

Agent-based Simulation of Ant Foraging Behaviour With Two Pheromones

Patrick Ellis

Chapter 1

Abstract

Agent-based modelling is a method to study emergent behaviours occurring in natural systems on an individual level. One natural system which is often studied is stigmatic communication of food locations between ants.

In this article, we investigate the foraging behaviour of ants using an agent-based simulation model with a stochastic and deterministic components of ant movement. The motion of ants is derived from the concentration of two types of pheromone deposited in the environment when the ants are seeking food or returning to the nest. The proposed model and simulation results demonstrate ants' ability to form effective pathways to and from food sources of various sizes and different distances from their nest.

Simulation results show that the effectiveness of ants forming a pheromone trail is greatly influenced by the distance between the nest and the food sources.

Chapter 2

Introduction and Background

2.1 Introduction

A stochastic agent-based model of pheromone-based ant foraging has been developed and investigated in Malíčková and Yates [10] in which communication between ants in the model is mediated through changes to the environment by the deposition of two attractive pheromones. Each pheromone has a different role as indicated in figure 1. As ants search for food they deposit pheromone A and follow trails of pheromone B. Ants searching for the nest deposit pheromone B and follow pheromone A.

In a similar vein, a model proposed in Panait and Luke [11] also implements a two-pheromone model however instead of continuous space employs a nontoroidal grid world. From any given square ants may move to any eight-neighbour square which is not overpopulated or obstructed (see fig. 2). This state-based model allows ants to propagate across the state space by at each time step choosing one of the surrounding squares to move to with a probability linked to the concentration of pheromone present on the square. Several evolutionary computation algorithms have been applied to such problem spaces to learn exploration/exploitation strategies using pheromones deposited via hardcoded mechanisms. For example, in Sauter et al. [13, 14] evolutionary computation is used to tune an agent policy within an application involving several digital pheromones. Similar approaches are applied in T. White [17] with regards to network routing.

There have been drastically fewer attempts to mimic the pheromone-depositing procedure itself; the most notable attempt is that of AntFarm, a system that combines pheromone communication and evolutionary computation. Antfarm, however, only makes use of one pheromone to mark trails – and rather than implementing a second, ants use a compass to direct themselves along the shortest path back to the nest.

Perhaps the most intriguing results of such models are those that demonstrate the ability of ants to react dynamically to drastic environmental changes. Work by Resnick Resnick et al. [12] expresses how ants are able to ‘forget’ previously discovered food sources once they are depleted and construct paths towards new ones. Many of the drawbacks to these models lie in their mono-pheromone model with the addition of some path tracking compass or alternative method for nest searching. As such it is clear that much of previous work has been ad-hoc, assuming a single ant pheromone to set up a gradient towards food sources with a high pheromone concentration to help guide ants towards it. However, such methods rely

upon an artificial solution for the movement patterns of ants after discovering food. This assumption is either stated explicitly or it is true implicitly through examination of the proposed techniques.

One model in which foragers do not display ad-hoc methods for nest searching movement is presented in Vaughan et al. [18]. Vaughan et al put forward agent behaviours that employ directed pheromones (pheromones indicating a specific direction), and produce high performing foraging simulations as well as real world robot foraging. Though impressive, this model could be improved – assuming agents are capable of depositing pheromones throughout the entire environment regardless of their location and distance from the deposition site.

Our proposed model bears much similarity to one of the few that does not follow this pattern in inaccurate previous work, a model discussed in Malíčková and Yates [10], making use of two pheromones in order to establish a gradient from the nest and from food allowing efficient travel between them over time. We have added our own diffusion model and environmental setups to investigate the results ourselves and expand upon them.

2.2 Background

Colonies of ants are capable of carrying out high level tasks almost entirely through indirect communication. Such behaviour gives rise to many emergent behaviours and cooperative functions across large numbers of individuals. Investigation into such biologically inspired behaviours in order to draw parallels to other fields is known as biomimicry. One such example is the solving of optimisation problems using ant models via ‘ant colony optimisation algorithms’ (ACO) Doerr [5], Dorigo [6].

There is a high degree of variation between both ant species and members of a colony with regards to anatomy and performance. For example, some species may rely on their sense of sight as a primary navigation tool; however, many species make use of the deposition and detection of pheromones as a means for colony-wide intercommunication Jackson and Ratnieks [9], Steck [16].

There are examples of species within this group that make use of several such pheromones with each differing in their purpose and physical properties, such as viscosity, which serves as an ant’s main form of pheromone identification Dussutour et al. [8], Sherman and Visscher [15]. The presence of at least two pheromones, one exploratory and one to guide ants back to the colony having retrieved food, are necessary for the system to function.

The use of pheromones allows the colony to more hastily mobilise its foragers when food is discovered Beekman et al. [1] and is especially beneficial when food sources are scarcely present Dornhaus [7], Sherman and Visscher [15], or when they are too large to be gathered by a single worker Detrain and Deneubourg [4].

Chapter 3

Methodology

3.1 Model Description

This section follows the ODD protocol for descriptors of agent-based models described in Volker Grimm [19].

3.1.1 Purpose

This model demonstrates the pheromone trail forming process within a single colony of ants to and from food sources located within close vicinity to the ant nest. It also serves as a tool to demonstrate the innate ability of ants to deconstruct paths to food sources which are no longer present and construct new ones to recently discovered food sources.

3.1.2 Entities, state variables, and scales

The model consists of one type of agent: ants. Individuals are characterised by their state variables; velocity, position, current activity, direction of motion, antennae length and ant length. A complete list is presented in table 1 below. In this model, these agents exist in a finite world space which consists of their home colony and food sources. The world is simply a flat 2D plane of land, with no variation in height. Modelling in 3D space would lead to a significant increase in computational complexity whilst not giving us better insight into the effects of pheromones on foraging trails.

See the table on the following page for a comprehensive list of parameter values and descriptions.

<i>PARAMETER</i>	<i>VALUE</i>	<i>REFERENCE</i>	<i>DESCRIPTION</i>
ANT VARIABLES			
Velocity	8.0	5-13mm/s[2]	Model utilises a constant movement speed
Antennae angle	$\pm \pi/6$	$\pm \pi/6$ [3]	Angle
Antennae length	0.7	1/3 body length	Length of antennae, required in order to know the exact point at which to test pheromone perception
Body length	2.1	2-15mm[2]	Body length of an ant
MOVEMENT VARIABLES			
Angle of random motion	$\pm 0-15\text{deg}$	Obtained experimentally	Random directional change at each iteration
PEROMONE VARIABLES			
D_A, D_B	1,5	mm^2/s	Diffusion constants for pheromone A and B
δ_A, δ_B	50, 100	s	Pheromone decay rates
m	0.01	g	Quantity of pheromone deposited
Ta, Tb	80, 80	s	How long is a pheromone deposited for
SIMULATION NUMERICS			
Number of ants (N)	200	-	Number of agents in the system
$[X_N, Y_N]$	variable	-	Nest position
$[X_F, Y_F]$	variable	-	Food position
S_S	0.5	-	Step size, 1 iteration = 0.5 seconds
Niterations	1200	-	Length of each simulation in iterations
S_C	1	mm^2/s	Size of each grid square in our model
Simulation size	200x300	mm^2/s	Total size of our model

3.1.3 Process overview and scheduling

Timesteps are evaluated at discrete 0.5 second increments. As pheromone trails are formed and deconstructed over minutes, this step size is a suitable choice in order to fully evaluate the process in sufficient detail.

At each time step t , each agent performs the following sequence of actions:

1. Evaluate pheromone concentration at the point at the tip of the left antenna and right antennae independently and compare.
2. Alter course of motion accordingly.
3. Derive new position coordinates.
4. Check if the new position is reachable in the model space, if not then alter direction vector by $\pm(1-20)$ degrees and repeat from step 1.
5. Update position vector.

3.1.4 Design concepts

Basic principles

Only surface level characteristics have been programmed, as noted in table 1 above, and much of the produced behaviour is therefore emergent. Equation 1 below derives a new movement vector at each time step:

$$\omega_{n+1}^i = \omega_n^i + f(c) + \sigma(c)\xi_n^i$$

Where w_n^i represents a direction value between 0 and 2π in the n th step of the i th ant.

