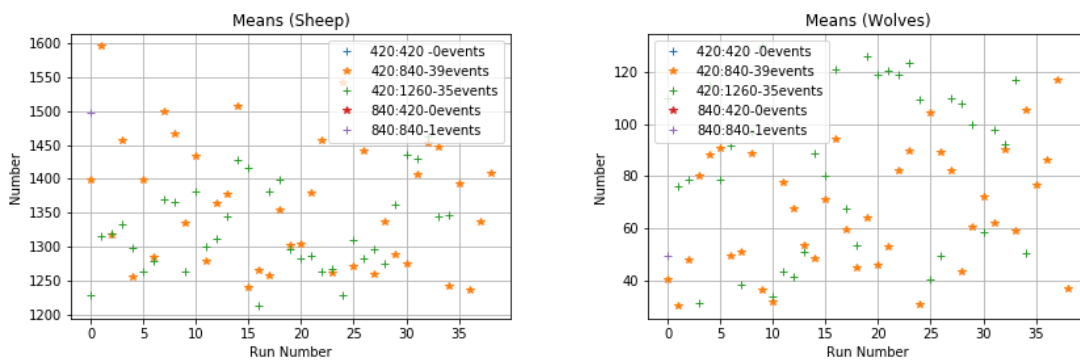


Figure 4.7: Plots for different ratios of initial number of Predator to prey (initial 500 time steps of the 50,000 time steps are shown) when $GRT = 10$.

Figure 4.7 shows the population dynamics (for all 50 samples) at different initial

population ratios of predator to prey when GRT was set at 10. It can be evidently seen that all the simulations except for (d), (e) and (i) led to extinction. In the cases where the simulation led to coexistence, oscillations were observed around a steady state value.

In Figure 4.7 (d), when the initial predator to prey population ratio was 420:840, the first case of oscillation can be seen. Out of 50 simulations, 39 resulted in oscillations and all the remaining runs resulted in extinction. In the case of predator to prey ratio of 420:1260 (Figure 4.7 (i)), it was 35 out of 50 simulations that resulted in oscillations while in the case of (e), that is for predator to prey ratio of 840:840 it was only in one run that oscillations were observed.



(a) Distribution of means for the prey. (b) Distribution of means for the predator.
(averaged over all the runs which lead to coexistence)

Figure 4.8: Plot showing the mean value of steady state when $GRT = 10$.

The steady state values were calculated by averaging over the last 1000 population values (from the 50,000 time steps) and these are shown in Figure 4.8.

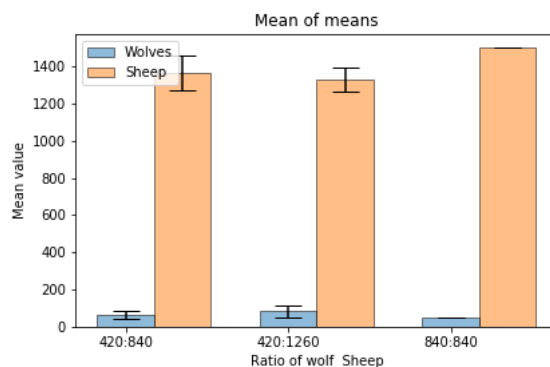


Figure 4.9: Bar plot showing the values of steady state averaged over 50 simulations when $GRT = 10$.

The variation of the steady state value over different population ratios is shown in Figure 4.9, it can be seen that the value of the steady state (when it exists) does not depend on the initial ratio of predator to prey population. Compared to $GRT=0$ and $GRT=5$, the steady state population sizes of sheep increased further and the number of wolves decreased.

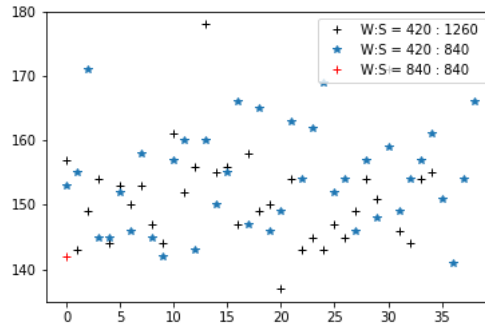


Figure 4.10: Period of oscillations.

The period of oscillation was calculated and it is shown in Figure 4.10, the values range from 137 to 178 for all initial population ratios (whenever it exists).

4.1.4 Limited Resources for prey ($GRT > 10$)

Grass Regrowth time was again increased and the simulations were run for GRT values 11, 12 and 15. For higher grass regrowth time, all the simulations resulted in immediate extinction as shown in Figure 4.11.

The route to extinction in this case showed variations in their dynamics. Depending on initial population sizes, either the wolves went extinct gradually first for not finding sheep in their neighbourhood (Figure 4.11 (a), (b), (d), (e), (f)) or increased continuously and then collapsed finally due to extinction of sheep (Figure 4.11(c)). The Prey population also showed interesting oscillatory dynamics of increase.

All the simulations for $GRT > 10$ resulted in similar extinction.

