Diseased Daisyworld:
Homeostasis is threatened by the introduction of virtual bacteria

By Mark Paterson Monash University

22643206 mwpat2@student.monash.edu

Abstract

Watson and Lovelock created Daisyworld to realistically model the coupled system of life and the environment. This world comprising of black and white daisies, is able to maintain homeostasis with an increasing solar radiation because the differing daisies absorb different amounts of radiation. This model was modified to become an agent based, 2D spatial model. The aim was to investigate what will happen to homeostasis when a pathogenic bacteria was introduced, becoming diseased. *Xylella fastidiosa* is one such bacteria that causes Pierce's disease in grapevines. It thrives in warmer temperatures in Central America. With climate change, it is likely to spread from America into Europe. This is important as if left unchecked, it could restrict the diversity of food and decimate the wine industry. The effects to homeostasis on Diseased Daisyworld were modelled using a computer simulation, which introduced virtual bacteria. By varying the infectivity of daisies to the bacteria, Diseased Daisyworld was tested how well it could maintain homeostasis. It was found that as the rate of infectivity increased, the average temperature of homeostasis increased and the total time homeostasis was maintained decreased. This shows that the virtual bacteria does directly influence the global environment of Daisyworld. Ultimately, knowledge of how bacteria interacts with the global environment will help to keep the Earth habitable in the future.

Keywords: Agent based model, Climate change, Daisyworld, Pierce's Disease, *Xylella fastidiosa*

1. Introduction

1.1 Modelling climate change

Climate change and global warming are a huge issue facing humanity in the 21st century (Houghton, 1996). Over the course of billions of years, according to Gaia theory, the entire biosphere of the Earth has evolved to become self-regulating and homeostatic (Lovelock, 2003). Since the industrial revolution humans have been changing the environment too fast (Change, 2007; Houghton, 1996). What is vital to know is how the ecosystem will evolve over time and will it still be able to support life? To answer this question, it is best to use a model. You do not want to wait and see what will happen in real life, only to discover that the Earth is no longer habitable and you have to find somewhere else to live. Instead, models allow far greater flexibility (Dorin, 2014 pg. 118). This allows for one perturbation to be isolated, with absolutely no risk involved for the planet.

1.2 Disease and Pathogenic bacteria

Disease caused by pathogenic bacteria is a real concern when dealing with climate change in the future. Increasingly bacteria is developing drug resistance to antibiotics, which potentially could become a healthcare crisis in the future (Magiorakos et al., 2011). Furthermore, disease including pathogenic bacteria is threatening our forests and agriculture and food supply.

Restricting diversity of food and being reliant on one food source can have disastrous effects. In the mid-19th Century, out of a population of 8 million people, 3 million Irish peasants were dependent on the potato as a staple of their diet (Braa, 1997). When the potatoes became diseased, 1 million people died and another 1.3 emigrated to other countries (Boyle & Grada, 1986). It is therefore important to learn from and not repeat the mistakes of the past.

Xylella fastidiosa is one such pathogenic bacterium that causes diseases in over 100 species of plants. It needs a warm climate to survive and is currently a big problem facing Central America (Schaad, Postnikova, Lacy, Fatmi, & Chang, 2004). Its optimal temperature for growth is 33°C and below 10°C, growth diminishes. It is so dangerous as there is no current way to kill it (Hopkins & Purcell, 2002). Diseases typically caused are typically of the leaf scorch variety (Chatterjee, Almeida, & Lindow, 2008). One disease that *Xylella fastidiosa* can cause is Pierce's disease in grapevines (Figure 1). The bacteria is spread from vine to vine by vector insects, such as the leafhopper and sharpshooter. It may not be possible to kill *Xylella fastidiosa*, however, you can control it. One way is through the vine's resistance to the bacteria. Vines have a full spectrum of resistance, ranging from the European type *Vitis Vinifera* that have little resistance, to the most resistant muscadine grapes *Vitis Rotundifolia*. It is then possible to genetically control to resistance of the vines to infection. When a grapevine is infected, its' leaves go brown, grapes shrivels up and the vine eventually dies (Hopkins & Purcell, 2002). If the global temperatures do rise, then there is a real threat of *Xylella fastidiosa* spreading throughout the rest of America and into Europe. Resulting in the loss of the food variety from grapes and the decimation of the wine industry.

Figure 1 Pierce's disease in different grapes: A and B leaf necrosis (tissue death) in red bunch grapes. C leaf scorch in Fiesta bunch grapes D leaf scorch in muscadine grape

It is important to understand how a bacterial disease could impact the Earth in the future. One way to achieve this, is through the use of a model.

1.3 Daisyworld

Daisyworld originated as a model from the closely coupled system of the biota and the environment. This is too complex to model on the Earth, so a simple world was created to display one property that is important to the Earth, temperature regulation (Wood, Ackland, Dyke, Williams, & Lenton, 2008). Daisyworld is this fictional world that is covered by two types of daisies. Dark daisies reflect less light than bare ground and light daisies reflect more light than bare ground (Watson & Lovelock, 1983). The growth rate of daisies β, is dependent on the local temperature T_L, with a steady state temperature at 22. 5°C (Figure 2) (Watson & Lovelock, 1983 eq. 3)
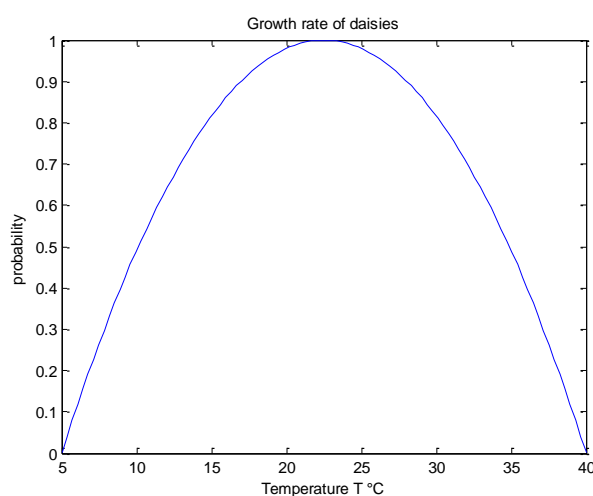
$$\beta = 1 - 0.003265(22.5 - T_L)^2 \tag{1}$$