Emergence

For this particular set of tests, emergence and fitness can largely be combined into one category. Fitness is an implicit characteristic of our model and is evident in our model results. For an ant colony model such as this one, fitness refers to the eventual formation of a ‘shortest trail’ between the colony and a food source. This behaviour is not pre-programmed, but rather a naturally developing characteristic of the model. As time passes ants innately begin to strengthen those trails which are stronger and ignore less efficient trails which eventually decay. Only one characteristic is modelled explicitly which is the ability of ants to be able to sense a food source from within a close proximity. This formation of the shortest trail is a clear example of emergent behaviour. Additional points of interest with regards to emergent behaviour is the presence of oscillating behaviour in many ants around areas of high pheromone concentration. This point is discussed further in the submodel section.

Adaptation

With regards to the equation above, the key source of adaptation in this model is the ability of the ants to respond to changes in pheromone concentration in their surrounding environment. When the perceived pheromone concentration is large, the component $f(c)$ takes a value of $\pm \pi/6$. This angles the ant towards the direction of highest pheromone concentration, in itself producing an emergent oscillating behaviour, as ants will constantly move off and back onto the path of highest concentration (a pheromone trail) as they overshoot their mark and adjust their bearing accordingly. This behaviour is well documented and a known trait of pheromone trail marking ants.

Sensing

Agents obtain information on the activity of other agents in the system as well as their environment entirely through evaluating the pheromone levels on their immediate left and right. Ants are not given any knowledge other than this with the exception of being able to sense when they are within one iterations travel range of the nest or food.

Interaction

Ants interact with each other only indirectly by each depositing pheromone A or B at a given time step. No other knowledge is passed from ant to ant as this would be a form of explicit communication and would undermine the validity of ‘emergent’ results.

Stochasticity

In the angular update equation, $\sigma(c)\xi_n^i$ represents angular noise whose magnitude varies with the perceived pheromone concentration. If the pheromone concentration is large, this random component of movement is significantly reduced. This stochastic nature of ant movement is vital to the behaviour of the colony as a whole, allowing for environmental exploration.

We demonstrate this by testing with multiple food sources in the local surroundings.

Observation

Different forms of data are extracted from the model to be evaluated. Key statistics we deemed relevant include the population of foraging and nest seeking ants at each time step, total quantity of food gathered from each simulation, and a visual plot of pheromone A and pheromone B distribution against time.

3.1.5 Initialisation

Agents are created from the following base input values represented in the table on the following page.

CHARACTERISTIC	STARTING VALUE	EXPLANATION
Position	Colony position	All ants are initially spawned at the colony
Activity	"Foraging"	Ants are defined as being in one of two states at any given time, "foraging" or "nest searching"
Carrying	0	Amount of food the ant is carrying, initially zero
Velocity	8.0	A pre-defined constant term
Direction	2π (randomly generated)	All agents begin the simulation with a random bearing

3.1.6 Submodels

This section provides a mathematical oversight of the model. Following equation 1, the updated coordinates for the position of an ant I in Cartesian form is calculated according to the following rules:

$$\begin{aligned}x_{n+1}^i &= x_n^i + L\cos(\omega_{n+1}^i) \\ y_{n+1}^i &= y_n^i + L\sin(\omega_{n+1}^i)\end{aligned}$$

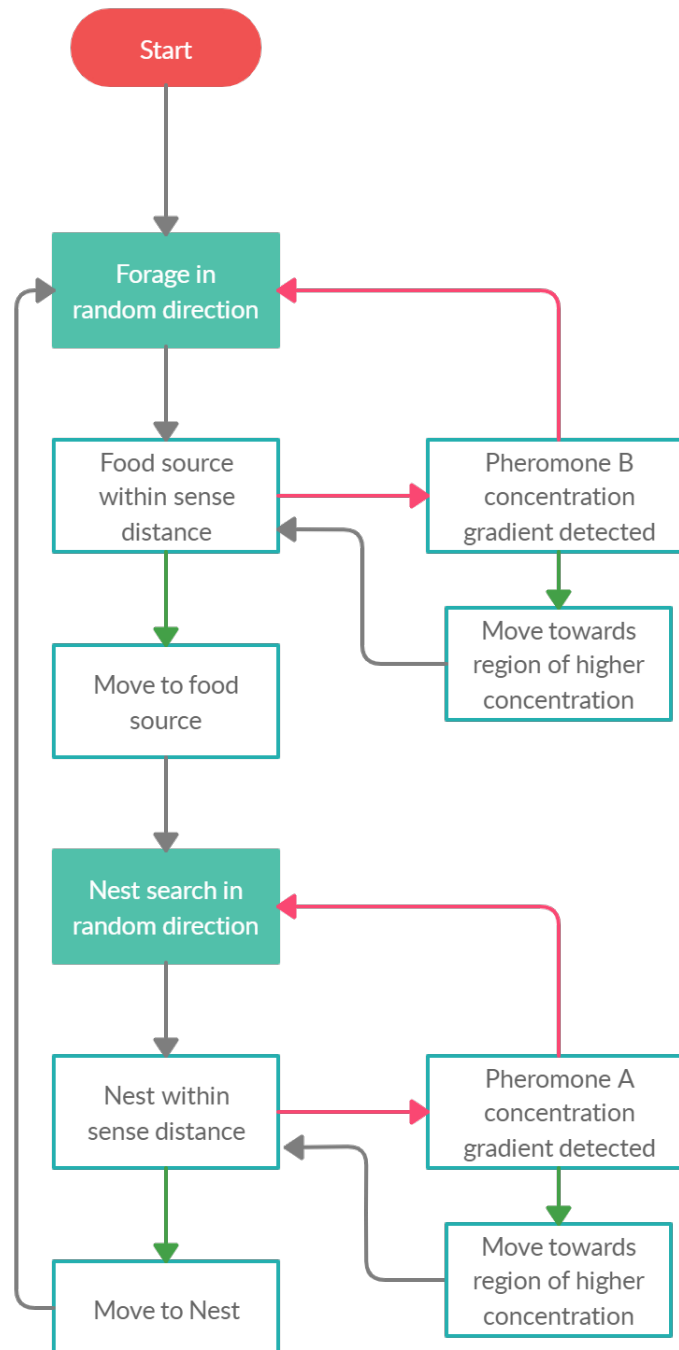
Where L is the constant spatial step size, assumed here to be equal to two ant body lengths. Function $c(x, y, t)$ gives the concentration of a given pheromone at location (x, y) at time t . The function $c(x, y, t)$ evolves according to the two dimensional diffusion equation:

$$\frac{\partial c}{\partial t} = D\left(\frac{\partial^2 c}{\partial x^2} + \frac{\partial^2 c}{\partial y^2}\right)$$

It should be noted that whilst there are similar models to this one, none accurately implement diffusion. Best solutions involve independently solving diffusion equations for all pheromone depositions individually, and then combining all solutions to produce the result. This is inaccurate due to the effect of concentration gradients affecting the diffusion path of pheromones, fixed through this models implementation. In the model above, D is replaced by either D_A or D_B ; the diffusion constants for pheromones A and B respectively.

The pheromone concentration has an effect on both the deterministic component of the angular equation, $f(c)$, and the amplitude of the stochastic component $\sigma(c)$.

Figure 3.1: Flow diagram to show model processes



Chapter 4

Results

4.0.1 Model Progression

As described previously, ants constantly leave a trail of pheromone as they forage and return to the nest with food. However, we first had to overcome the parameter connectivity between the ants' pheromone decay rate and the diffusion of the pheromone, without which the pheromone trail may not point in the right direction (backwards to a particular ant path's origin). After diagnosis, we found the problem only occurs when the decay of the ant's pheromone release is less than the pheromone diffusion rate. We hence adjusted the model to remove this problem.

Another issue with the model is "ant loss". At the beginning of each simulation no pheromone B or A trails are established, and the angular update is defined purely based on the stochastic component of the equation. As a result, even when a trail has been formed, many ants become "lost" as they stray too far from the nest and cannot pickup nearby trails. One solution of this problem was first attempted by recalling all ants back to the colony after 10 percent of ants had returned with food. This allows ants to pick up on the pheromone B trail that has just been established and effectively forage. Lost ants do not have a significant impact on results, however they do significantly affect the time taken for trails to form. Later in the development process, this problem was solved by correcting the sensitivity of ants to extremely low quantities of pheromone.