Predator-Wolves Grass Prey-Sheep

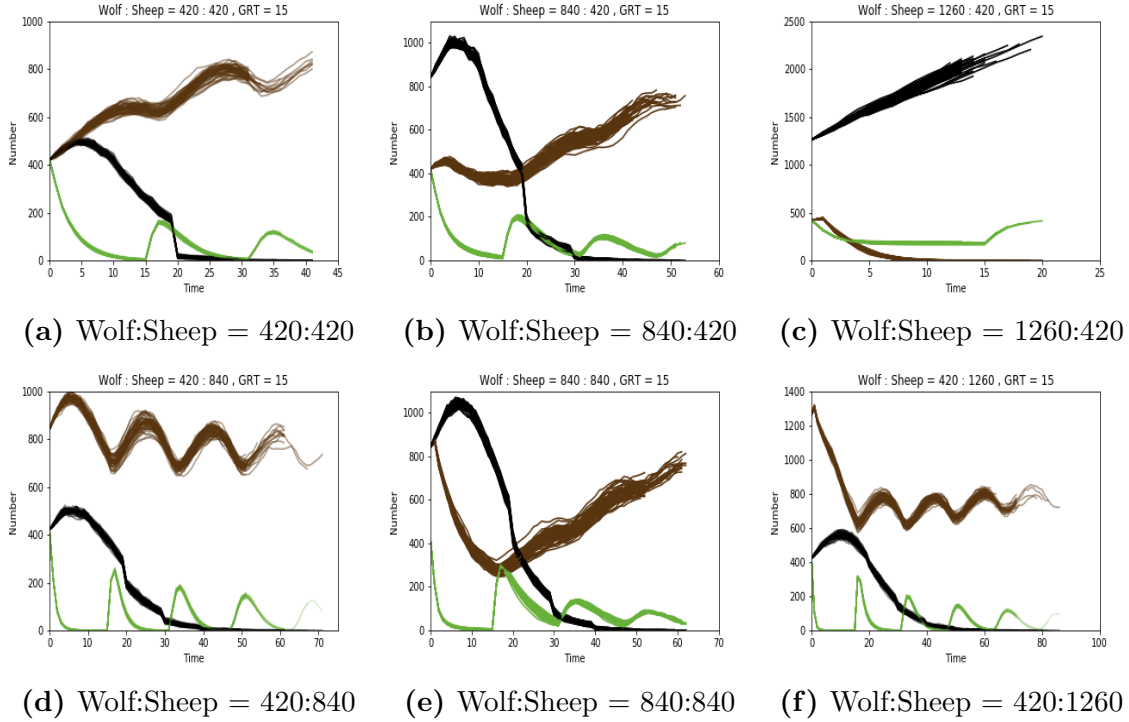


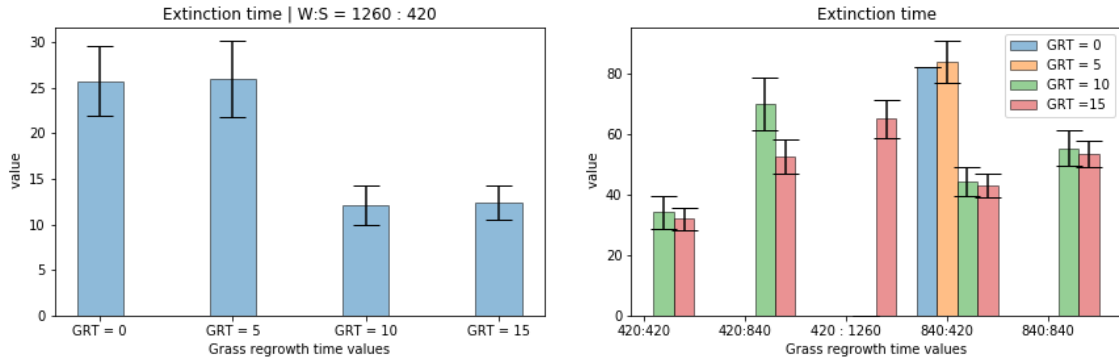
Figure 4.11: Plots for different ratios of initial number of Predator to prey (initial 500 time steps of the 50,000 time steps) are shown when $GRT = 15$.

4.1.5 Extinction

For all values of GRT , cases of extinction were seen, in a few cases the frequency of this happening was higher than in the others. The Figure 4.12 shows the distribution of the extinction times (the time taken by the species to go extinct).

Population Ratios	GRT 0	GRT 5	GRT 10	GRT 15
W:S = 420:420	All Coexist	All Coexist	All Extinct	All Extinct
W:S = 420:840	All Coexist	All Coexist	Extinct (11/50) Oscillations(39/50)	All Extinct
W:S = 420:1260	All Coexist	All Coexist	Extinct (15/50) Oscillations(35/50)	All Extinct
W:S = 840:840	All Coexist	All Coexist	Extinct (49/50) Oscillations(1/50)	All Extinct
W:S = 840:420	Extinct (1/50)	Extinct (17/50)	All Extinct	All Extinct
W:S = 1260:420	All Extinct	All Extinct	All Extinct	All Extinct

Table 4.1: Table summarising results from agent-based prey-predator model



(a) Case of sheep going extinct first

(b) Wolf going extinct first

(data for W:S ratio 420:1260 has been excluded)

Figure 4.12: Distribution of Extinction times.

Extinction times can be of two types - one in which the predator population (wolves) goes extinct first and the prey population may survive. The other in which the prey population (sheep) goes extinct and consequently the predator population also goes extinct due to unavailability of food. Figure 4.12 (a) corresponds to the sheep going extinct first while both (b) and (c) correspond to the wolves going extinct first.

Contrasting the standard range of extinction time of less than 90 time-steps seen in all the other cases there are three outliers in the case of GRT 10 making the range of extinction time as 0 to 47935. The data for W:S ratio of 420:1260 has been removed from Figure 4.12 for the same reason.

Chapter 5

Modelling the spread of infection

The results for SI ABM and SIS ABM are shown in the sections 5.1 and 5.2. The plots corresponding to the dynamics of the number of infected and susceptible hosts at various parameters have been shown. The models were studied and quantities like infection time (the time taken to infect the entire population) were calculated.

The dynamics of the system (S and I) was studied for different values of initial number of infected hosts (infected hosts = 1 , 5 , 10) to understand the effect of initial conditions on infection time. For each value of initial number of infected, simulations were done for total population values of 422 hosts, 1056 hosts, 2112 hosts, 3168 hosts and 4225 hosts (10%, 25%, 50%, 75% and 100% of maximum number of the available patches respectively). All the simulations were run 50,000 times and sampled 50 times for each set of parameters.

