



Observing coevolution in simulated bacteria

Using asexual reproduction and simple direct mapped functions for decision-making

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1 Abstract

In this report we have presented the results of a program which performs simulations of artificial bacteria with the ability to evolve different characteristics and behaviours through genetic algorithms. Over time unfit bacteria will die out, and the more fit bacteria will produce offspring with slightly mutated variants of it's genetic code resembling the evolutionary process. The simulation does not follow the traditional macro-scale hand-picked sexual reproduction often used in genetic algorithms to produce optimal results, but it instead uses individual asexual reproduction which more closely resembles how bacteria reproduce in nature. Furthermore we do not use traditional neural networks for decision making, but simple functions which directly map the bacterias inputs to their decisions.

The purpose of this study was to observe whether bacteria with different initial starting populations would coevolve, and specialize into heterogeneous populations. Furthermore we have tried to analyze how the populations interact with each other and how changing the different parameters of the simulation would affect the populations. We have performed three separate experiments that differ in their initial conditions, one with pre-created and heterogeneous herbivores and carnivores, one with homogeneous omnivores, and one with bacteria whose genetic values have been decided at random. The result of our experiments was that we observed coevolution in the bacteria, and that they would despite very different initial starting conditions always grow towards stable heterogeneous populations with very few exceptions.

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2 Introduction

This report evaluates the result of a program which has been developed to simulate artificial bacteria and evolution through genetic algorithms. The bacteria eat, fight, reproduce and die over the course of the simulation, the weaker bacteria will perish while the stronger will be able to evolve to take on different characteristics which help them adapt better to their environment. We hope to be able to observe the bacteria evolving from a homogeneous neutral state to an heterogeneous end state through coevolution.

3 Purpose

We will perform three different experiments, each with different starting conditions. We will perform one experiment where the starting bacteria will be either heterogeneous herbivores or carnivores whose genetic values have been decided by us, one experiment where all the starting bacteria will be homogeneous omnivores, and lastly one experiment where the genetic values of the bacteria will be set at random. As the bacteria evolve, we will observe how they interact with each other and whether there is pressure to from other organisms in the simulation to push evolution in certain direction, and hopefully observe coevolution where two (or more) different species will evolve in certain ways based on the presence of each other in the same environment and how they are affected by different starting conditions.

Our primary problem statement is whether we can observe homogeneous populations of bacteria coevolving towards specializing into heterogeneous populations. Our hope is to observe these bacteria coevolving into different species and being able to coexist in the simulation. The largest obstacle towards achieving this consists will consist of observing how our simulation rules affect the simulation, a major part of the work will go towards discovering how these rules should be implemented to allow for such scenarios to occur.

4 Background

4.1 Evolution

In “On the Origin of Species” by Charles Darwin, it is argued is that all life on earth is based on variation. Over time tiny genetic variations occur in organisms and through natural selection those with advantageous variations will be more likely to pass on those genetic variations to their offspring as they have better adapted to their environment and can then pass on their genetic material. These variations during an extended period of time causes the organisms to gradually evolve and further adapt better to their environments, and at times even evolve into separate species. This is what is known as evolution. (1)

4.2 Genetic algorithms

As evidenced from the diversity of species on earth, the ability for organisms to adapt to their environment in many different ways is truly remarkable. If one views this as a problem of adapting a species with the environment as parameters, then nature with it's millions of years of evolution can provide a far more simple and efficient solution than conventional algorithms. (2)

Genetic algorithms is the field of trying to emulate the naturally occurring selection by having solutions of a problem both fight with each other for survival and mate for reproduction, just like in nature the solutions adapt over time to become improved. Genetic algorithms are a non-deterministic heuristic where solutions are generated randomly, and then mutated in order to create better solutions. Initially a set of random solutions are generated, and among those solutions the most fit are selected and their genetic material passed on with small mutations. The same process is then repeated for this new set of solutions, over and over again until a sufficient result has been achieved. There are many different ways of implementing genetic algorithms, and exactly how one should choose to implement them depends on the specific problem. (3)

Genetic algorithms can be used even for very simple problems, but they are especially effective in finding solutions for problems with large numbers of variables which can be combined into very complex amounts of possible solutions. For example, when designing complex structures a genetic algorithm can improve on a solution several factors faster than engineers simply by applying random mutations and keeping improvements and discarding mutations that do not help the final solution. (4) As genetic algorithms involve random mutations, they are non-deterministic and can often yield different results from the same initial conditions.