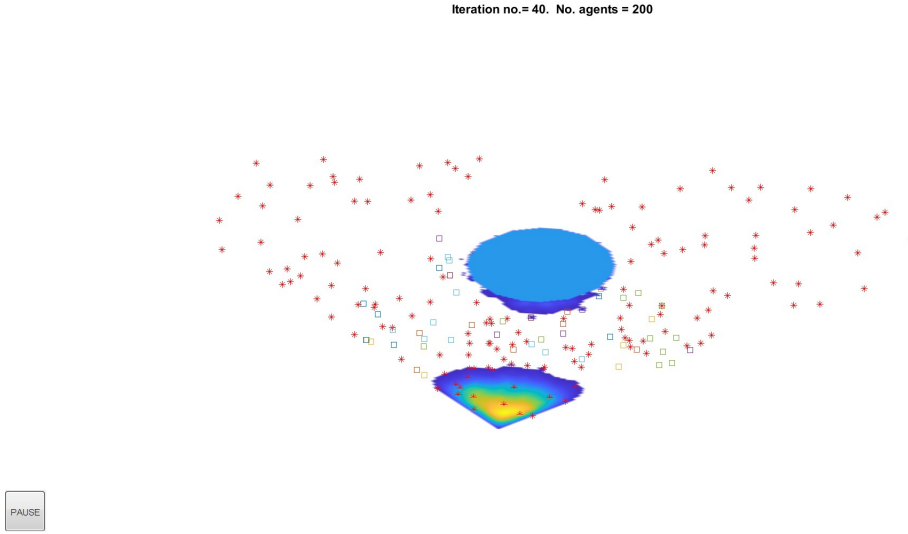
Shown in an alternate branch of our code, even if the ants correctly follow the pheromone when on it, there are a large amount of lost ants outside the region.

4.0.2 Results

Model Parameters between runs

- World Size: 200 x 300 (mm^2)
- Number of Ants: 200
- Number of iterations: 1200
- Primary Colony Position: 100, 150

Figure 4.1: Showing many ants lost



These parameters require a careful balance between adequate simulation space and simulation run time. There is a disproportionate increase in computational power required as the problem space is increased. We ran the simulation with 50 and 100 ants and observed bridges forming in every simulation, however 200 was used here as ant behaviour is more graphically evident.

The “total completed deliveries” statistic has been computed as an estimator of colony performance for each test scenario, which counts the amount of food delivered to the colony. It should be noted that only in cases where ants struggle to form a bridge is this statistic a useful comparison tool between simulations. In other simulations the construction of a bridge is inevitable and this becomes a measure of the distance between the colony and food source. This is the only limiting factor in the parameters growth.

We then altered the position of the food source(s) for each scenario and measured this statistic, as well as qualitatively inspected the visuals every 25 iterations to look for bridges forming, for exactly 10 runs for each scenario (this took a significantly long time to compute given the high number of iterations, see below). We have also calculated standard deviations for each test case which gives a more detailed insight into the consistency of results.

These terms are used in the descriptions below and equate to these values.

Term	Grid Squares/distance (mm)
Far distance	150
Medium distance	100
Close distance	50
Large food size (radius)	30
Medium food size (radius)	20
Small food size (radius)	10

Where two sources are used, each is in directly opposite directions from the nest

Test No.	Environment Description	Average	Standard Deviation
2	2 Sources, both medium distance and medium size	2603.4	29.50
3	2 Sources, both medium distance, one medium other smaller	2134.1	50.40
4	2 Sources, both medium distance, one large other medium	2767.8	23.52
5	2 sources, one far distance, other medium distance, both medium size.	1371.6	14.50
6	2 sources, one close distance, other medium, both medium size	14522	114.32
7	2 sources, one further and small, other medium and large	1537.1	11.66
8	2 Sources, one large and close, other far and small	30122.6	95.92
9	2 sources, 1 large and 1 small, both medium distance	2768.2	9.70
10	2 sources, 1 large far 1 small close	10383.9	56.25
At this point, we made it so one of the food sources removes at the 300th time step			
11	2 sources, 1 close small that removes at 300 time steps, 1 large far away	2535.5	26.16
12	2 sources, 1 medium distance medium size that removes at 300 time steps, 1 large far away	691.2	12.63
13	2 sources, 1 far medium size that removes at 300 time steps, 1 large far away	454.6	25.64
14	2 sources, 1 far large that removes at 300 time steps, 1 large far away	29518.5	166.35

As discussed before, here are some images for a few of the test scenarios, a full table of all test scenarios can be found in the appendices.

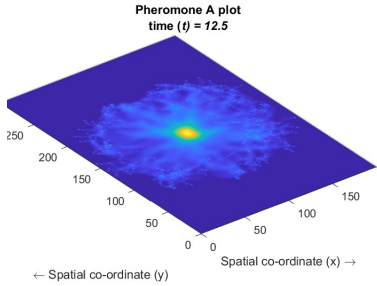
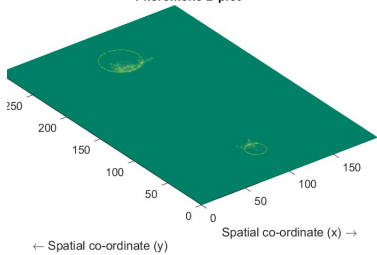
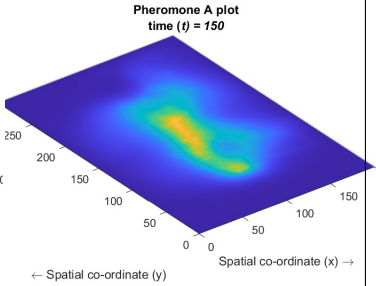
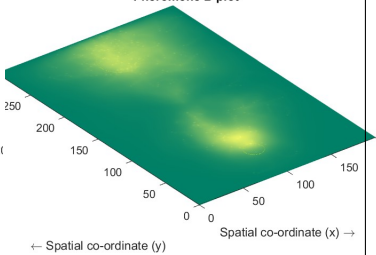
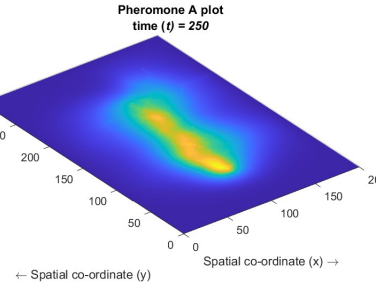
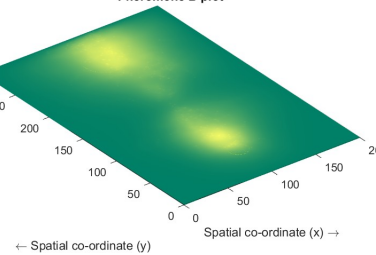
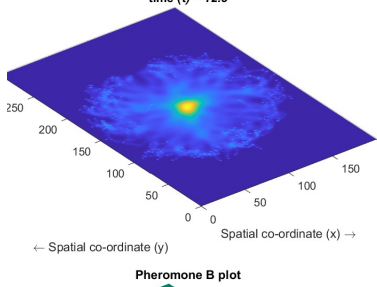
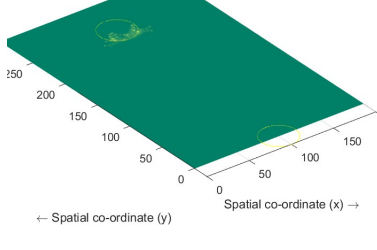
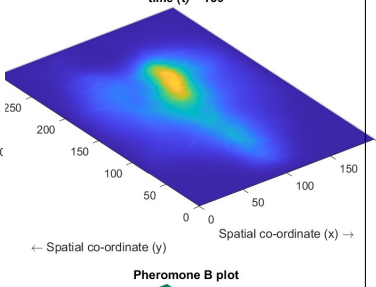
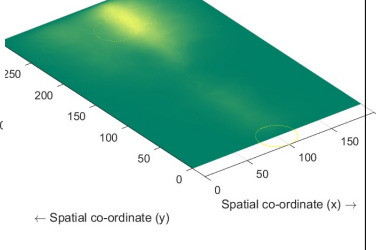
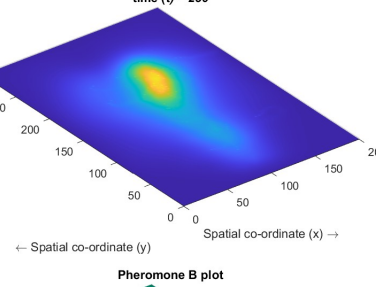
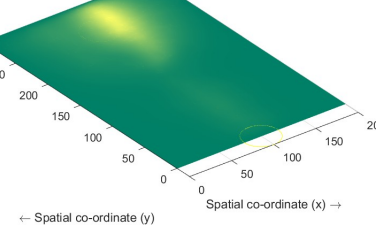
Test No	Iteration 25	Iteration 300	Iteration 500
3	<p>Pheromone A plot time (t) = 12.5</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p> <p>Pheromone B plot</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p>	<p>Pheromone A plot time (t) = 150</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p> <p>Pheromone B plot</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p>	<p>Pheromone A plot time (t) = 250</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p> <p>Pheromone B plot</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p>
5	<p>Pheromone A plot time (t) = 12.5</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p> <p>Pheromone B plot</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p>	<p>Pheromone A plot time (t) = 150</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p> <p>Pheromone B plot</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p>	<p>Pheromone A plot time (t) = 250</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p> <p>Pheromone B plot</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p>