5.1 Agent-based SI Model

The SI ABM model followed a similar temporal trend to that of the differential equation model (2.2). The simulation resulted in all the hosts becoming infected for all parameter values since the SI ABM did not allow a change in the total population size of the system, only a change in the state of the host was possible (from susceptible to infected).

5.1.1 Initial number of infected = 1

Figure 5.1 shows the population dynamics of both the infected and the susceptible hosts when the initial infected number was kept at 1. It has to be noted that all the graphs in Figure 5.1 were normalised with the corresponding total population.

It was observed that the infection time decreased with increasing population and increasing patch occupancy in a bounded area. It can also be seen that the curve became sharper with increase in total population.

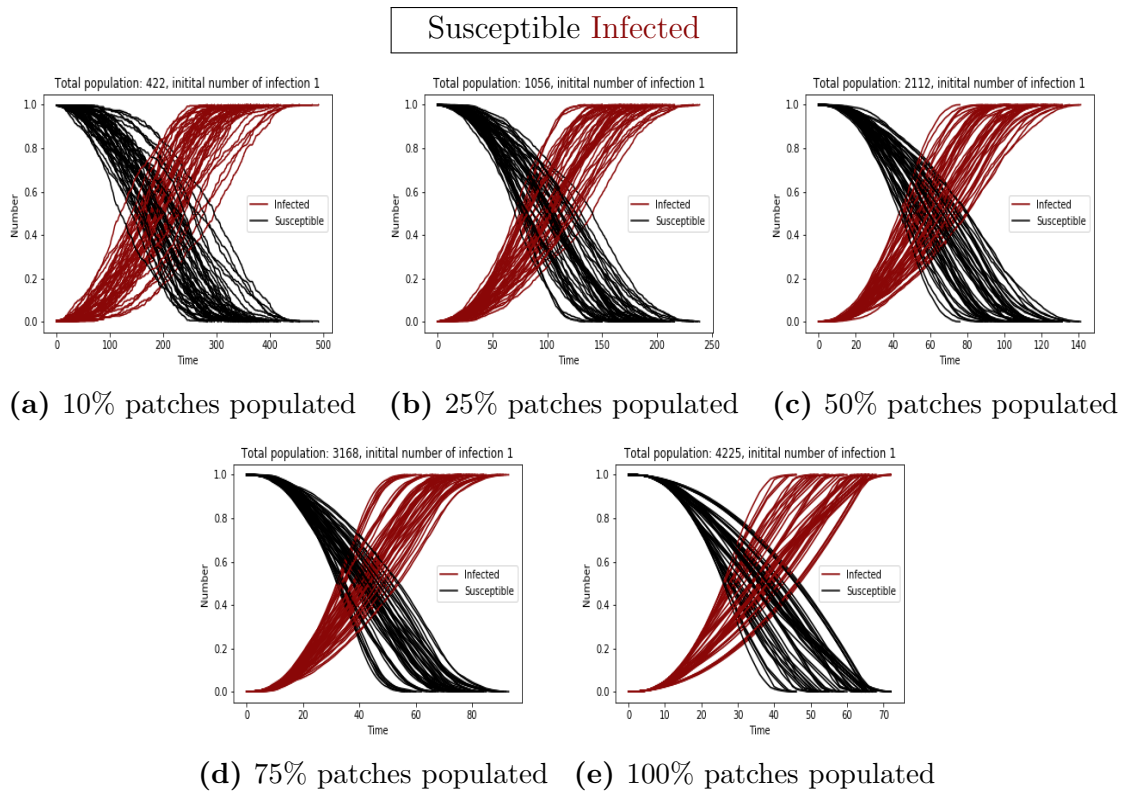


Figure 5.1: Temporal dynamics of the number of infected and susceptible hosts when initial infected population is 1.

5.1.2 Initial number of infected = 5

The population dynamics of S and I when the initial infected number of infected is 5 (Figure 5.2) was similar to that when compared to Figure 5.1 for initial infected host 1. These 5 infected hosts were distributed randomly in the environment. Again, all the plots were normalised with the total population size in the environment. Further, the infection time followed a similar pattern in which it decreased with increase in

population size when the total number of patches (the area enclosed) was constant.

