

# Predator Prey Model

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November 2011

When writing this report, a lot of emphasis was put on interactivity, so, a reader would benefit from reading an electronic version (PDF) rather than a paper one

# Contents

<b>1</b>	<b>Introduction</b>	<b>1</b>
<b>2</b>	<b>Design &amp; Implementation</b>	<b>3</b>
2.1	Code . . . . .	3
2.1.1	Structure . . . . .	3
2.1.2	Algorithm . . . . .	4
2.2	Input/output . . . . .	6
2.2.1	GUI . . . . .	7
2.3	Tools . . . . .	8
2.3.1	IDE . . . . .	8
2.3.2	SVN . . . . .	8
2.3.3	Ant File . . . . .	8
2.3.4	Unit Testing . . . . .	8
<b>3</b>	<b>Results</b>	<b>10</b>
3.1	Output Analysis . . . . .	11
3.2	Performance Analysis . . . . .	11
<b>4</b>	<b>Conclusions</b>	<b>15</b>

# Chapter 1

## Introduction

This project involved writing a computational simulation of a predator-prey model. The focus of the task was to produce an efficient algorithm and a readable extendible code base. This was done by making use of a number of useful development tools and employing good set of programming practices throughout. The problem was as follows:

- An island represented by a rectangular domain, where every grid point is either land or water
- Density of prey (hares) and predators (pumas) are changing with time depending on parameters  $r, a, b, m, k, l$ .<sup>1</sup>
- differential equation governing changes in population density where H is prey population density, P is predator population density,  $\Delta t$  is discrete timestep size:

$$H_{ij}^{new} = H_{ij}^{old} + \Delta t(rH_{ij}^{old} + aH_{ij}^{old}P_{ij}^{old} + k((H_{i+1j}^{old} + H_{i-1j}^{old} + H_{ij+1}^{old} + H_{ij-1}^{old}) - N_{ij}H_{ij}^{old}))$$

$$P_{ij}^{new} = P_{ij}^{old} + \Delta t(bH_{ij}^{old}P_{ij}^{old} - mP_{ij}^{old} + l((P_{i+1j}^{old} + P_{i-1j}^{old} + P_{ij+1}^{old} + P_{ij-1}^{old}) - N_{ij}P_{ij}^{old}))$$

- Aim to simulate a grid up to 2000x2000 points updating populations for a certain time.

We designed the program in such a way as to take advantage of Java's object-orientated, modular nature. Due to the large size of our group we also decided to incorporate a GUI. The program can also be run from the command line, as in some situations (ssh) a GUI is not available.

There is always some compromise between readability and performance in coding, and we tried to keep this balance in mind when designing our code. We made best use of class structure whilst still keeping our implementation of the given algorithm as efficient as possible.

The predator prey algorithm implemented in this project crudely models the interaction between population densities of different animals, specifically hares and pumas. Each population has a self-interaction coefficient (birth for Hares, death for Pumas) and a coefficient describing how it interacts with other species' populations.

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<sup>1</sup>Where  $r$  is prey birth rate,  $a$  is predation rate,  $b$  is predator birth rate,  $m$  is predator death rate,  $k$  is prey diffusion rate,  $l$  is predator diffusion rate

These populations exist in a 'world' consisting of land and water and are also able to diffuse across land squares with a rate determined by a diffusion coefficient. Thus, each population has  $N+1$  coefficients which determine its behaviour, where  $N$  is the number of animals.