Table 4.1: Above figures display test results for tests 3 and 5. In both cases, an initial 'probing' phase is evident where ants spread out in all direction in search of food, depositing only pheromone A. Once pheromone B trails are established the A trails are quickly narrowed towards optimal paths.

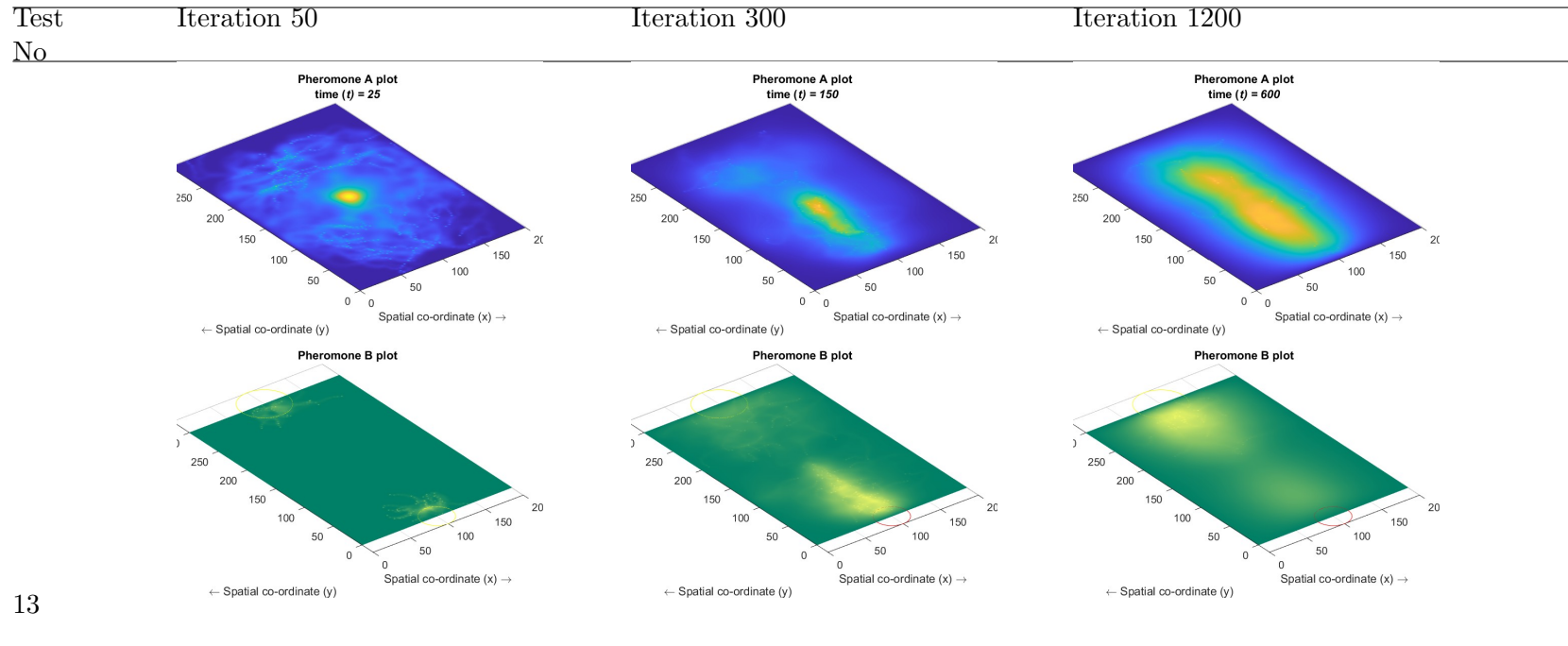


Table 4.2: The above results show the effect of removing a food source, to which a pheromone pathway has already been established, on the ant behaviour. It also shows that if a food source is removed, ants quickly redistribute themselves to form a bridge to the remaining food source. It should be noted that the decay rates for pheromone A and B are not the same. Pheromone A, marking foraging trails, is much more permanent. Pheromone B is a relatively short lived pheromone and its trail quickly dissipates once the food source is removed at iteration 300. After 900 iterations a new bridge has been fully formed.

We also plotted the ratio of foragers to seekers, as well as the total number of food deliveries over the course of each run.

Figure 4.2: Showing the graphs of test 5

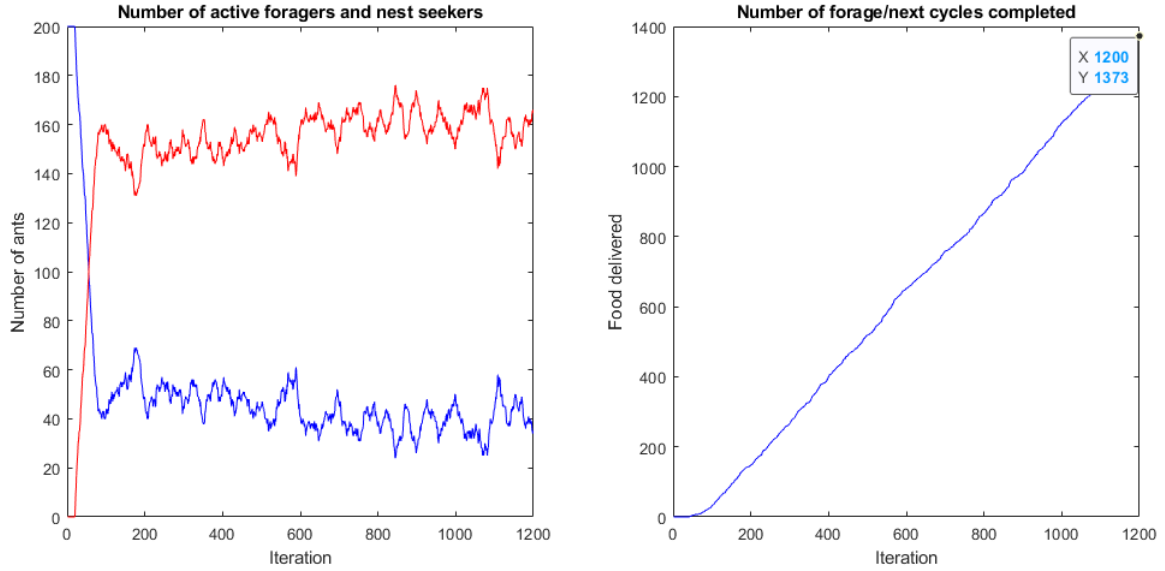
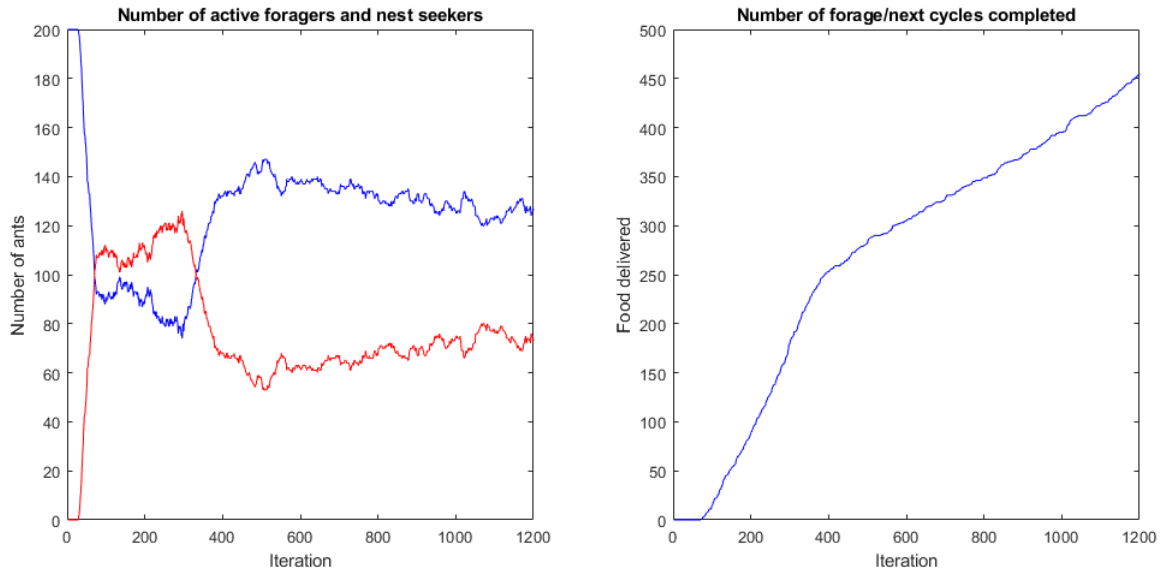