Figure 2 Growth rate of daisies

Mark Paterson 22643206
mwpat2@student.monash.edu

The dark daisies increase the temperature of the planet and the light daisies decrease the temperature of the planet with respect to bare ground. Daisyworld was subjected to increasing solar radiation over time. When Daisyworld is too warm, it grows more light daisies. When Daisyworld is too cold, it grows more dark daisies. By balancing the number of light and dark daisies, Daisyworld maintains homeostasis (Figure 3) (Dorin, 2014 pg. 112 - 114). The global temperature of Daisyworld was governed by a series of mathematical equations (Watson & Lovelock, 1983 eq. 4). This is only concerned with the overall population of each type of daisy and ground, with the position irrelevant.

$$\sigma(T + 273)^4 = S \times L(1 - A) \tag{2}$$

Where T is the temperature (converted to kelvin), σ is the Stefan's constant, S is solar flux, L is the luminosity and A is the planetary albedo.
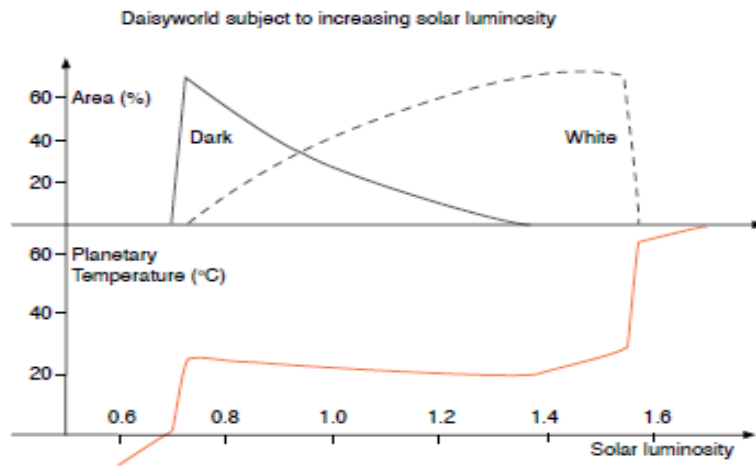

Figure 3 (top) Graph of percentage of area covered by Dark and White daisies and (bottom) graph of planetary temperature versus solar luminosity (Dorin 2014 pg. 113)

An extension to the original model, is to make a 2D spatial Daisyworld (Wood et al., 2008). Daisies and bare ground are represented with a cellular automaton grid, having explicit diffusion between cells. Each cell is either occupied or unoccupied and during every time step, an occupied cell may die and an unoccupied cell may grow a daisy.

One of the more popular models, has multiple types of daisies and a regrowth rule (Von Bloh, Block, & Schellnhuber, 1997). Choose a random neighbour of an unoccupied cell. That cell can colonize the unoccupied cell according to the growth rate. Then the new daisy has an albedo that randomly mutates from the albedo of its neighbour. Resulting in a spectrum of albedos ranging from 0 to 1. The temperature of each individual cell is governed by an equivalent equation to equation (2) (Von Bloh et al., 1997 eq. 6)

$$C \frac{\partial T(x,y,t)}{\partial t} = D_T \left(\frac{\partial^2}{\partial x^2} + \frac{\partial^2}{\partial y^2} \right) T(x,y,t) - \sigma T(x,y,t)^4 + S' \tag{3}$$

With two new constants C and the diffusion constant D_T. Laplace's equation can then be estimated with a difference equation (Abramowitz & Stegun, 1972 pg. 885).

$$\frac{\partial^2}{\partial x^2} + \frac{\partial^2}{\partial y^2} \approx T(x-1,y) + T(x+1,y) + T(x,y-1) + T(x,y+1) - 4 \times T(x,y) \tag{4}$$

A similar approach is agent based modelling. Where instead of using cells to determine how the system behaves, the agent based model uses agents.

1.4 Agent based models

Agent based models look at systems at the individual level. This greatly increases the complexity of the model, therefore it must be run as a simulation on the computer (Grimm et al., 2006). The requirements for an agent based model are to have a set of agents, a set of interactions between agents and an environment for the agents (Macal & North, 2010). The most important feature is that an agent acts autonomously. All agents are able to act and interact with each other uniquely. Furthermore, agents do have the ability to move around their environment. Agents may grow, develop, reproduce and ultimately die. This in turn modifies the environment and taken together, determines how the overall system behaves.

In evolutionary agent based models, the goal of agents is to pass on their genes to the next generation, by maximising their fitness (Grimm & Railsback, 2005 pg 2). Every agent is uniquely different from each other. Differences that enhance survival increase their fitness and the number of offspring they have. Over time the agents with the higher fitness should accumulate and agents with the lower fitness should be eradicated (Dorin, 2014 pg 122).

There are different ways to model transmission of infectious diseases (Riley, 2007). Patch models construct patches based on location (Figure 4A). All individuals of the same patch have the same risk of infection. If one individual of the patch is infected, then the rest of the individuals in the patch all have an equal risk of infection. Conversely, there is no risk if no individuals in the patch are infected. Distance Transmission places all individuals within a certain range at risk of infection (Figure 4B). With a greater risk the individual is to the infection. Containment and Groups place individuals in groups (Figure 4C). Individuals can belong to multiple groups. Individuals belonging to multiple groups connects different groups together. If an individual in a group is infected, then the rest of the group and other groups that the individual is connected to are at risk. Networks connect individuals to other individuals (Figure 4D). There is only a risk of infection if an individual is connected to another infected individual.
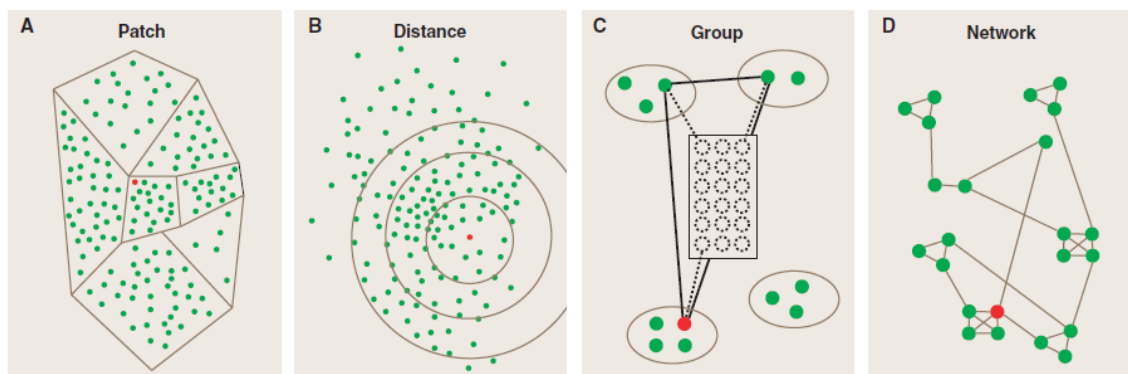

Figure 4 Red dot marks the infected member A. Patch models, B. Distance Transmission, C. Containment and Groups, D. Networks (Riley, 2007)

The structure of the rest of the paper will be as follows: Section 2 will detail the method of creating an agent based Daisyworld with virtual bacteria. Section 3 will outline the results to of how Diseased Daisyworld maintains homeostasis after running experiments. Section 4 will discuss and analyse the results. Section 5 will discuss any future work that is needed. Section 6 will present the conclusion. Section 7 lists the Bibliography and lastly, section 8 has the Appendices, will contain a Test Report and a READ ME section.