## Chapter 2

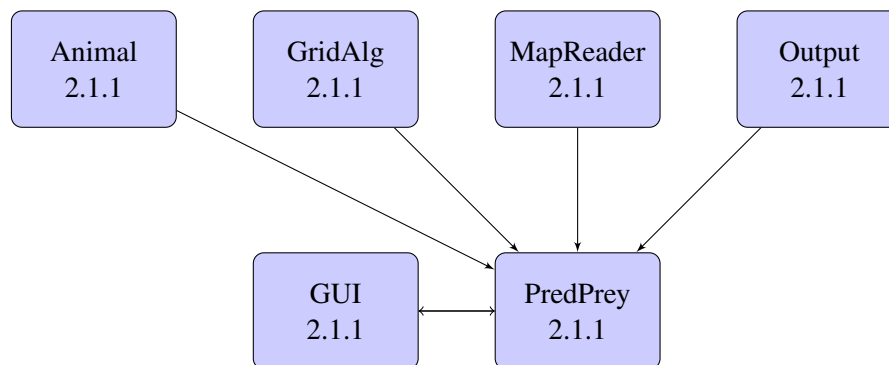
# Design & Implementation

### 2.1 Code

#### 2.1.1 Structure

The language our group decided to code the predator-prey model in was Java. Using Java gave us easy access to numerous tools such as Javadoc and Swing for creating GUIs, and the main advantage for most of us was the familiarity of working with object oriented code design. Object orientation provided us with the opportunity to design the central workings of the code with extensive extendibility, leaving just the user interface specifically designed for the problem at hand.

##### Classes Flow Chart



##### Animal

The Animal class holds the information about the animal; it's density distribution and how it is updated relating to other animals. It is called in the PredPrey class where it's values are initialised from those taken from the GUI or input file. Discussion of the implementation of the main algorithm can be found in section 2.1.2

## **GridAlg**

The Grid Algebra class governs methods for updating the animal densities across the grid. The constructor takes the array of animals passed after creation in the PredPrey class and the 2 dimensional array of neighbours passed from the MapReader class. Upon creation the GridAlg class initialises the densities of each animal in each grid cell to a uniformly distributed random number between 0 and 5, changing this range are only seen to change the scale of the simulation. A couple of different methods of updating the grid are held in the class, these is discussed further in subsection 2.1.2.

## **MapReader**

The MapReader class is responsible for reading the file which holds where the land and water are and outputs an array holding the neighbours of all the land cells, this is discussed further in section 2.2.

## **Output**

The output class is sent density distributions of the animals and from that calculates and outputs the average density as well as an image of the density distribution. The format and creation of these files is discussed further in section 2.2

## **GUI**

This class is responsible for displaying a GUI for a user to input parameters of the simulation discussed further in section 2.2.1

## **PredPrey**

A main class, PredPrey, governs the creation of occurrences of all of the other classes as required. When running the program from the command line there is an option to run with or without a GUI, this is determined by whether the input file names are given as arguments. If the arguments are passed, the input parameters are read from the file, if they are not then the user can input them in themselves via the GUI.

### **2.1.2 Algorithm**

The equations shown in the problem Model are specific to Hares and Pumas located in the cells of the world grid. Our initial approach was to write a computational algorithm that simply iterated the equations for the density arrays of the two animals. The next stage in the development was creating an abstract Animal class, for which subclasses provided the implementation of the kernel specific to that animal. It was soon realised that this abstraction could be removed, and the problem generalised even further resulting in the current algorithm: A general Animal class is used to represent any species present in the world. Instances of Animal are created at runtime for all such species. These objects contain all of the information about the animal, most importantly:

Listing 2.1: The fundamental fields of the animal class.

```

// The density of the animal in each cell
double[][] densities
// The diffusion rate of the animal
double diffusionRate
// The coefficients controlling the effect of other animals on the animal
double diffCo[]

```

To illustrate more clearly what values `diffusionRate` and `diffCo[]` take, they are shown for the simple hare puma case that was used for the entirety of testing.

Listing 2.2: Behavioural coefficients for the hare instance of animal.

```

diffusionRate = k
diffCo[0] = r    // How hares effects the hare
diffCo[1] = -a   // How pumas effects the hare

```

Listing 2.3: Behavioural coefficients for the puma instance of animal.

```

diffusionRate = l
diffCo[0] = b    // How hares effect the puma
diffCo[1] = -m   // How pumas effect the puma

```

The governing class (`PredPrey`) creates an array of `Animals`, passing each their diffusion rate, and the array `diffCo` dictating how the of the other animals effect them. Armed with these tools, the `Animal` objects are able to iterate the equations shown in the model themselves. As long as the constants governing the effect of each animal on others are known, the size of the array of `Animals` can be increased to as many as desired. At each time step, the code loops over the animals, invoking the `calcNextDensity()` method. Part of this method is shown in listing 3.4.