Figure 4.3: Showing the graphs of test 13



As seen, the mean value of total deliveries displays massive variation between test scenarios, but when observing the graphs we saw that after a brief period of stabilisation tests 2 - 10 are all remarkably linear. This is mostly because once a bridge has been established the ants can consistently deliver food where the only factor altering the gradient is length of

the pheromone pathway or distance to the food source.

Furthermore, the ants managed to discover new pathways to food seen in tests 11 to 13. Test 13 (figure 4.3) shows they managed to make a bridge to the new food source, as seen in the graph: the change in gradient represents when they are now going to and from a different food source at a further distance i.e. a new bridge has been formed.

We can conclude that the distance from the colony to the food source greatly affects the reliability with which the colony is able to construct the optimum bridge, whilst size is a much less significant factor.

4.0.3 Computational Performance

We measured the performance of our system by altering various statistics of the base running criteria. We used the tic function as suggested by the example report to measure the actual times of each one of these settings.

To be accurate to the first running conditions of our system we continued to have graphs being printed. We also used the “test one” for all the performance tests as there are no significant computational differences between different test cases.

First we changed the number of iterations at different numbers of iterations, while keeping the ant population at 200.

We would expect the program run time to scale linearly with iterations as it must perform the same calculations in each.

Number of Iterations	Running time (s)
50	49.4
100	102.7
500	477.5
1000	1006.25

From these results you can see that when the graphs are being plotted the program requires roughly one second per iteration. You can see from the above results that running one run of the program takes over 20 minutes, which resulted in over 4 hours of running for our image-capture tests.

To improve this, we carried out many tests without plotting results except from one plot per 100 iterations, improving run times. The bulk of time still remains within the internal calculations and so there is a limit to this techniques effectiveness.

Number of Iterations	Running time (s)
50	12.3
100	18.3
500	65.8
1000	142.6

These much improved running times allowed us to complete the rest of the tests in a roughly equivalent time to the initial capture.

Secondly we changed the amount of ants. Although this would mean the diffusion calculations should not take any longer, as these use vectored calculations and are fast regardless. The actual agents of the system require $O(n)$ computational steps unavoidably.

Number of Ants	Running time (s)
50	16.2
100	19.2
500	37.5
1000	64.46

4.0.4 Possible improvements

You could potentially improve the performance by allowing ants that have been on a particular trail for some time to “automatically” follow a nearby ant without having to perform additional calculations, although this would be at the detriment of the accuracy of the model.

Alternatively you could allow the “lost” ants to be removed from the simulation if they have not found a trail in a certain amount of iterations. (although with the improvements in our model there are many fewer ants getting lost, so the improvement may be negligible).

The diffusion calculations are already very fast due to quick vectored calculations. However, with bigger world sizes they may become more of a problem, in which case you could reduce the rate of diffusion calculations instead of being performed every iteration.

Ants which collide with the edge of the model simply rotate until they are able to move forwards. This is unrealistic behaviour and one way to handle such events would be to make these ants despawn. This creates issues however as the only ants that would not collide with the model boundaries are those on a direct course with food, and forming a bridge with such a low number of ants would take several thousand iterations.

Chapter 5

Discussion

Relating back to our research question, which is to investigate the systems behind the ability of ants to form effective pheromone trails to and from food sources, we can see that the model does successfully demonstrate that under these parameters the agents are able to rapidly construct and often deconstruct pathways efficiently.

They successfully replicate real ant biology by detecting the pheromones and acting on these senses i.e. being able to follow a path of highest concentration and they realistically leave a path of pheromone of decreasing strength as they progress, and use two types of pheromone for each direction of their travel much like in the paper Malíčková and Yates [10].

In terms of emergent behaviour, they frequently successfully form a pheromone "bridge" between the food source and the nest, allowing future ants to follow the same path and increasing food delivered to the nest. They also have a minimal ability to adapt to the loss of a particular food source and form a new path way to a full food source, as observed in nature Jackson and Ratnieks [9], Steck [16].

From this model we found that if one food source is closer and continues to be plentiful, the ants will prefer to establish just one bridge to it instead of maintaining multiple bridges.

We also found that the size of a food source would not impact the potential to form a bridge beyond the fact that it would result in a closer point of contact for the colony. It does however reduce the time to form the bridge as ants searching for the food source to begin with can find it quicker with a larger footprint.

By using an ABM as opposed to a cellular automata approach, we open up the possibility for much more complex agent-environment interactions as the state space becomes infinitely larger. For our specific application, this is useful for several reasons but most importantly our system requires us to compare pheromone concentrations at two exact Cartesian coordinates at each agent's left and right antennae. Whilst investigating complex trail structures it stands to reason that continuous space would be more suitable for plotting gradient like structures including pheromone diffusion. These advantages come at the expense of computational complexity and runtime, and use of a CA would allow us to scale up the number of agents without significantly effecting the time taken for each simulation. Combinatorial explosion is a risk of agent based modelling, as the majority of the problems that we would like to model often require large amount of parameters to make the model more realistic. Hence, we have to use a smaller number of parameters which will inevitably make the model less realistic.

However, while the model does have great success in modelling these aspects of the ants

behaviour, there are several improvements that could deepen our understanding further. First of which could be to remove the food sources as they are eaten instead of after a short time. This would work much like in nature; as the food source is consumed, its radius is decreased - mimicking a loss in mass, therefore making the food source harder to discover for ants.

One interesting application for this model which we did not have time to delve into was to add impassable terrain into the model and applying the ant colony to tasks such as maze solving. Additional tests include the recreation of the clock experiment, spawning and removing food sources surrounding the colony in a clock like setup to demonstrate the ants ability to break and reform trails more rigorously, which would allow us to test the situations discussed in Dornhaus [7], Sherman and Visscher [15].

One ambitious addition to the model would be interaction with neighbouring and rival ant colonies. By introducing competition for food sources we could observe any associated emergent behaviour, potentially implementing fighting or other such rivalry mechanics.

Chapter 6

Conclusions

In this report we have evaluated the performance of our simple model and its ability to mimic and reproduce the foraging behaviours of ants. These ant agents are able to forage in dynamically changing environments with multiple food sources at varying distances from the colony. There is significant room for improvement and further experimentation in order to increase the likeness of our ages with ants from nature. For example, expanding the system to allow ants to detect difference in food source quality, and adjust worker distribution if food is particularly far from the nest. There are also clear inaccuracies with our model such as worker interaction with the edges of the simulation boundaries which could be addressed a variety of different ways we discussed previously. However, the ability of our agent to break down and form new trails is an impressive example of emergent behaviour which ought to be investigated more thoroughly than the scope of this project allows.