2 Method

2.1 Overview

Diseased Daisyworld is an agent based extension to the original Lovelock and Watson model. It is a world made up of black and white daisies and bare ground with increasing solar luminosity from the sun over time. Virtual bacteria will be introduced that will be based on the bacteria *Xylella* fastidiosa and will be represented by a new type of daisy called a diseased daisy (Figure 5).
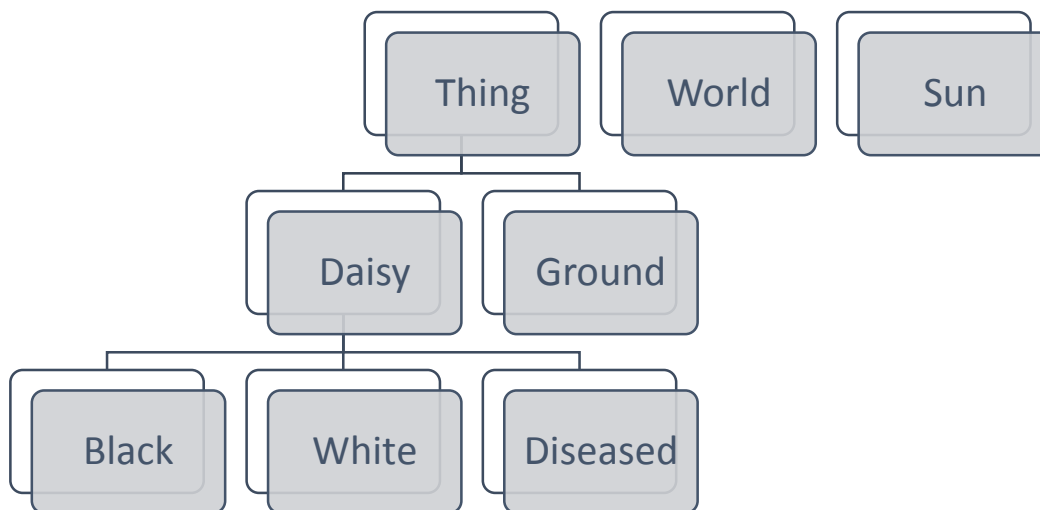

Figure 5 Class diagram

The energy that heats the world comes from the sun.

2.2 Sun

The sun provides Diseased Daisyworld with solar luminosity. Luminosity initially starts at 0.65 and increases by 0.005 each time step. Solar luminosity multiplied by the Solar flux constant of 917 Wm^{-2} provides the energy needed to heat the World.

2.3 World

The World is represented by an n by n torus shaped grid. There will be two representations of the world: one representing the agents (daisy, ground) and another being a heat map. The heat map will represent the temperature of each agent with a colour. From coolest to hottest they are dark blue, light blue, green, orange, red and black.

Each agent in the grid is classified as a Thing that is either a daisy, or ground. Each Thing has a local temperature. The World has a global temperature that is the average out of all the individual local temperatures. The initial global temperature is set to 0°C and the grid is initially populated with bare ground.

2.4 Ground

Ground has only one function, it can grow daisies according to the parabolic function from Lovelock and Watson, dependent on the local temperature T in kelvin (Figure 2):

$$\beta = 1 - 0.003265(22.5 - T_L)^2 \tag{1}$$

Daisies can only grow and survive between 5°C and 40°C, with a maximum growth rate, or steady state at 22.5°C.

There is an equal chance of growing a black, or white daisy before the number of daisies reaches a threshold.

$$Threshold = 0.8 \times Number\ of\ bare\ ground \tag{5}$$

Then it is dependent on the immediate 8 neighbours. The probability of growing a white daisy, is the proportion of white daisies to the total number of white and black daisies. The reverse holds for growing a black daisy.

$$P_{White} = \frac{N_{White}}{Total} \; ; P_{Black} = \frac{N_{Black}}{Total} \tag{6}$$

Take Figure 6 as an example. The ground at (x, y) has 8 neighbours. Of those 8, there are 5 black daisies and 1 white daisy. That means the ground has 5 black daisies and 1 white daisy neighbours. That means it has 5/6 chance of growing a black daisy and a 1/6 chance of growing a white daisy.

Black(x+1,y-1)	Black(x+1,y)	Black(x+1,y+1)
White(x,y-1)	Ground(x,y)	Diseased(x,y+1)
Black(x-1,y-1)	Ground(x-1,y)	Black(x-1,y+1)

Figure 6 Probability of growing a black, or white daisy dependent on its immediate 8 neighbours.

2.5 Black and White Daisies

At each time step, black and white daisies can either continue living, or die. The daisies die according to the deathrate γ of 0.05, or if their local temperature is outside the range $5°C \leq T_L \leq 40°C$. They can become diseased from the virtual bacteria.

2.7 Diseased Daisy

A diseased daisy is a daisy infected with virtual bacteria, based on the bacterium *Xylella* fastidiosa. The disease is introduced to a healthy daisy, at a probability of 0.0001. Diseased daisies can continue living, die, or infect neighbouring black and white daisies. As the disease is lethal, the deathrate of diseased daisies are twice that of black and white daisies. Like black and white daisies, diseased daisies will also die if their local temperature is outside the range $5°C \leq T_L \leq 40°C$. *Xylella* fastidiosa is spread by vector insects from vine to vine causing Pierce's Disease. Pierce's Disease does not infect all vines that have *Xylella* fastidiosa and can appear to popup randomly over individual grapevines. Although from vineyard to vineyard, it does spread to nearest neighbours. One daisy can represent a vineyard and a diseased daisy can therefore infect their immediate four neighbours. In Figure 7, the diseased daisy (x, y) can only infect black and white daisies. That means it can infect Black$(x + 1, y)$ and