Listing 2.4: The key part of the computational kernel within animal - called when the density for a single cell is to be updated to the next time step.

```

// Loop over the total number of animals/behavioral coefficients.
for (int k = 0; k < animals.length; k++) {

    /*
    Add the contribution to the new density depending on the weather
    the animal is this or not.
    */
    if (animals[k] == this) {
        newDensity += dt*getDiffCo()[k]*oldDensity;
    }
    else {
        newDensity += dt*getDiffCo()[k]*animals[k].getDensity(y, x)*oldDensity;
    }
}

// Add the contribution based on the animals diffusion rate
...
...
...

```

The GridAlg class controls the order in which the cells are updated which is an important feature of the algorithm. In the final version, all of the animals and all cells are updated simultaneously. This is implemented by temporarily storing the results of a time step and not actually applying the new densities to the system until all other calculations are complete. In doing this, it is ensured that the all densities used in calculations within the kernel are from the same time step.

## 2.2 Input/output

In our model the "world", or landscape, is represented by a rectangular grid of alterable dimensions  $N \times N$ , where  $N$  can be as large as 2000. We designed the code in a way such that it can read in an ASCII file that contains a set of numbers, those being either 0 or 1 and representing water and land, respectively, parses them and stores in a two-dimensional array. This means that the code can be used to model landscapes of different sizes with various distributions of land and water.

The boundary conditions are assigned to the model by setting the values for density of both, pumas and hares, to 0 at the edges of the grid. Initially, pumas and hares are randomly distributed across the land cells. All these tasks are implemented in methods within the MapReader class.

The initial values for parameters that appear in the PDE's governing the evolution of the system with time can be set up by the user, who will be able to interact with the program by means of a GUI. Specifically, it is allowed for the user to initialise the values for the birth, death and diffusion rates of both types of animals as well as the time step ( $dt$ ), which controls how often the system is updated with new data. The user can also control the frequency of creating the output files, by choosing a value for the parameter  $T$  in the GUI window. The output gets created every  $T$  time steps. We have also included an optional "range" feature which allows the user to set a range of initial values for all the differential coefficients and an increment. In this case the code will run several times creating separate outputs for every simulation. In the next section we talk about the GUI in more detail.

Alternatively, the user can execute the code directly from within the terminal by specifying two arguments. The first argument required is the name of the file containing initial values for all the parameters, and the second is the name of the input ASCII file that will be used to create the grid.

The methods responsible for creating the output are included in the Output class. Depending on the user's preference, the code will create one output directory (for single initial values) or a number of such directories (for the range of initial values), i.e. one for each run. In both cases the user will be able to view the distribution of both populations across the landscape every  $T$  time steps. The form of the output is a number of \*.ppm files which can be viewed as images, or "maps", similar to these showed in the figure below.



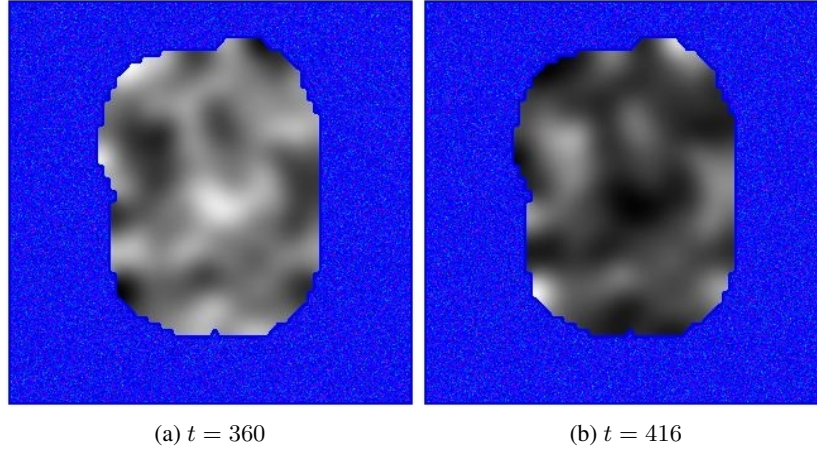


Figure 2.1: This figure shows examples of the output files created during a simulation using a  $500 \times 500$  grid and default initial conditions. Various shades of grey represent the density of pumas after 900 (a) and 1040 (b) timesteps, with timestep size set to 0.4.