4.3 Coevolution

Coevolution means that a certain organism evolves in a certain way to adapt to the evolution of another organism, in order to better adjust to the new circumstances. Coevolution is observable all over nature at all levels from tiny

microorganisms to large animals. In short, it means that the evolution of different species affect each other and the success of a new mutation can depend on the success of another mutation in a different creature. (5) This is what we hope to be able to observe in our simulation.

4.4 Terminology

4.4.1 Herbivore

A herbivore is an organism that survives by eating only plants and other vegetative materials. (6)

4.4.2 Carnivore

A carnivore is an organism which eats other animals as a source of food. (6)

4.4.3 Omnivore

An omnivore is an organism that can eat a wide range of foods, such as both plants and other organisms as a source of food. (7)

4.4.4 Heterogeneity

Heterogeneity is when elements of a group differ in structure. (8)

4.4.5 Homogeneity

Homogeneity is when elements of a group are similar in structure. (8)

4.4.6 Lotka-Volterra model

The Lotka-Volterra model was devised by two different mathematicians and scientists independently during the 1920s. It is a model which can predict the population development according to a system consisting of predators and prey. If there is an abundance of carnivores, there will be fewer herbivores as they are more likely to get eaten, this in return means there will then be starvation among the carnivores which leads to a rise in herbivore population and a drop in carnivore population. At this point the abundance of food for carnivores means the carnivore population will rise once again, and so the cycle repeats. (9)(10)

4.4.7 Tick

A tick refers to a unit of time where our simulation applies the rules of the simulation, essentially meaning one turn of the simulation. Each tick all bacteria will act, interact and react to other entities. Assuming the computer can keep up, we perform this 100 times per second.

4.4.8 Asexual reproduction

Asexual reproduction is where the genetic material of offspring is a copy of the genetic material of the parent, usually done through cell division. Asexual reproduction requires only one parent. (11)

4.4.9 Direct mapped function

We will refer to our decision system for the bacteria as a direct mapped function. It means that whenever the bacteria senses anything in a certain direction, that impulse is scaled by the bacterias genetic attraction to that object and is then directly translated to a movement vector for the bacteria. Therefore there occurs no advanced decision making, but rather that all inputs are directly translated into the movement of the bacteria.

5 Implementation

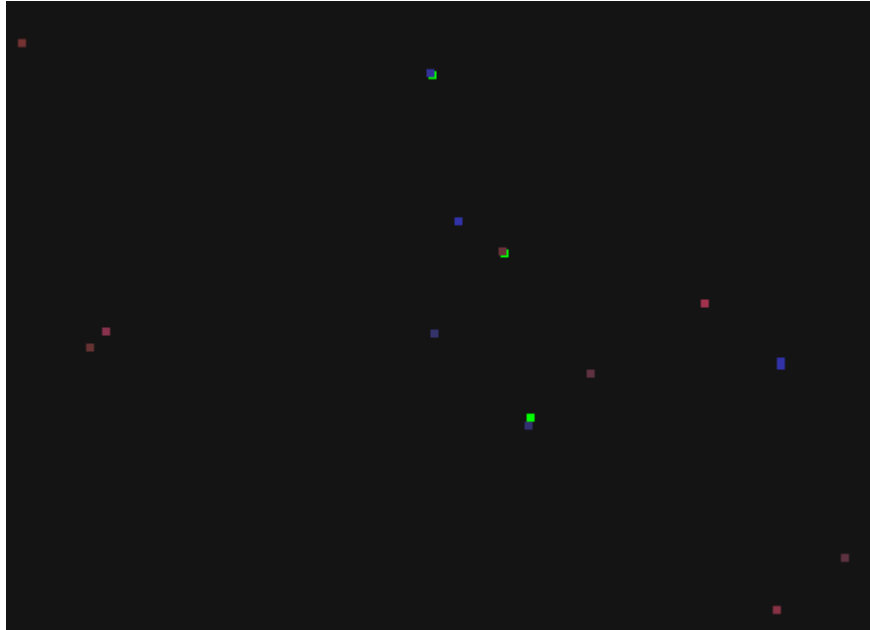


Figure 1: A visualization of our simulation. The green dots represent plants, the blue dots represent herbivores, the red dots represent carnivores and the colours in between represent omnivores. The darker the color a bacteria, the less energy it has.