White$(x, y-1)$ and cannot infect Diseased$(x, y+1)$, or Ground$(x-1, y)$. The bacteria can only survive in a diseased daisy host.
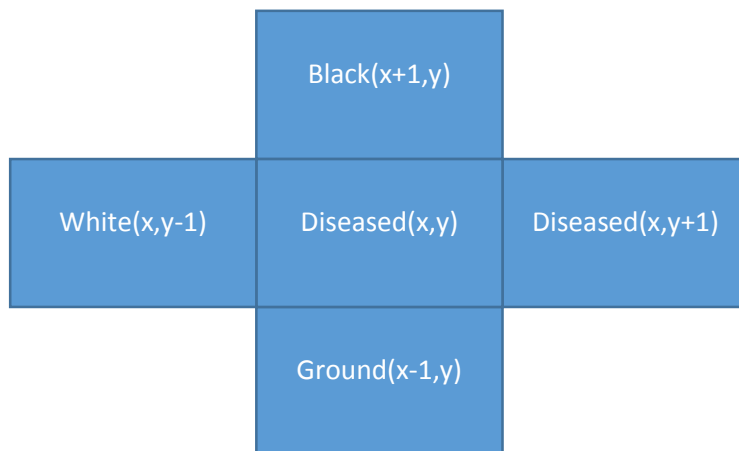

Figure 7 Disease spread at position (x,y). Black: black daisy, White white daisy, Diseased: diseased daisy, Ground: bare ground

2.8 Running the Simulation

Diseased Daisyworld will initialised with a grid of bare ground and a sun, each bare ground agent will have a local temperature of 0°C. The global temperature will also be 0°C and the sun will have an initial luminosity of 0.65.

The algorithm will consist of two sequential loops. The first loop is to build up a sufficient number of black and white daisies, so they can reproduce on their own according to equation 6. The second loop is from when there is a sufficient number of daisies, until there are no more daisies left (Figure 8). Each time step represents a month in duration.
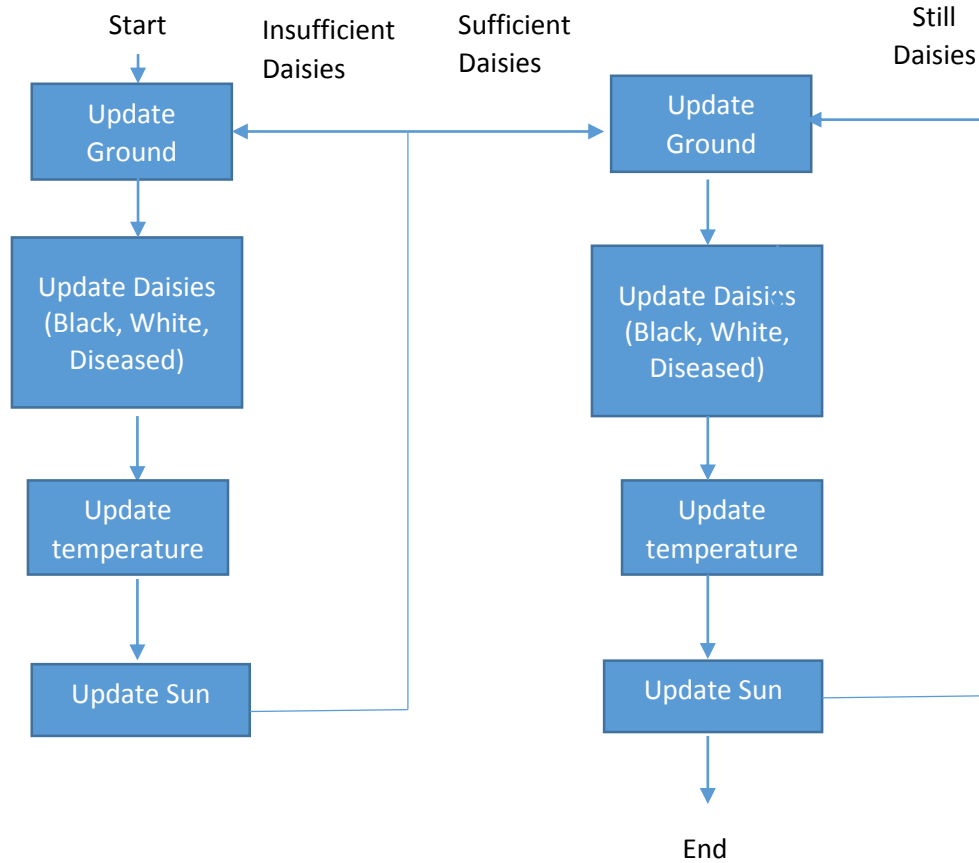
Figure 8 Flowchart of algorithm to run Daisyworld

Updating ground, involves growing daisies. Updating daisies involves killing daisies and spreading the disease and updating the sun increases the luminosity. Each bare ground and daisy agent then updates their local temperature based on the current luminosity, their albedo and their own local temperature and that of their neighbours. Therefore, heat diffuses across Diseased Daisyworld with each time step.

The change in local temperature is calculated using the heat equation from Von Bloh

$$C \frac{\partial T(x,y,t)}{\partial t} = D_T \left(\frac{\partial^2}{\partial x^2} + \frac{\partial^2}{\partial y^2} \right) T(x,y,t) - \sigma T(x,y,t)^4 + S' \qquad (3)$$

Where the Laplace equation is estimated with a difference equation (Figure 9)

$$\frac{\partial^2}{\partial x^2} + \frac{\partial^2}{\partial y^2} \approx T(x-1,y) + T(x+1,y) + T(x,y-1) + T(x,y+1) - 4 \times T(x,y) \qquad (4)$$
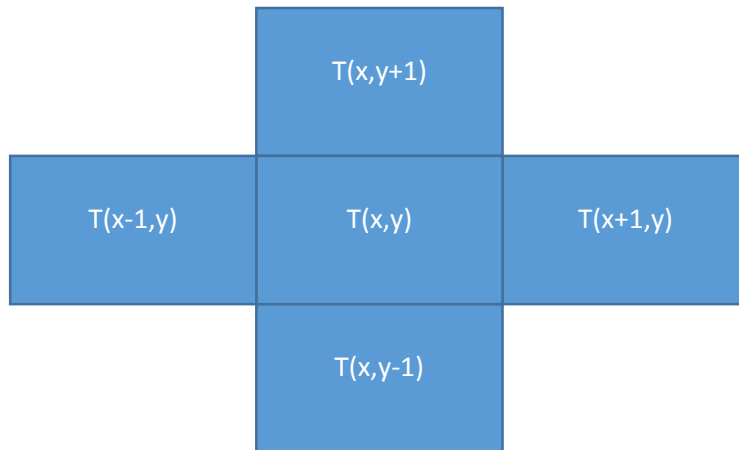
Figure 9 Cell temperature diffusion

The variable S' from Von Bloh is equivalent to $Solar\ flux\ S \times Luminosity\ L$ of the original Watson and Lovelock model.