Bibliography

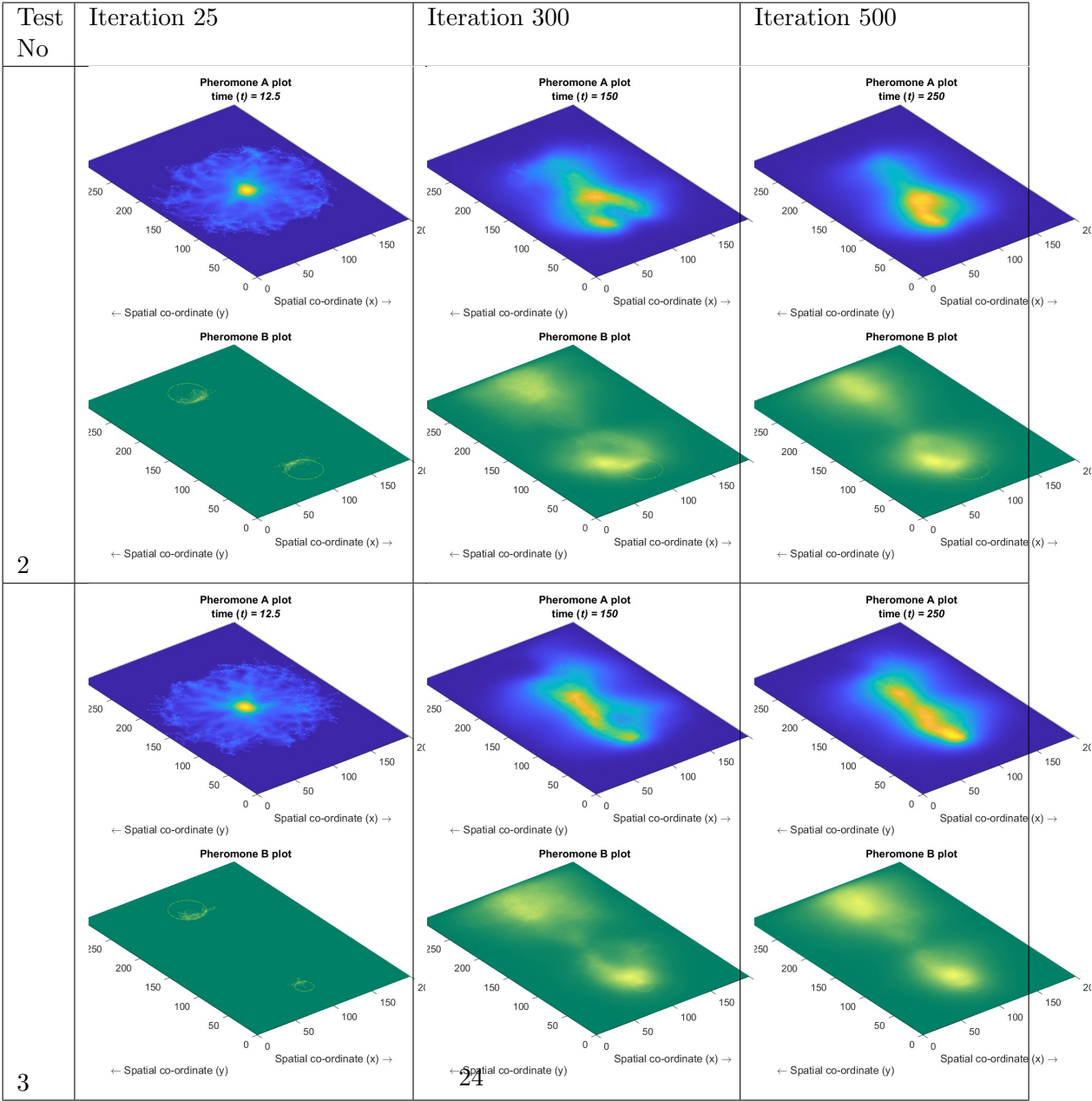
- [1] Beekman, M., Sumpter, D. J. T., and Ratnieks, F. L. W. (2001). Phase transition between disordered and ordered foraging in pharaoh’s ants.
- [2] Bicak, M. (1970). Agent-based modelling of decentralized ant behaviour using high performance computing: Semantic scholar.
- [3] Couzin, I. D., Franks, N. R., Couzin, I. D., Franks, N. R., Centre, N. R. F., of Ecology, I. D. C. I. D. C. D., of Ecology, I. D. C. D., and Biology, E. (2003). Self-organized lane formation and optimized traffic flow in army ants.
- [4] Detrain, C. and Deneubourg, J.-L. (2006). Self-organized structures in a superorganism: do ants ”behave” like molecules?
- [5] Doerr, B., H. A. K. T. (2012). Ants easily solve stochastic shortest path problems. page 17–24.
- [6] Dorigo, M., B. M. (2010). Ant colony optimization. pages 36–39.
- [7] Dornhaus, A. (2002). Significance of honeybee recruitment strategies depending on foraging distance (hymenoptera: Apidae: Apis mellifera).
- [8] Dussutour, A., Nicolis, S. C., Shephard, G., Beekman, M., and Sumpter, D. J. T. (2009). The role of multiple pheromones in food recruitment by ants.
- [9] Jackson, D. E. and Ratnieks, F. L. W. (2006). Communication in ants.
- [10] Malíčková, M., B. K. and Yates, C. (2015). A stochastic model of ant trail following with two pheromones.
- [11] Panait, L. and Luke, S. (2004). A pheromone-based utility model for collaborative foraging.
- [12] Resnick, M., Kafai, Y. B., Burke, Q., Rocha, L. M., Bedau, M. A., Husbands, P., Watson, R. A., and Ikegami, T. (1994). Turtles, termites, and traffic jams.
- [13] Sauter, J., Matthews, R., and Brueckner, S. (2002). Evolving adaptive pheromone path planning mechanisms.
- [14] Sauter, J. A., Parunak, H. V. D., Brueckner, S. A., and Matthews, R. S. (1970). [pdf] tuning synthetic pheromones with evolutionary computing: Semantic scholar.