The number of the \*.ppm files created depends on the initial parameters specified by the user,  $dt$  and  $T$ . To maximise the level of output clarity we decided to make separate landscape "maps" for each type of animal, here pumas and hares. In each "map" the pixels corresponding to water cells are shown in blue, while the land cells are white. The variation in density of pumas/hares across the land cells is represented by different shades of grey, with black colour corresponding to the maximum value.

For each type of animal, every  $T$  time steps, the code also calculates the mean population density and writes it along with the corresponding time into a file.

### 2.2.1 GUI

GUIs are not used in HPC as they use memory and slow down computations and are generally not necessary as all the interactions with HPC machines is done through a command line. However, our group has chosen to code in Java, and GUI is one of Java's strengths as it should look the same on every machine. So it was decided that we are not taking advantages of our chosen language unless we create a GUI. GUI created is responsible for the input parameters of the simulation. Initially, it would just take the values and run the simulation. However, in later versions, *range* option was added to be able to run multiple simulations changing one of the parameters. The frame is divided into three parts (all on separate frames): input, input2, button. Input holds labels and text fields for parameter inputs. Input2 holds second text field and radio buttons to chose which parameter to range over, is not visible unless range is selected. Button holds start button, choice between range and preset values and parameter values that are general like input file, steps before output. GUI is still very simplistic and could be enhanced more but was not due to time constraints.

## 2.3 Tools

### 2.3.1 IDE

IDE stands for ‘Integrated Development Environment’, which is widely used in modern program development, especially in object-oriented projects. Because Java is a completely object-oriented programming language, IDEs became an indispensable tool during this project. Most of the group members used the Eclipse IDE to develop the program. Eclipse provides many useful features that aid the development process including an extensive debugger, realtime error checking, comprehensive autocompleting and support for JUnit testing. In addition to Eclipse a number of other tools were utilised, details of which can be found in the following sections.

Compared to Eclipse, Netbeans is a new IDE for Java developed by Sun, which provides more powerful debugging and performance scanning tools. The performance analysis section was held on Netbeans IDE by Netbeans Profiler.

### 2.3.2 SVN

We chose to host the SVN repository using a Google Code project. The home page can be found at <http://code.google.com/p/ps-predator-prey/>. Doing so allowed us to make use of the many excellent tools that are available for managing such projects; the most obvious example being the ability to quickly and easily browse all of the revisions from r1 current via the web interface. The fact that the code was hosted externally on a 24/h server meant that it could be accessed from anywhere at any time. There was also no issue with compatibility: Some of the group members opted to use the SVN Eclipse plug that interfaces seamlessly with the Google Code while others chose to use the more traditional approach of checking code in and out via the command line. Another invaluable feature was the ability to compare side by side any and all changes between revisions. See for example the changes made to Output.java in revision r29<sup>1</sup>. This feature is compatible with all text files, and so also proved useful for the group editing of latex files.

### 2.3.3 Ant File

To automate the building of the software, we have coded an Ant file using the XML language. The Ant file contains the appropriate sections that ensures compilation uses the correct files in the right packages. In order to maintain portability, we included a lib/ directory that contains libraries necessary to the Ant program, so it needs not search the local file system. The scripts also produces a .jar file containing the whole project for easy transportation.

### 2.3.4 Unit Testing

Every class of the project form a functional unit according to the design elaborated at the beginning of the project. In order to ensure the software’s good functioning and correct behaviour, all classes have been tested using the Java JUnit framework with test cases to tackle programming errors and code bugs.

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<sup>1</sup><http://code.google.com/p/ps-predator-prey/source/diff?spec=svn29&r=29&format=side&path=/code/Output.java>

The libraries necessary to the tests are thus accessed from the test cases using Java import statements and extending the `TestCase` superclass in the class declaration:

Listing 2.5: Test case headers

```
import org.junit.Before;
import org.junit.Test;
import junit.framework.TestCase;

public class TestAnimal extends TestCase {
    ...
}
```

The test cases, for each class, follow the normal directives in use for Unit testing with JUnit. The most relevant methods were submitted to thorough tests, where their properties, return values and correct functioning were evaluated by comparing the actual results they provide with the expected ones. These procedures were implemented by test methods in each test case using the format required by the JUnit standards.