2.9 Constants of Diseased Daisyworld

World	
C	50
D_T	0.025
deathrate γ	0.05
deathrate DiseasedDaisies	0.10
degrees to kelvin	273
initTemp	0°C
Introduce disease	0.0001
Max daisy temperature	40°C
Min daisy temperature	5°C
Solar flux S	917 Wm^{-2}
Stefan-Boltzman Constant σ	5.6696×10^{-8} Wm^{-2}K^{-4}
BlackDaisy	
Albedo A	0.25
WhiteDaisy	
Albedo A	0.75
DiseasedDaisy	
Albedo A	0.4
Ground	
Albedo A	0.5
Sun	
Luminosity L	0.65
Luminosity increase	0.005

Table 1 Constants

2.10 Experiments to test hypothesis

Will conduct a series of experiments to test the hypothesis that adding virtual bacteria will impact the global environment of Diseased Daisyworld. The rate of infectivity of the disease spreading to daisies will be tested and this can simulate plants genetic resistance to disease. The simulation will be run until all of the daisies die and the global temperature will be recorded. For different rates of infectivity, how temperature changes with time will be graphed. As it is a stochastic simulation, it will need to run

multiple times and the mean temperature, with error bars will be graphed. Error bars will be recording the 95% confidence interval. It is impossible to know in advance how many times to run the simulation for varying values of infectivity. The number of runs will depend on the magnitude of the error bars. Comparitively small error, means run fewer times and converesely large error, means run more times to be confident with the mean temperatures. At a bare minimum, 10 runs for each rate of infectivity. If there is a large change between 2 successive values of infectivity, then do some more testing between these points.

Characteristics to graph will be the global temperature over time, the start time of homeostasis, the end time of homeostasis and the average temperature of homeostasis all over rate of infectivity.

3 Results

The dimensions used in constructing Daisyworld, was a 40 by 40 grid. Diseased Daisyworld was graphically represented, with a unique colour indicating each type of agent (Figure 10a). To complement the agent representation, is a heat map that shows the local temperature of each agent as a colour (Figure 10b). For every time step, you can see for each position in the grid, what type of agent it the corresponding local temperature.

a)   Daisyworld agents   b)   Heat map
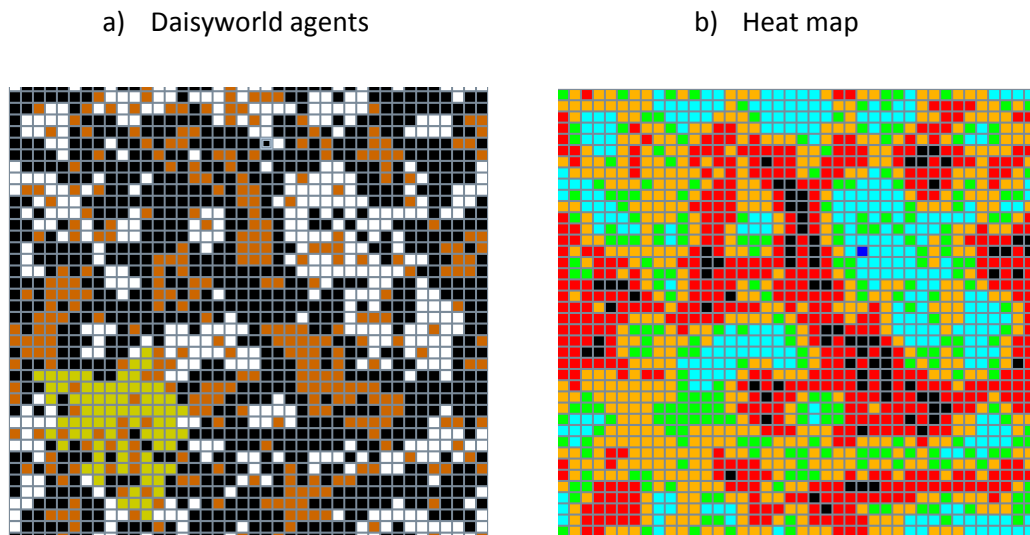

Figure 10   a) Diseased Daisyworld (colour, agent): (black, black daisies), (white, white daisies), (gold, diseased daisies), (brown, ground)   b) Heat map colour in order of heat lowest to highest: dark blue, light blue, green, orange, red, black

The simulation was initially run for 250 time steps, for infectivity rates of 0.1 between 1.0 incrementing by 0.1 each time (Figure 11). As it is a stochastic simulation, it needed to be run multiple times with a random number generator. To have some control about repeatability for each run, the seed value was controlled. The first run had a seed value of 1, with each subsequent run incrementing the seed value by 1. To begin with, I did 10 runs for each infectivity rate. Then plotted the mean temperature at each time step, with a 95% confidence interval (Lane, 2015).

$$x \pm 1.96 \frac{\sigma}{\sqrt{n}} \tag{7}$$

With x the sample mean, σ is the standard deviation and n is the number of terms.

The number of runs to do for each infectivity rate, is dependent on the size of the confidence interval. The confidence interval was larger for values of infectivity between 0.2 and 1.0. I did another 10 runs for the value 0.2 and another 20 runs for rates of infectivity between 0.3 and 1.0 inclusive.
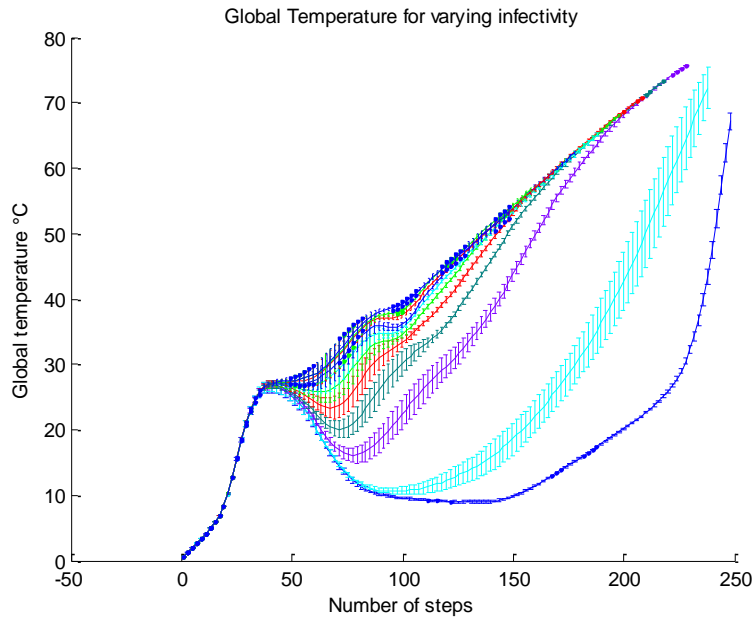
Figure 11 Varying infectivity rates from bottom to top: 0, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0