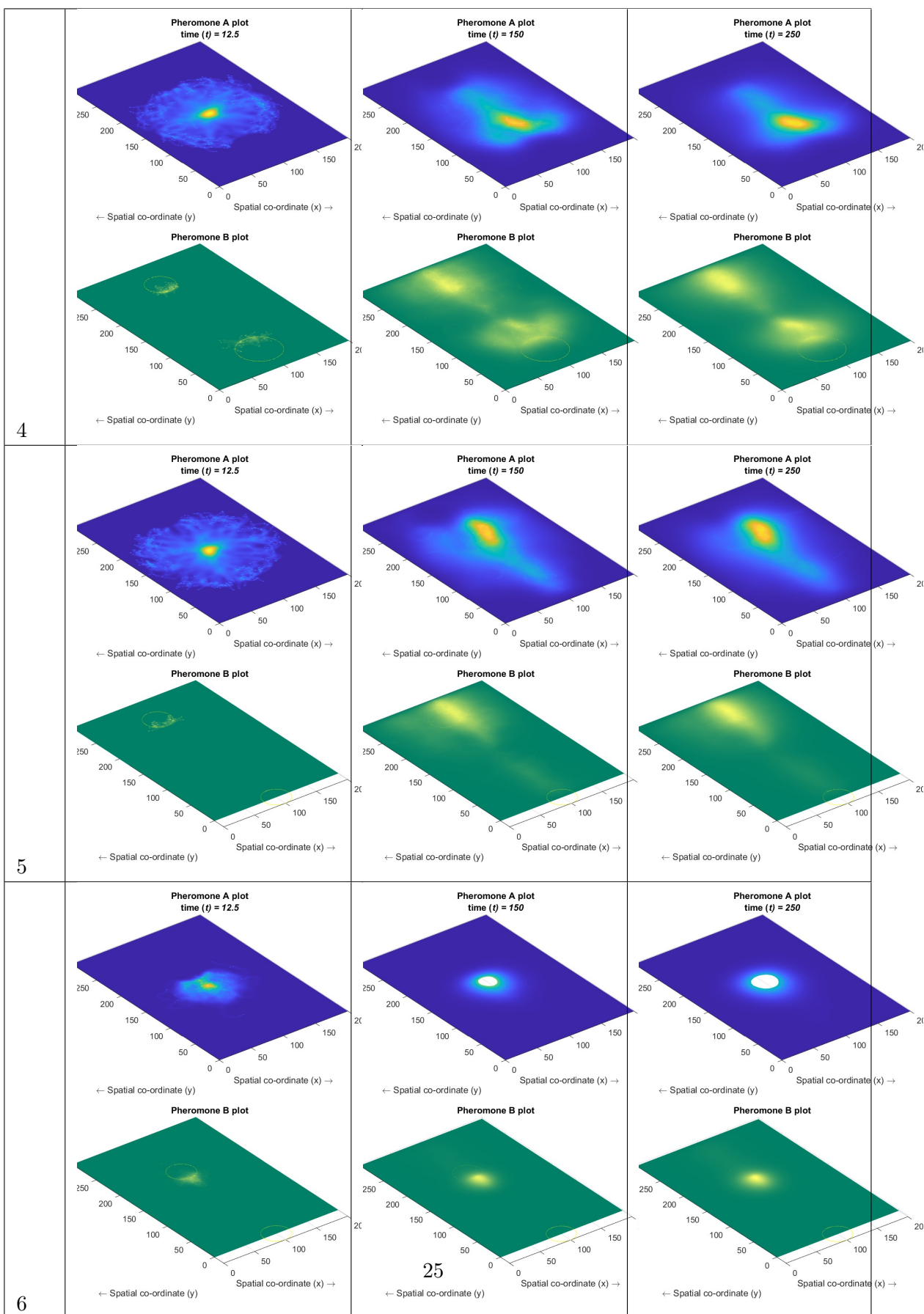
- [15] Sherman, G. and Visscher, P. (2002). Honeybee colonies achieve fitness through dancing.
- [16] Steck, K. (2011). Just follow your nose: homing by olfactory cues in ants.
- [17] T. White, B. Pagurek, F. O. (1998). Asga: improving the ant system by integration with genetic algorithms.
- [18] Vaughan, R. T., Støy, K., Sukhatme, G. S., and Matarić, M. J. (1970). Blazing a trail: Insect-inspired resource transportation by a robot team.
- [19] Volker Grimmer, Uta Berger, D. L. D. J. G. P. J. G. S. F. R. (2010). The odd protocol: A review and first update.