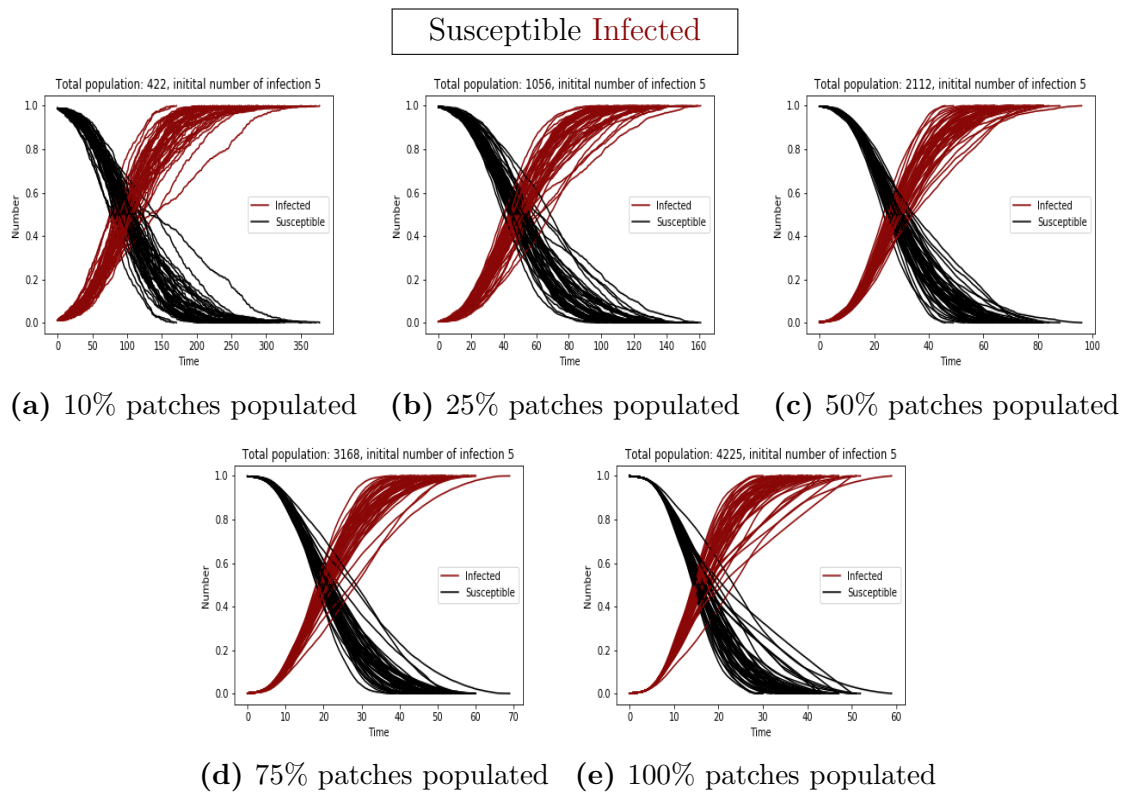


Figure 5.2: Temporal dynamics of the number of infected and susceptible hosts when initial infected population is 5.

5.1.3 Initial number of infected = 10

The case when number of initial infected hosts was 10 had the shortest infection time compared to the other two values given in the previous sections.

From Figures 5.1, 5.2 and 5.3 we can see that the spread and the value as such of infection time decreases with increase in population size and initial infected number, this has been summarised in Figure 5.4.

The decrease in infection time with increase in population can be explained by the fact that with an increase in the total population the probability of interaction increases and thus the chance of an infected host interacting with a susceptible host increases drastically. In the cases when the total population was 100% of the total number of patches available, in the initial steps, every patch had a host in it because of the model structure and this resulted in the population following a similar increase in infected hosts for all 50 runs which can be seen in Figure 5.1, 5.2 and in 5.3.

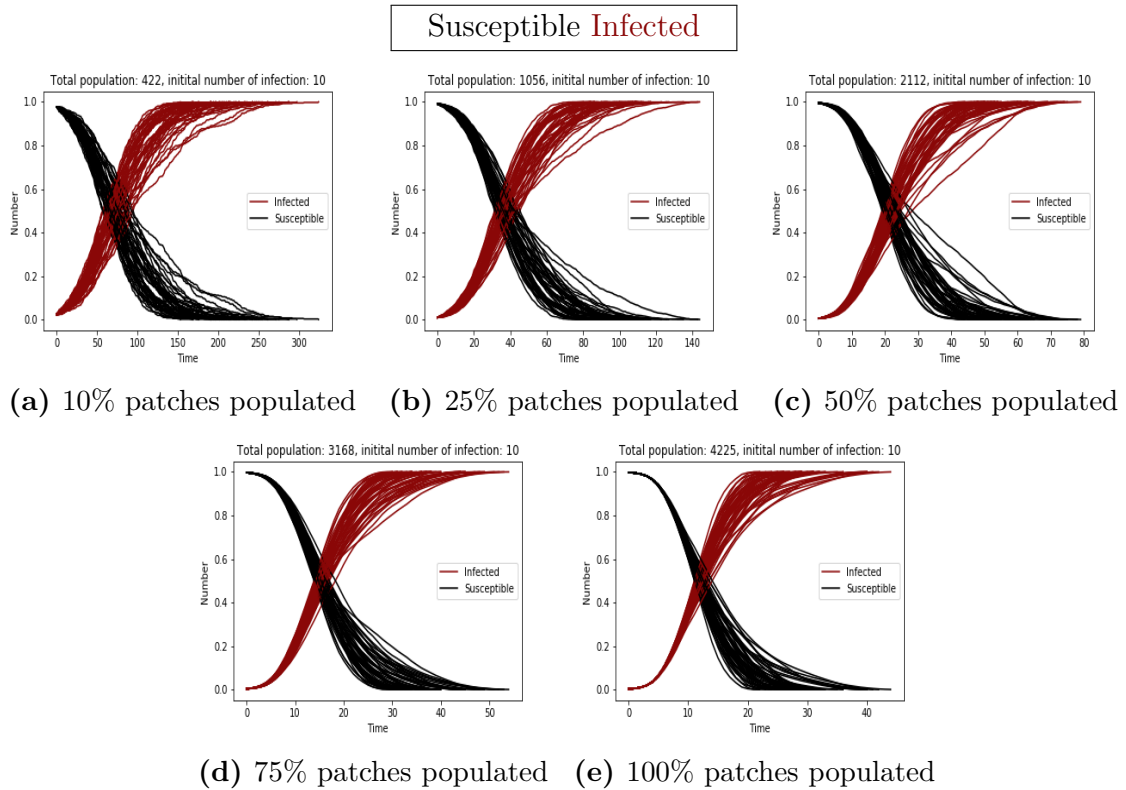


Figure 5.3: Dynamics of the number of infected and susceptible hosts when initial infected population is 10.

The difference in the rate of increase of the infected curve (the slope) for different initial infected (I) values can be explained by the simple fact that an increase in initial infected will lead to multiple centres for the spread of infection as all of the initial hosts are randomly distributed.