There is a large gap between infectivity rates 0 to 0.1 and 0.1 to 0.2. To see what is happening, I conducted more testing for rates of infectivity of 0.02, 0.04, 0.06, 0.08, 0.12, 0.14, 0.16 and 0.18 (Figure 12). With 10 runs for each value of infectivity.
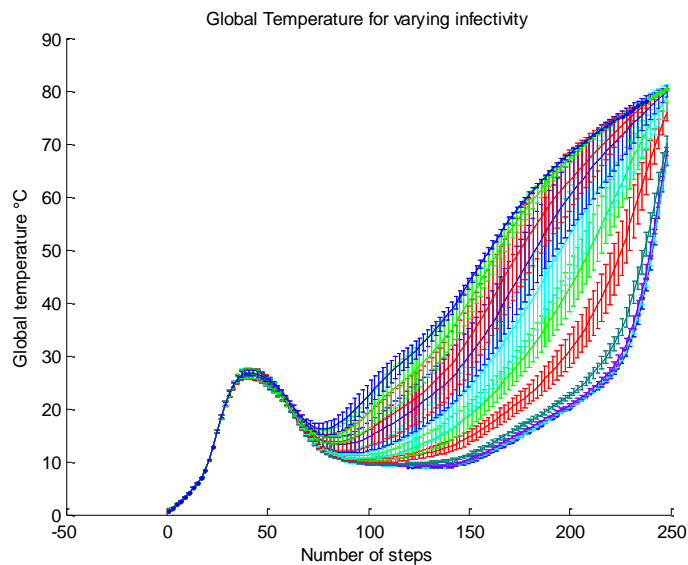

Figure 12 Varying infectivity rates from bottom to top: 0, 0.02, 0.04, 0.06, 0.08, 0.1, 0.12, 0.14, 0.16, 0.18, 0.2

Visually by inspection, varying the rate of infectivity has influenced the global environment. To quantify the results, I have produced graphs for the start time of homeostasis, the end time of homeostasis and the average temperature of homeostasis (Figure 13). Each graph has two distinct turning points. The start of homeostasis was taken from the first turning point of the graph, where it goes a positive gradient, to a negative gradient. This remains constant at 39 steps for varying rates of infectivity (Figure 13a). The end of homeostasis was taken from the second turning point of the graph, where it goes from a negative gradient, to a positive gradient again. As the rate of infectivity increases, the end of homeostasis decreases asymptotically from 140 steps to 55 steps (Figure 13b). The average

temperature of homeostasis was calculated by taking the mean between the start of homeostasis and the end of homeostasis. It was found that as the rate of infectivity increased, the average temperature of homeostasis also increased asymptotically from 14°C to 27°C (Figure 13c).
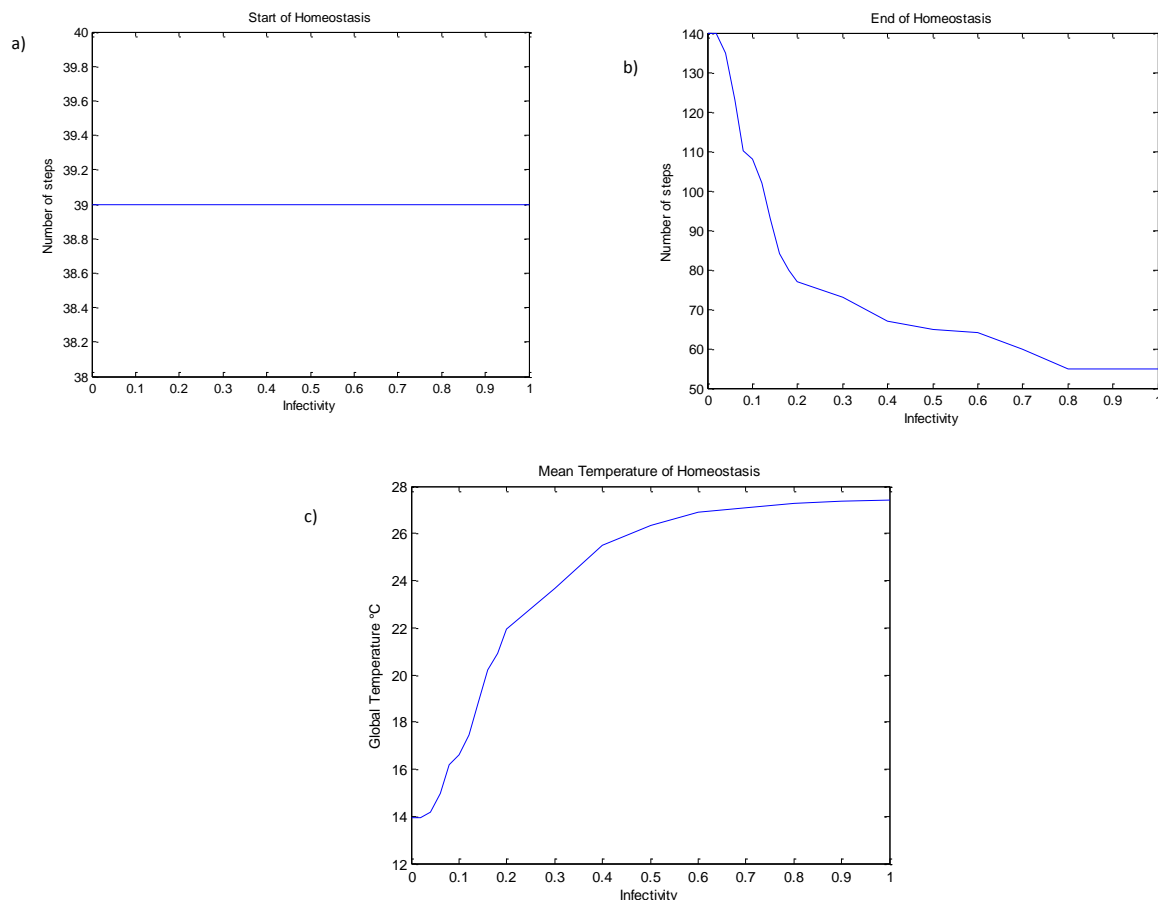

Figure 13 a) Start of homeostasis b) end of homeostasis c) average temperature of homeostasis

4 Analysis and Discussion

Adding virtual bacteria and varying the infectivity of disease was shown to increase the average temperature of homeostasis and decrease the length of time homeostasis was maintained. The main reason the virtual bacteria was able to have such a significant effect is that initially daisies cover most of the grid at any time step. That means that all daisies in Daisyworld are highly connected to each other. If you pick one daisy at any time step, you could connect that daisy, through neighbours to a majority of the other daisies in the grid. That means just one outbreak has the potential to infect the whole world (Figure 10a).