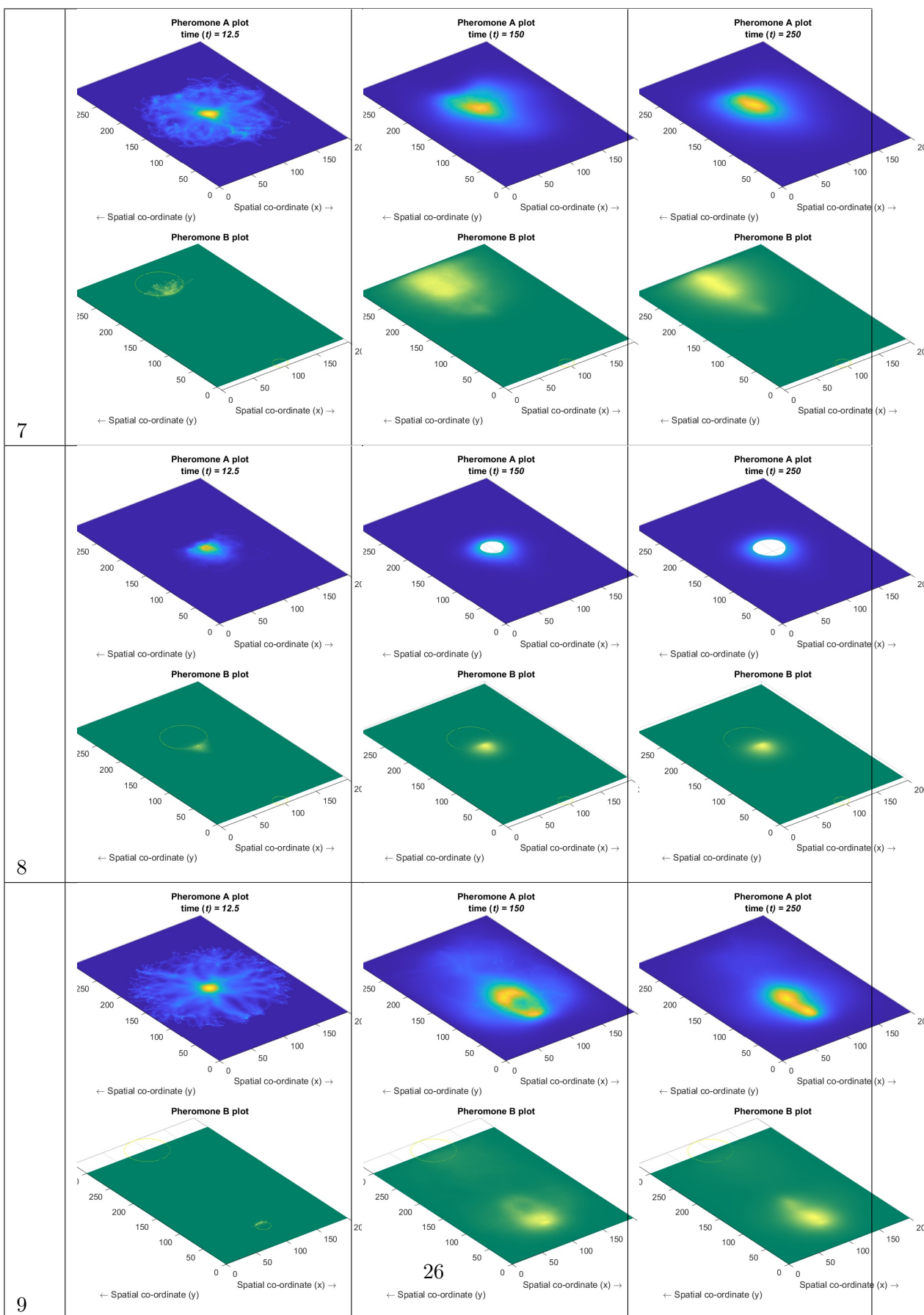
Appendices

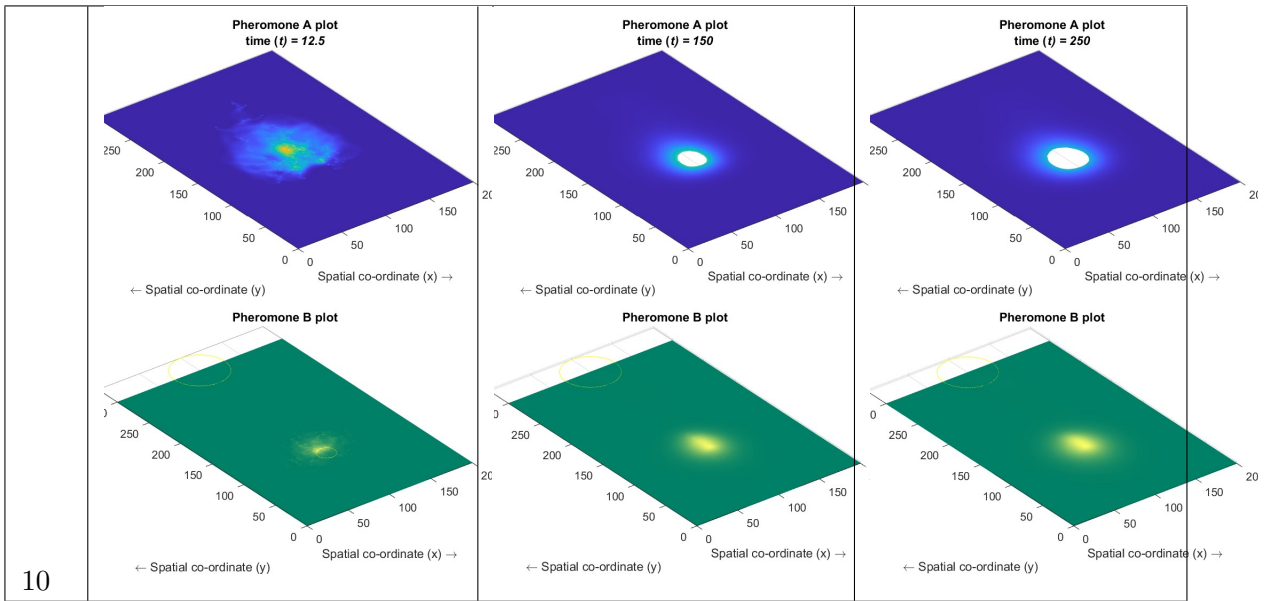
Appendix A

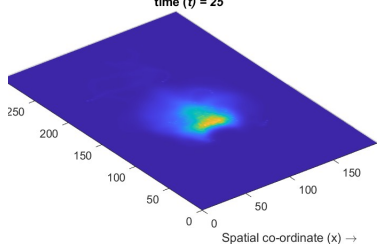
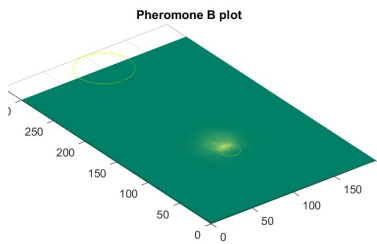
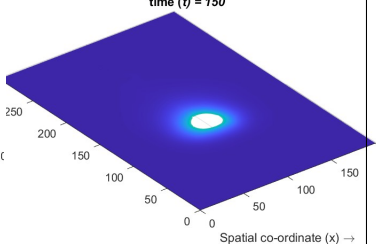
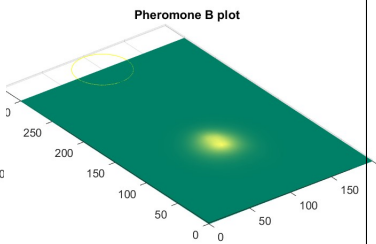
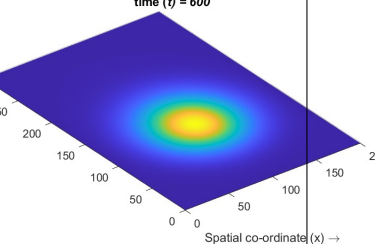
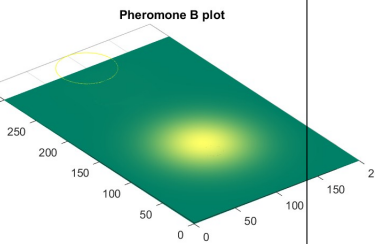
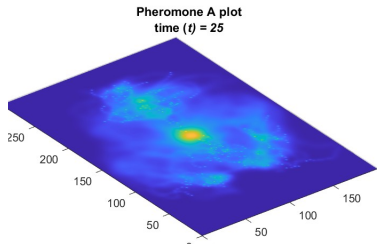
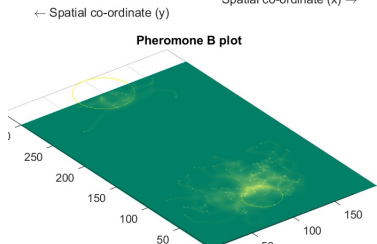
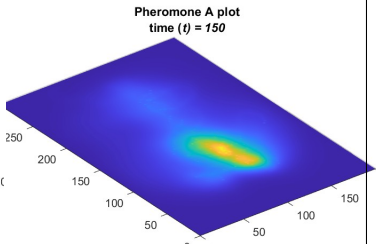
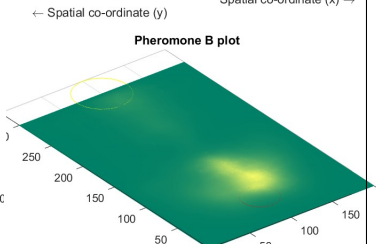
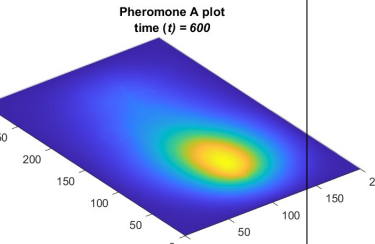
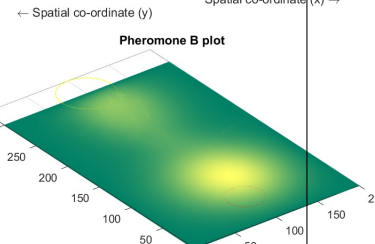
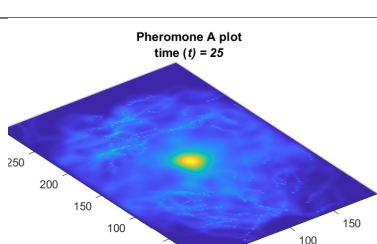
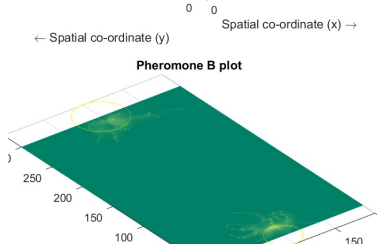
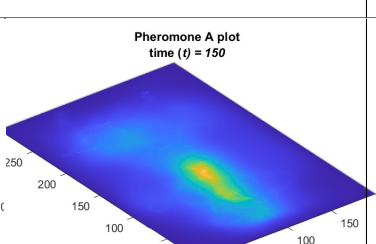
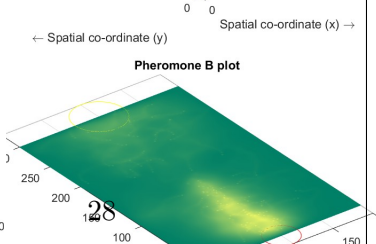
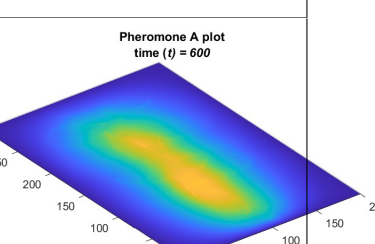
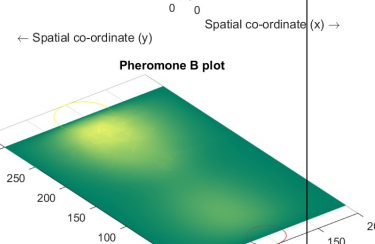
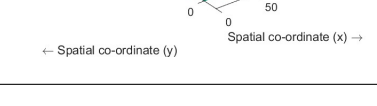
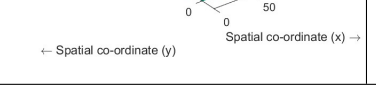
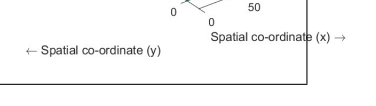
Test Results Images









Test No	Iteration 50	Iteration 300	Iteration 1200
11	<p>Pheromone A plot time (t) = 25</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p> <p>Pheromone B plot</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p>	<p>Pheromone A plot time (t) = 150</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p> <p>Pheromone B plot</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p>	<p>Pheromone A plot time (t) = 600</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p> <p>Pheromone B plot</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p>
	<p>Pheromone A plot time (t) = 25</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p> <p>Pheromone B plot</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p>	<p>Pheromone A plot time (t) = 150</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p> <p>Pheromone B plot</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p>	<p>Pheromone A plot time (t) = 600</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p> <p>Pheromone B plot</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p>
13	<p>Pheromone A plot time (t) = 25</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p> <p>Pheromone B plot</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p>	<p>Pheromone A plot time (t) = 150</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p> <p>Pheromone B plot</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p>	<p>Pheromone A plot time (t) = 600</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p> <p>Pheromone B plot</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p>
	<p>Pheromone A plot time (t) = 25</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p> <p>Pheromone B plot</p> <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p>	<p>Pheromone A plot time (t) = 150</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p> <p>Pheromone B plot</p> <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p>	<p>Pheromone A plot time (t) = 600</p>  <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p> <p>Pheromone B plot</p> <p>← Spatial co-ordinate (y) Spatial co-ordinate (x) →</p>