Every test case includes a `setUp()` method that builds the initial object and its different parameters. Directives like `@Before` and `@Test` for every method declaration were thus inserted in the code where appropriate. The functioning of a method is then assessed comparing the expected results with the actual ones with JUnit testing methods such as `AssertEquals()`, `AssertNotNull()`, etc...

Listing 2.6: Use of JUnit directives in test cases

```
@Before
public void setUp() {
    ...
    testAnimal = new Animal(numAnimals);
    testAnimal.setName("Puma");
    ...
}

@Test
public void testAnimal() {
    assertNotNull(testAnimal);
    assertNotNull(testAnimal2);
}

...
}
```

Where possible and where the tests were failing, we corrected and bettered the code until all tests passed correctly. We have employed several different methods and tools to debug the code, mainly with Eclipse IDE's debugger and JDB (Java Debugger) at the command line, that enabled us to verify the variables in use in classes and methods are holding the correct desired values during runtime. We have in this manner corrected many mistakes and wrong operations until the software was performing as expected. We also have used certain programming techniques such as Test Driven Development, unfortunately in just a few classes, although the procedure would deserve more time and practice to achieve a reasonable degree of maturity and efficiency to prove a powerful tool.

## Chapter 3

# Results

After the code was completed and was outputting sensible ppm files like the ones shown previously, we needed to confirm that the density profiles behaving correctly. The most obvious way of doing this was to plot the mean densities over time for both of the animals. This plot is shown in figure 4.1 for the default parameters given in problem specification. As expected both animals start of with an average density of 2.5 (after having initialised the densities with uniform random distributions between 0 and 5). As the pumas begin to eat the hares, the predator densities increase, corresponding to a decrease in the density of hares. The pumas eventually eat all of hares in their areas, and start to die off, corresponding to an increase in hare population. The hares then begin to spread, and the cycle repeats itself.

### 3.1 Output Analysis

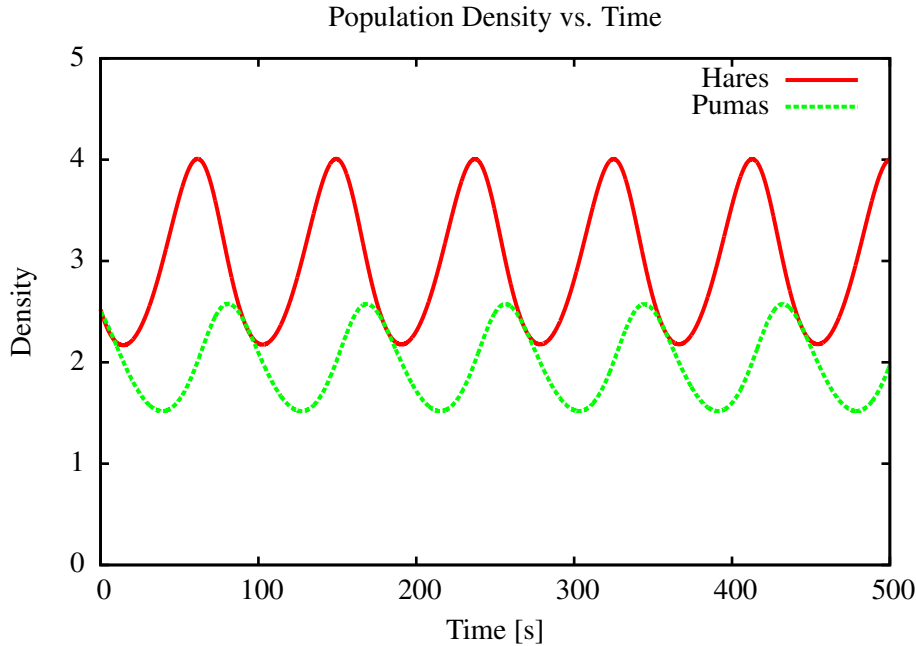


Figure 3.1: Population density vs. time for Hares and Pumas. This periodic behaviour is typical of predator-prey interactions.

### 3.2 Performance Analysis

Because most optimisation in Java is done at runtime using Just-In-Time (JIT) compilation, there is not much to choose from in the way of compiler flags. The way in which a problem is laid out is always very important, however, so our main aim in performance testing was to identify inefficiencies within the code itself, such as unnecessary loops and calls to methods.