For bare ground to grow a new daisy, it needs to have at least one black, or white neighbour. With a high infectivity rate, bare ground may not be able to grow daisies even if it is at an optimal temperature (Figure 14). This is because, all of the neighbouring daisies are diseased, not black or white daisies. Once the diseased daisies begin to die off deserts begin to take form.
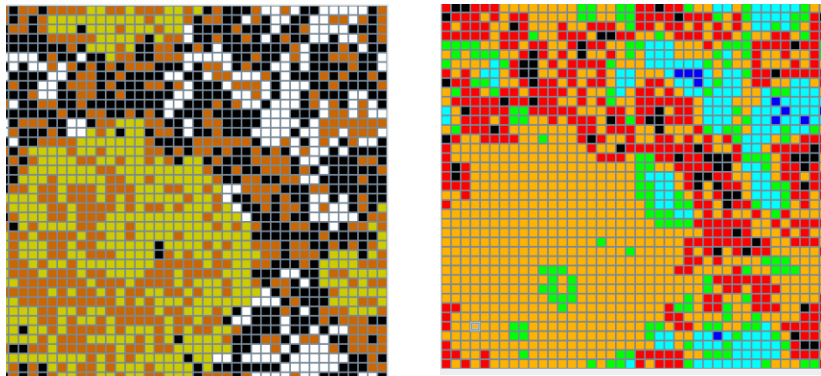
Figure 14 Desert formation in Daisyworld agent representation on the left and heat map on right

With a low infectivity rate, black and white daisies are able to keep up with the spread of disease. In this instance there are no desert formation. Bare ground can continue to grow new daisies as long as the local temperature is not too hot.

There was shown to be a limits to the maximum average temperature of homeostasis and the end time of homeostasis (Figure 13 b and c). This occurs because of desert formation. When the infectivity is high, the disease spreads right throughout the world killing off most of the daisies. What is left is isolated groups of white daisies that have avoided infection. These groups are completely independent from the rate of infectivity unless the disease is randomly reintroduces the disease.

5 Future Work

The limiting factor of this paper, is that the scale is small. Ideally, the experiments would be more meaningful on a 200 by 200 grid over 10,000 time steps. The constants C, D_T, the size of the grid and the rate luminosity increases with each time step all need to be juggled to stabalise the number of black and white daisies needed to maintain homeostasis. The extent it is possible to upscale the experiments is also dependent on the hardware available.

In this report, the disease was spread to all immediate neighbours. This looks at a macro approach of each daisy representing a vineyard. A more realistic model may be to have the bacteria spread by vector insects. Having daisies represent individual grapevines. One possibility would be to have a number of insects that move in a random direction each time step. If they land on a diseased daisy they carry the virtual bacteria for a certain amount of time steps. While they are carrying the bacteria, they can infect healthy daisies.

Managing pathogenic bacteria including *Xylella fastidiosa*, is vital to ensure the Earth stays habitable. Options are to kill the bacteria, increase the resistance of plants to infection, or limit the spread. A solution could involve combination of the options listed.

6 Conclusion

Varying the infectivity of daisies to disease does directly influence how the global environment is able to maintain homeostasis. As the rate of infectivity increases, the average temperature increases and the total time that Daisyworld is able to maintain homeostasis decreases. The preservation of grapevines, is vital to keep the Earth habitable in the future. It is therefore vital to accumulate knowledge of how bacteria interacts with the global environment.

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8 Appendices

The appendices contain a Test Report followed by a READ ME section on how to run Diseased Daisyworld.

8.1 Test Report

Before conducting the experiments of this paper, it is first vital that Diseased Daisyworld is behaving correctly.

8.1.1 No Daisies

First want to make sure that Daisyworld works correctly without any daisies. To do this, for each time step do not update bare ground. Want to check that Daisyworld works for a stable luminosity and an increasing luminosity.

When Daisyworld has a stable luminosity and no daisies, the global temperature should remain constant.

The global temperature slowly decreases to -3.74°C, before remaining stable. This indicates that the initial luminosity of 0.65 is not quite eligned with the initial temperature of 0°C. Of course, Diseased Daisyworld corrects this by itself, so will not have any effect on homeostasis.

When Diseased Daisyworld has an increasing luminosity and no daisies, the global temperature should increase as the luminosity increases.

The temperature initially dips a little before increasing linearly. This indicates that the initial temperature does not exactly match the initial luminosity. As the relevent information is when Diseased Daisyworld is in homeostasis, it does not matter to the experiment that the initial temperature is not exact.

Next, will add one type of daisy to Diseased Daisyworld and again check that it performs correctly.

8.1.2 Black Daisies only

Want to make sure that Diseased Daisyworld behaves correctly with only black daisies. The two conditions to test are that black daisies warm the environment and that the world is able to maintain homeostasis with only black daisies.

To check that black daisies warm the environment, luminosity remains constant. It is easiest to tell on a large scale, so will have a world full of black daisies that never die. The global temperature should increase at a constant rate.

The temperature does increase at a constant rate, until it approaches an asymptote. As the temperature approaches the asymptote, the rate of increase approaches 0. This implies that the luminosity provides a bounds on the range of global temperatures that are possible in Diseased Daisyworld.

Next, check that Diseased Daisyworld is able to maintain homeostasis with only black daisies. Intially, only create black daisies. Diseased Daisyworld should be able to maintain homeostasis, however, it should be at and increased temperature. Average homeostasis should be greater than 30°C.

Diseased Daisyworld is able to maintain homeostasis with only black daisies. However, the average temperature is around 40°C. This coensides with the upper bound of the range of temperatures that daisies can survive ($5°C \leq T \leq 40°C$).

Now that Diseased Daisyworld functions correctly with only black daisies, will want to check that it functions correctly with only white daisies.

8.1.3 White Daisies only

Want to make sure that Diseased Daisyworld behaves correctly with only white daisies. The two conditions to test are that white daisies cool the environment and that Diseased Daisyworld is able to maintain homeostasis with only white daisies.

To check that white daisies cool the environment, luminosity remains constant. It is easiest to tell on a large scale, so will have a world full of white daisies that never die. The global temperature should decrease at a constant rate.