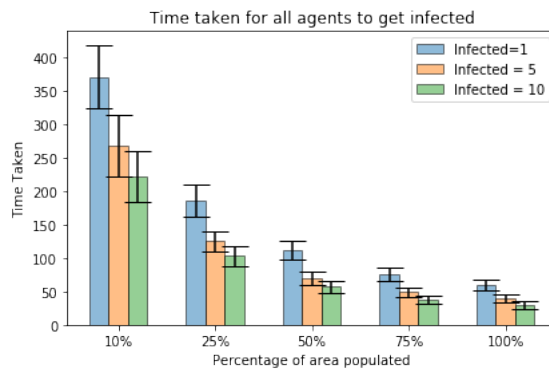


Figure 5.4: Distribution of Infection Time

Even though there was a decrease in the value of infection time with an increase in the value of initial infected, it was not linear. This is also seen in the differential equation models where the increase in I is not linear with time.

5.1.4 Infection spreading patterns- localised release of infected host.

The pattern in which infection spreads spatially has been given in the Figures 5.5, 5.6 and 5.7. Three different cases for three different population sizes can be seen below corresponding to the initial infected host being in one of the corners of the environment, the center of the confined environment, and center of one of the edges.

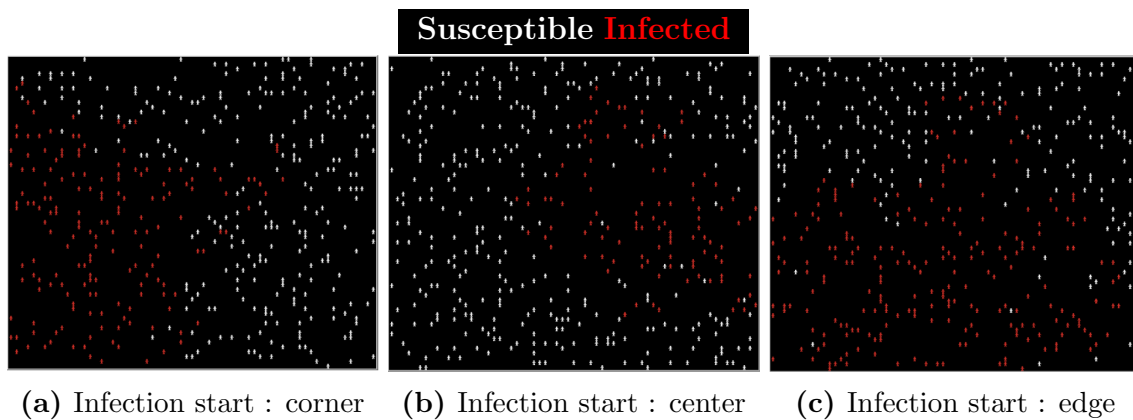


Figure 5.5: 10% of the total patches are populated at the beginning.

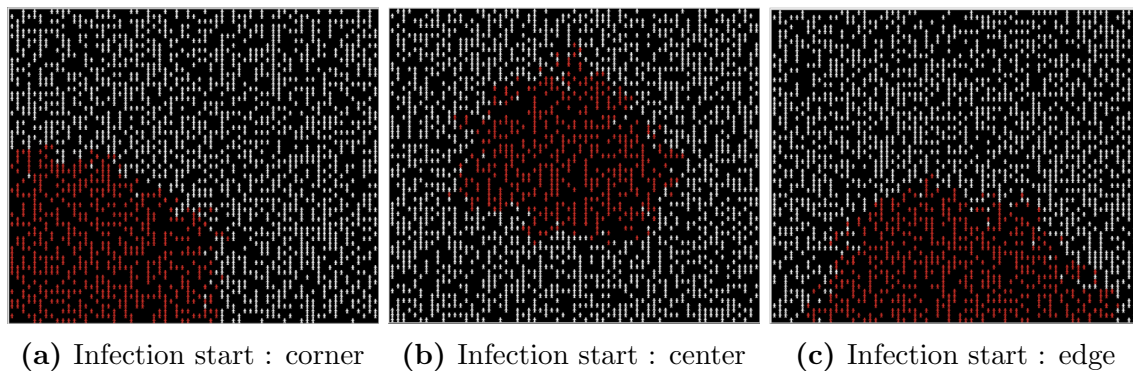


Figure 5.6: 50% of the total patches are populated at the beginning.

It is clear that infection spread is quite unpredictable when the population size is small, and it can reach far in space depending on interactions with the susceptibles. Spread is clearly localised in fronts when population size is large. This can have implications employing measures to control spread of infection in spatially distributed populations.

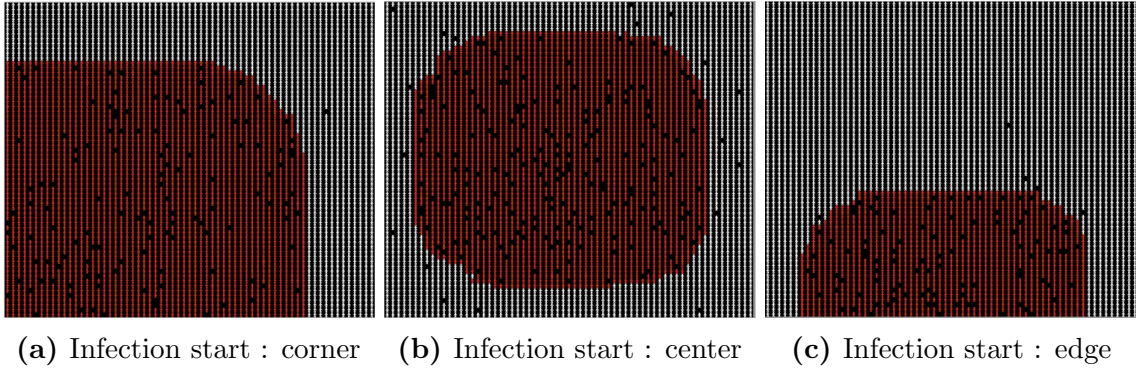


Figure 5.7: 100% of the total patches are populated at the beginning.