Profiling of the code was done mostly with NetBeans and the unix *time* command. Parameters were varied to assess the effect of a number of factors, most notably overhead, output write time, and the effect of map size and complexity.

One of the main things which we identified very quickly as a bottleneck was the output. Fortunately, implementing a buffered writer is very easy in Java; this alone increased performance by a factor of 5-6 (see Figure 3.2).

The performance of the program could be increased even further by having the output in a more efficient format. This can be shown more simply by running the code with an output frequency of 50 timesteps compared with an output frequency of 5000 timesteps (a single output for a  $t=0..500$ ,  $timestep=0.4$  simulation). This gave run times of  $\sim 21.5$  and  $\sim 17.0$  seconds respectively, even with buffered output. This output then accounts for  $\sim 17\%$  of the computation time of a simulation,

which is obviously not ideal.

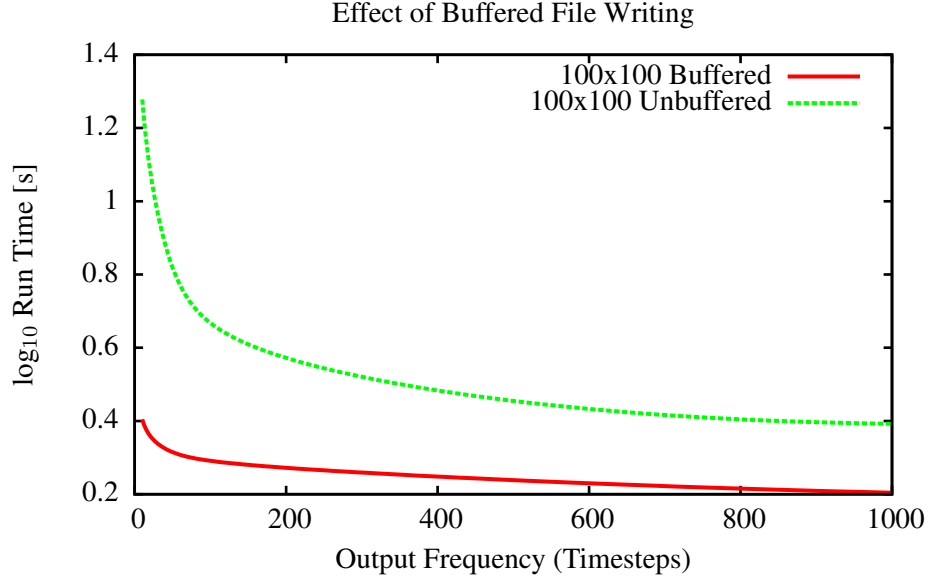


Figure 3.2: This graph shows the advantage of using a buffered file writer over repeated calls to the `printf()` method. The data was generated from a simulation using a 100x100 grid, but results will be similar for all grid sizes, since write time and computation time (neglecting overhead) both scale linearly with the number of cells.

In Figure 3.3 we attempt to quantify the overhead in our code. This is done by calculating the total time spent on each cell in a simulation, relative to the size of the simulation. With this metric, the code actually becomes ‘slower’ for smaller simulations. This is because a significant fraction of the simulation time is being spent on finding arrays of neighbours and other ‘non essential’ tasks. The graph shows that our code only begins to run as efficiently as possible once grids of  $\sim 100 \times 100$  are used, above which the simulation time scales almost exactly as the number of cells (the flat part of Figure 3.3).

Using this, we can find how long our program takes to update a single cell, giving us a useful way of quantifying the speed. The value on the graph is roughly  $10^{-3.27}$ s per cell over the whole simulation. Thus,  $10^{-3.27}/1200$ , where 1200 is the number of timesteps, gives us the time per cell per timestep:  $\sim 450$  nanoseconds. This allows us to predict how long a given simulation should take (on the machine used to generate this data, at least). For instance, if we had a  $10000 \times 10000$  array, this would should take  $10000^2 \times N$ , where  $N$  is the number of timesteps. For the same number of steps this is about 15 hours!