The temperature does decrease at a constant rate, until it approaches an asymptote. As the temperature approaches the asymptote, the rate of decrease approaches 0. This implies that the luminosity provides a bounds on the range of global temperatures possible in Diseased Daisyworld.

Next, check that Diseased Daisyworld is able to maintain homeostasis with only white daisies. Initially, only create white daisies. Diseased Daisyworld should be able to maintain homeostasis, however, it should be at a reduced temperature. Average homeostasis should be less than 10°C.

Diseased Daisyworld is able to maintain homeostasis with only white daisies. However, the average temperature is around 5°C. This coensides with the lower bound of the range of temperatures that daisies can survive ($5°C \leq T \leq 40°C$).

Now that Diseased Daisyworld functions correctly with black daisies or white daisies, the next thing to test is that Diseased Daisyworld works with black and white daisies.

8.1.4 Black and White Daisies

The first property to test with black and white daisies is reproduction. Bare ground with all black daisy neighbours should produce a black daisy 100% of the time and bare ground with all white daisy neighbours should produce a white daisy 100% of the time.

This test was conducted on a 3 by 3 grid, with one bare ground surrounded by 8 neighbouring daisies. The results found that when surrounded by 8 black daisies, bare ground always grew a black daisy. Conversely, when surrounded by 8 white daisies, bare ground always grew a white daisy.

Now that Diseased Daisyworld is able to reproduce black and white daisies correctly, the next property to test is that Daisyworld is able to maintain homeostasis with a fixed luminosity. This should be maintained through balancing the number of black and white daisies.

Test it by building up a sustainable population of black and white daisies as normal, while increasing luminosity. Next, fix luminosity and switch to growing new daisies based on their immediate neighbours.

Daisyworld is able to maintain homeostasis with both black and white daisies. With a luminosity fixed to 0.82, the average global temperature of homeostasis is around 16.5°C.

So, daisyworld is able to reproduce and maintain homeostasis with a fixed luminosity. The next thing to test is whether it can maintain homeostasis with an increasing luminosity.

Daisyworld is able to maintain homeostasis. Initially black daisies dominate and the global temperature increases. Daisyworld becomes too hot to sustain daisies and white daisies dominate. The number of black daisies left are too few to bounce back as the global temperature drops. This means that the average temperature of homeostasis is on the low side, around 10°C. This is still acceptable, as it is a baseline to compare results to when the disease from virtual bacteria is added.

Diseased Daisyworld, does run adequately. Now before adding virtual bacteria, need to check that it behaves correctly.

8.1.5 Virtual Bacteria

Daisies that are infected with virtual bacteria become diseased. Diseased daises can then spread the virtual bacteria to their immediate 4 neighbours. The probability that the neighbouring daisy will also become infected, or their rate of infectivity is going to be varied in this paper. To check that the disease spreads correctly, the rate of infectivity will be fixed to 1.0. The disease should then spread to all 4 neighbours.

The grid size will be reduced to a 3 by 3 grid. Diseased daisy will be in the middle cell, surrounded by 4 non-diseased daisies. The Infectivity rate of daisies will be fixed to 1, the rate of spontaneous infection fixed to 0 and the death rate fixed to 0. Then call update daisies and all daisies should become diseased.

All 4 neighbours correctly identify that they are adjacent to a diseased daisy. However, the disease is not spreading to all neighbouring daisies. The algorithm to infect new daisies works. The discrepancy comes from updating the daisies. The updating algorithm loops through all daisies of a particular type, with the stopping condition the number of that type of daisy. When a daisy becomes diseased, it is removed from the black or white list and placed in the diseased list. This reduces the number of daisies and as such, not all daisies are updated. They are updated on the next iteration. On a macro scale, with hundreds, or thousands of daisies the discrepancy will not make enough difference to influence the simulation. All it may do is delay the spread of disease fractionally.

8.2 READ ME

Open Diseased-Daisyworld.jar file and you are greeted with the two windows in Figure 15. The left window represents the agents as colours. Brown for ground, black for black daisies, white for white daisies and gold for diseased daisies. The right window is a heatmap using colours to represent temperature. The order from coldest to hottest is dark blue, light blue, green, orange, red and black. The window titled 'Diseased Daisyworld' has a menu bar that provides everything you need to run the simulation. First, click on 'Infection Rate' and choose an infection rate between 0 and 1 from a drop down list. You have buttons to either 'Step' through one time step, or 'Run' the simulation to completion. The right hand corner of the menu bar displays the global temperature, that is initially set to 0°C. You can pause the simulation at any time by pressing the 'Stop' button and return to the initial state by pressing the 'Reset' button. When finished you can save the current run by pressing the button 'Write to file'. Each run is saved to a file corresponding to the rate of infection used.
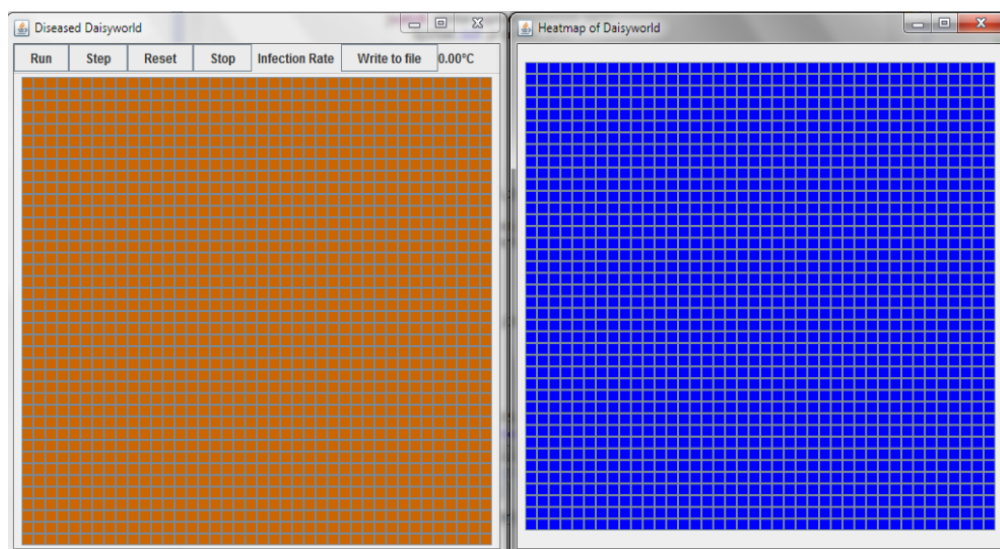

Figure 15 Initial screen