5.1.5 Effect of boundaries on pattern of infection spread

The model environment was slightly modified to study the effect of a boundary wall (centered horizontally in the environment) with a slit on infection time (Figure 3.2). Again, multiple population sizes were studied for three different cases,

- Slit positioned at the center of the boundary wall.
- Slit positioned at the edge of the boundary wall
- Slit positioned in between the center and the edge of the boundary wall.

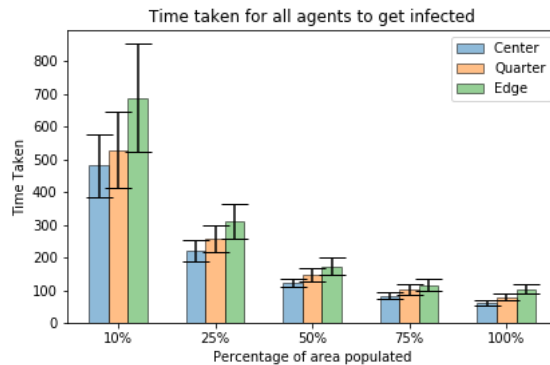


Figure 5.8: Distribution of Infection Time

The observation that the infection time decreased with increase in population size when the environment was confined, stands true even when the environment had a boundary wall in the middle. Among the three cases studied, the average infection time was maximum when the slit was at the edge and minimum when it was at the center. This might be due to the fact that the average maximum distance an infected host has to travel to move from the left section of the environment to the

right was more in the case when the slit is at the edge. When the patch occupancy was high, the effect of the position of the slit was statistically insignificant. Interestingly, comparing the time taken for infection spread in Figure 5.4 and Figure 5.8 shows that the boundary wall certainly delayed the spread to the whole population.

5.2 SIS Model - An ABM approach

Many diseases allow clearing of infection and the host goes back to the Susceptible state again to be re-infected. To incorporate the transition from Infected state to Susceptible state for a host, a parameter called *susceptible time* (Time required by an infected host to go into susceptible state) was introduced. The dynamics of the system was studied for different values of susceptible time (10,15 and 20) when the initial infected (I) was kept at 1.

The SIS ABM mainly showed three kinds of behaviours depending on the total population size and the extent of patch occupancy,

- Both the number of Infected and Susceptible hosts coexisting.
- The infection dying out.
- Infection dying out in a few cases and in the remaining cases it coexists.

Note: All the population dynamics plots have been normalised with the corresponding total population sizes.

5.2.1 Susceptible time = 10

Figure 5.9 (a) shows the case when the infection died out completely. Since the population was really low, the probability of interaction was less, and the susceptible time of 10 was too less for the infection to prevail. Figure 5.9 (b) shows the case when the infection persisted upto 50,000 time-steps in most cases (42/50 times) and in the remaining runs (8/50) it died out (Figure 5.9 (e)). Figure 5.9 (d) and (f) represent the cases when both S and I host populations coexisted always with the population

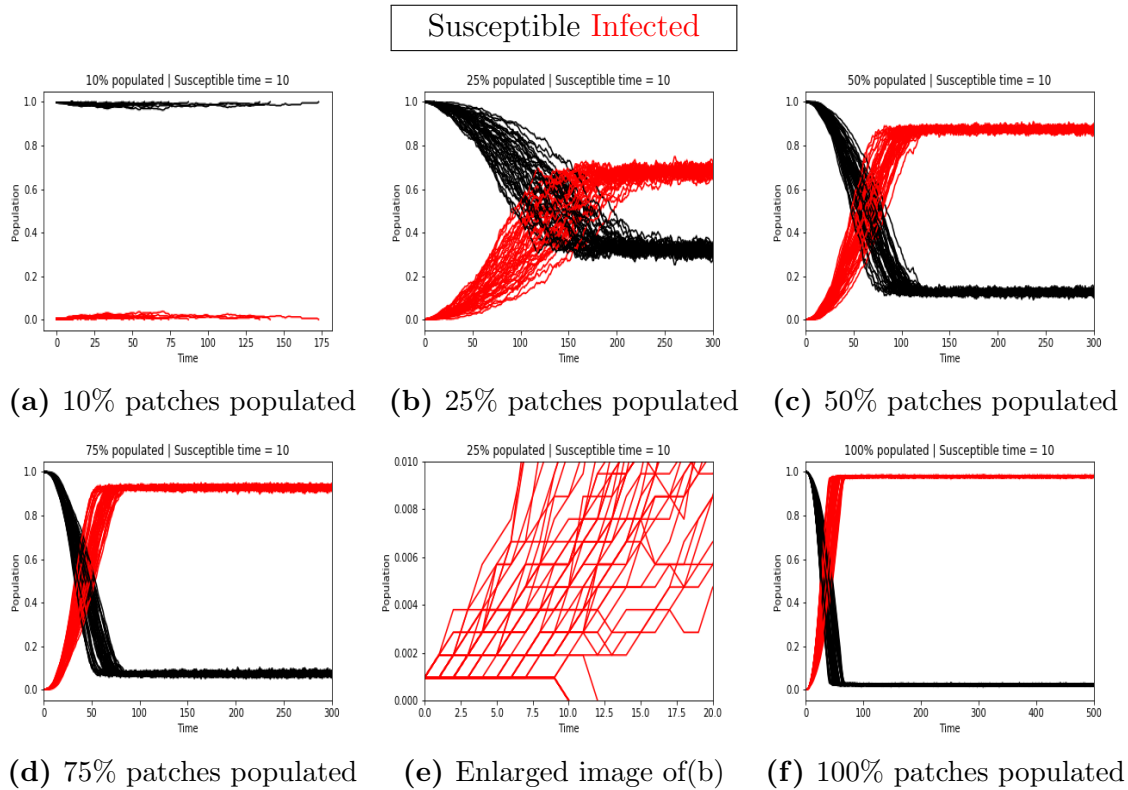


Figure 5.9: SIS Model-Dynamics of the number of infected and susceptible hosts when susceptible time is 10.

of I being high. The results also showed that for infection to be contained at a low amount, patch occupancy needs to be low.