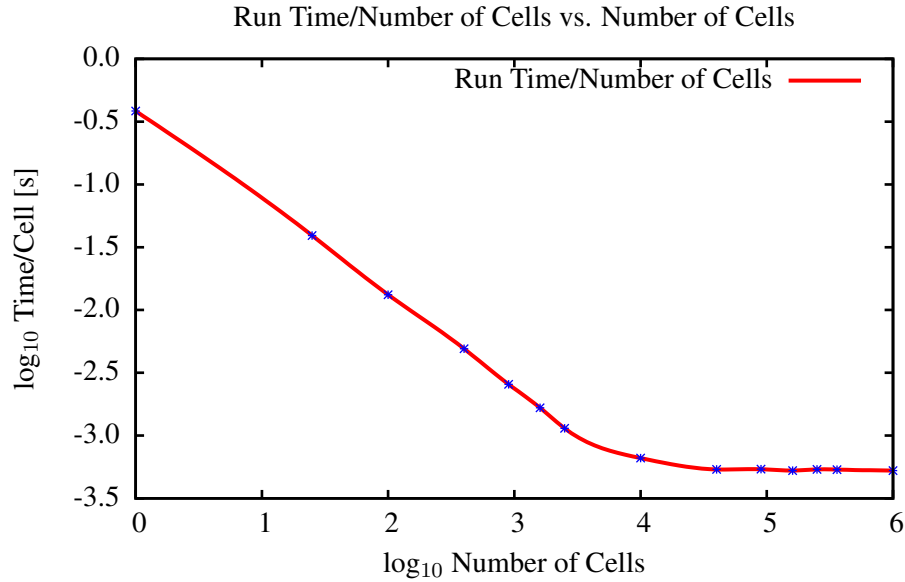


Figure 3.3: This is a graph of total time spent on each cell, which shows that overheads such as array initialization take up a significant fraction of computation time with grids smaller than  $\sim 100$  by  $100$ .

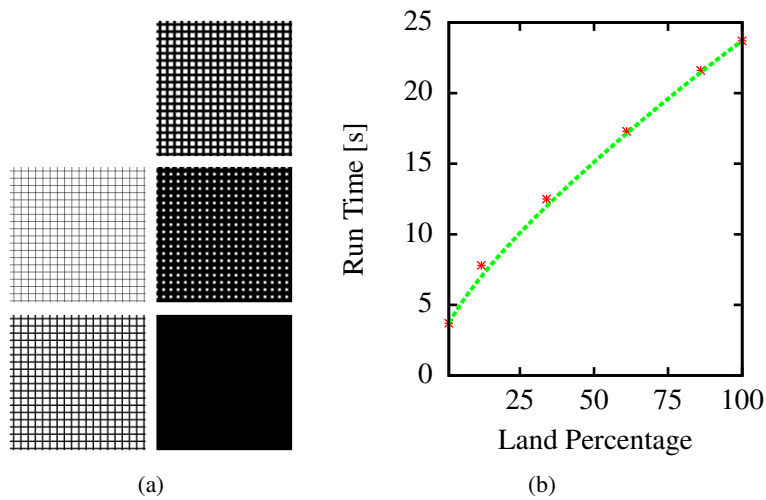


Figure 3.4: This shows the effect of fill percentage on run time. The six panels in a) are the input maps used, all of which were  $300 \times 300$ . As expected, the computation time increases fairly linearly with the amount of land, since the bulk of the main algorithm is only run for land cells.

The effect of map complexity is also discussed in Figure 3.4. As expected, we found that the code was totally insensitive to complexity, being affected mostly by the total number of land cells. This is because most of the density update algorithm is never implemented for water cells, and checking whether a cell is land or water does not take much time compared to a full density update.



## Chapter 4

# Conclusions

The Google Code SVN combined with the ability to compile and run Java code on any platform provided a universal code base that could be accessed from anywhere at any time.

We chose to write the program with a generalised algorithm, such that it could be easily extended to handle more animals. While this gives a results in slight decrease in efficiency over a more primitive less extendible alternative, it was felt that it offered a solution that was more in line with good programming practices.

GUI was not necessary for this task, however it did provide a more user friendly experience and the possibility to range over values. Possible improvements: output animations of the island to the GUI, add options to run performance tests.

The group performed well and achieved with success the task proposed at the beginning of the project. The solution is a fully working piece of software that models the diffusion of pumas and hares on a grid over time. The group has also been able to complete tests and analysis of the results obtained from the software and to plot these results on a series of graphs that visualise the behaviour of the model in time.