5.2.2 Susceptible time = 15

Figure 5.10 shows the dynamics in the case of susceptible time 15. Figure 5.10 (a) represents the case when the total population size is equivalent to 10% of the total number of patches, here 33/50 times the I populations went extinct. The steady state values of the susceptible hosts and infected were close. 5.10 (d) is an enlarged image of 5.10 (a) plotted for longer time. It can be noticed that there were cases when infection died out at 47804th time step also. Such rare events can only be seen through the agent based modelling approach.

In the case when the total population is equal to 25% of the total number of patches, the infection died out only 3 out of 50 runs. In all other cases, the infection persisted till 50,000 time-steps and was stable in dynamics.

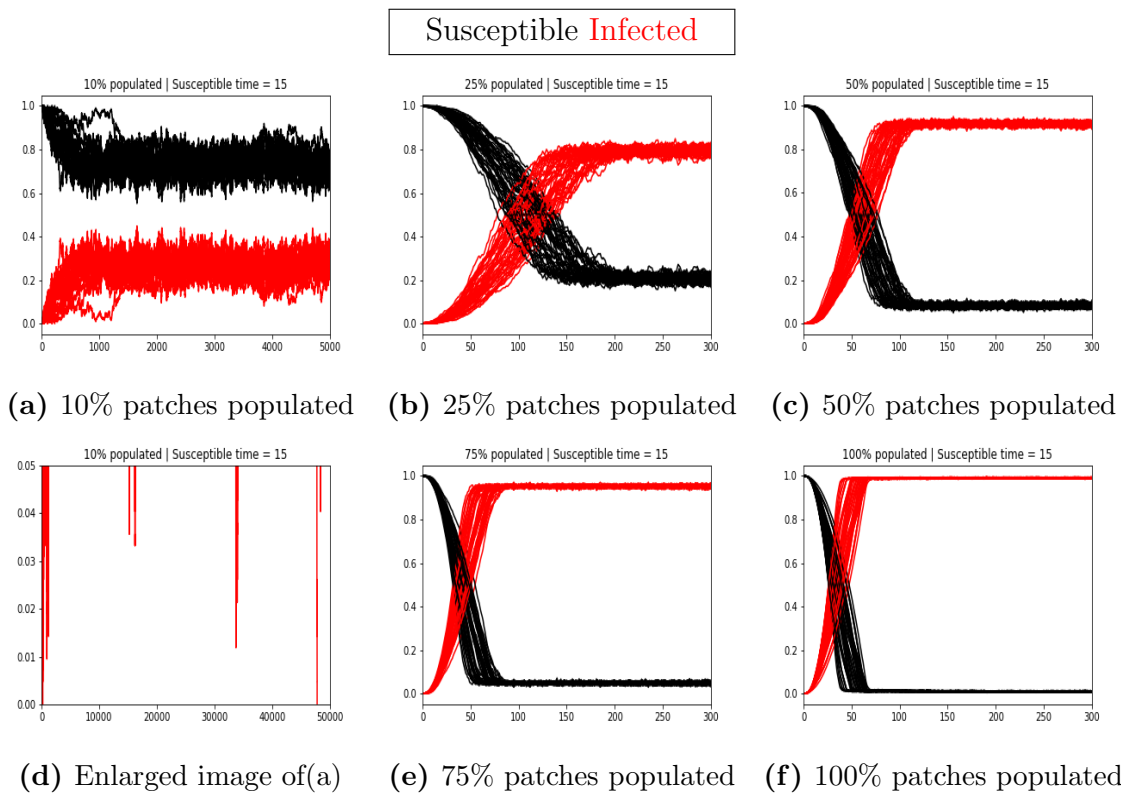


Figure 5.10: SIS Model-Dynamics of the number of infected and susceptible hosts when susceptible time is 15.

5.2.3 Susceptible time = 20

In Figure 5.11 (a) it was noticed that the steady state values (whenever it exists) for both the susceptible hosts curve and that of infected hosts overlapped with each other. In this case, 30 out of 50 simulations resulted in the infection dying out in the initial few time-steps. Infection persisted in all the other cases.

From the Figures 5.9, 5.10 and 5.11 it can be seen that the rate of infection increased with increase in population. This is again because of the increase in the probability of interaction between an infected host and a susceptible host.

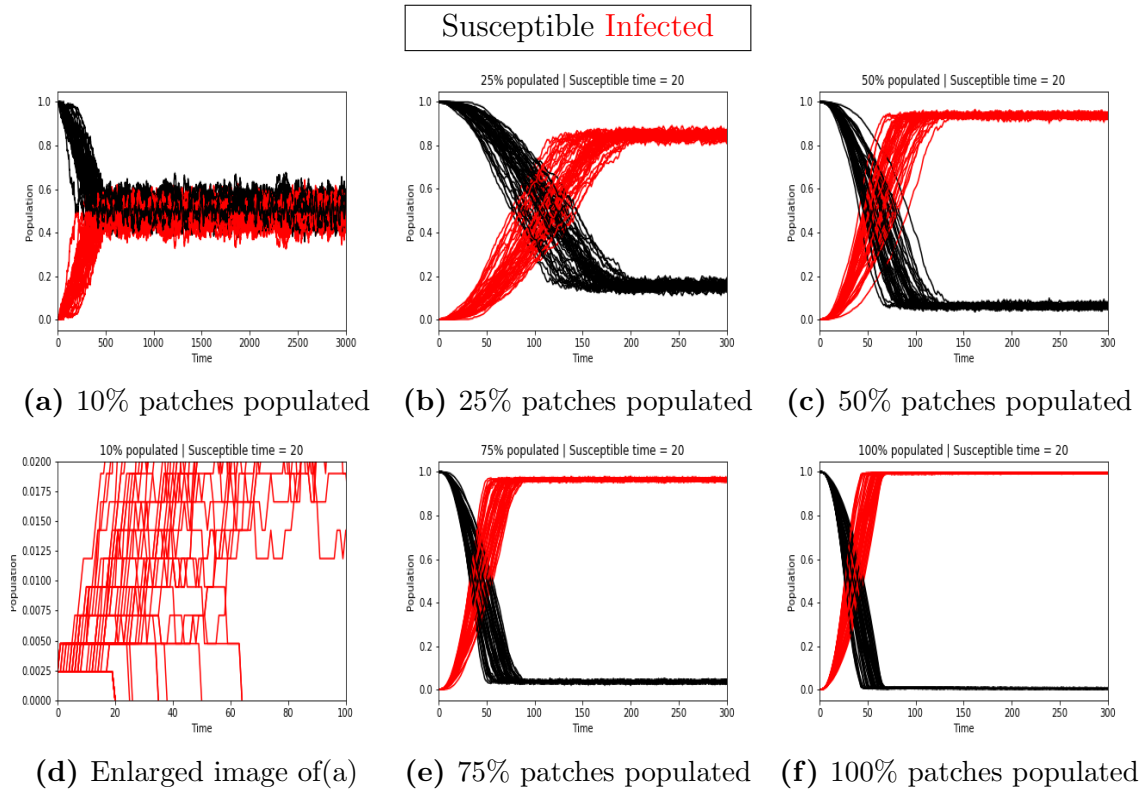


Figure 5.11: SIS Model-Dynamics of the number of infected and susceptible hosts when susceptible time is 20.

Steady State Analysis

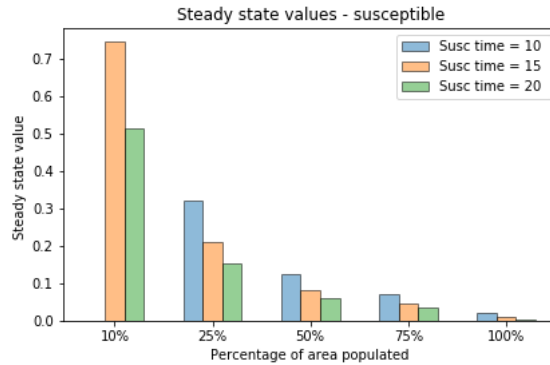


Figure 5.12: Average Steady State values for susceptible host population (SIS model)

Figure 5.12 shows the average steady state values of the susceptible host population whenever it existed for different total population values for multiple susceptible times. The data has been normalised with the corresponding total population size. The normalised steady state value decreases with increase in crowding (increase in population size) and increase in susceptible time.

Chapter 6

Summary and Future directions

6.1 Summary

The agent-based modelling approach for studying collective behaviour is known to be closer to real life systems than the averaged approach of ordinary differential equation (ODE) models, as in ABM each individual's interaction with their neighbours is considered. It also allows heterogeneity in individuals to be modelled easily. In this thesis, I have taken two examples from Ecology and Epidemiology to compare and contrast the two types of modelling approaches. The situations are not exactly the same as in differential equation models spatial distribution of individuals is not accounted for. In ABM, on the other hand, spatial distribution plays a major role in implementing the interaction rules. This allows different dynamical outcomes in ABM even when all other parameters are kept constant. Such initial condition-dependent behaviour is not normally observed in ODEs.

In the Ecological example, the prey-predator interaction has been studied for many variations in the proportions of their initial population sizes, resource availability for the prey, etc. The results are interesting as in many cases both survival and extinction of populations were found even when all the parameters were kept constant. The periodic variability in resource availability (grass regrowth time GRT) is more realistic as food availability changes in nature with seasons, rather than constant carrying capacity. The populations showed stable co-existence of both species, oscillations in

populations, and extinction in the ABM model.

For ABMs in epidemiology, the SI model showed that the time for infection decreases with increasing population size and initial number of infected hosts. The SIS model showed different types of persistence behaviour - the infection dying out and coexistence. The importance of the initial population sizes and the time required by an infected host to return to susceptible state again (Susceptibility period) was shown to have an important influence on the persistence of infection in populations.

6.2 Future Directions

This preliminary study opens up many directions of investigations in both ecological and epidemiological problems. An important direction is to investigate the role of structured environment in population/infection spread. These have important biological underpinnings. For example, to understand the effect of "refuges" in prey population survival have implications in biodiversity and conservation studies. It will be interesting to study a real ecological problem where yearly resource variation data is available from the field and ABM results can be matched with prey species populations.

The spatial structures like boundaries with different porosity can indicate ways to contain the infection in cities. The time taken for percolation of information (infection here) can be vastly increased with planned spatial structures modelled using ABMs. Different diseases have different epidemiological groups. The SIR (susceptible - infected - recovered) and SIRS (susceptible - infected - recovered - susceptible with varying degrees of immunity) models need to be studied using the agent-based modelling technique.

Such structured environment AB modelling can be also used for effective distribution of crowds in events such as football fields, melas, temples, etc.

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