The program involves simulating bacteria with specific properties which interact and live according to certain rules which we have decided for the simulation. Across the simulated world, food in the form of plants has been scattered which when eaten by certain bacteria replenishes their energy. If a bacteria reaches maturity and is of good health it can reproduce asexually into two different offspring which will inherit similar properties of the parent with a few mutations which will make their genetic material different. We have included a user interface (UI) which provides a real time overview of the simulation which will be the easiest way to get an overview of the world state, and we have included logging tools with which we are able to export the massive amounts of simulation data which can be statistically represented using MATLAB.

5.1 Decision systems

An artificial neural network is a simplified implementation of a biological neural network. A biological neural network is what all living creatures, including humans, have in the brain to make decisions based on various parts of informa-

tion. A neural network works as a directed graph with many nodes, information comes in at one side of the network and is then processed by various parts of the network until a conclusion is reached at the other end of the nodes. This can then not only be used to determine behaviour but also to help in detecting patterns in machine learning. (12)

We have decided to not use neural networks for multiple reasons, primarily because they can be very difficult to implement. Implementing a well-functioning artificial neural network takes a lot of time and knowledge, which is out of the scope of this project. Furthermore, the objective of our report is not to develop and analyze a neural network, it's to simulate evolution. As we are not searching for an optimal solution to a problem, but rather how the solutions (organisms) interact with each other it is not of vital importance.

We have instead decided to implement a simple direct mapped behaviour system based on the genes of the bacteria. This works by for each object in vision range, inversely scaling the distance by the genetic attraction to that object and then directly feeding the result as a movement vector to the bacteria. One could argue that this is a very simple and very scaled down version of a neural network, but it is significantly smaller and that the functionality won't be as advanced, but hopefully good enough for our purposes. One major inspiration for our implementation has been the report by Tegelund, Wikström(13) where they instead of neural networks use simple direct mapped functions for generating decisions to achieve successful results, so we know that the methods chosen by us are viable.

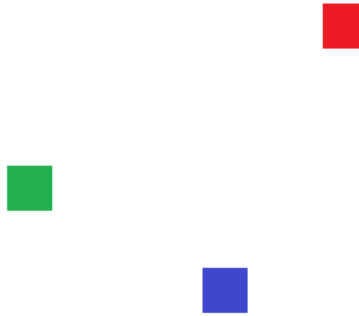


Figure 2a: A herbivore (blue), a carnivore (red) and a plant (green).

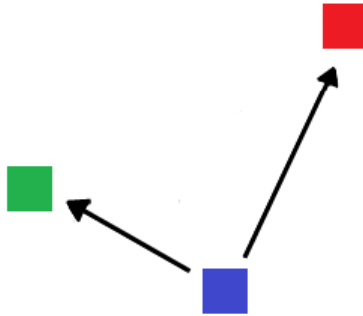


Figure 2b: The distance vectors between the herbivore and every object in vision.

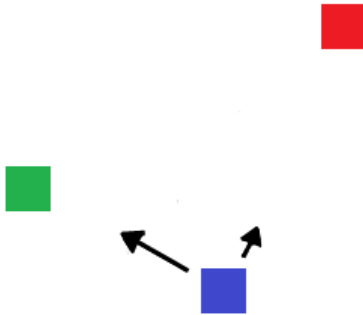


Figure 2c: The distance vectors are scaled proportionally to the inverse of the length.

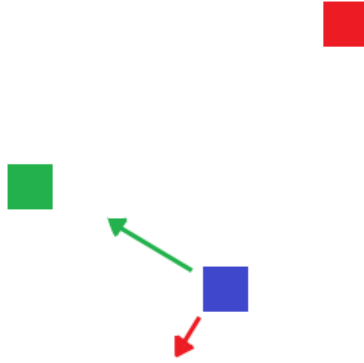


Figure 2d: The vectors are further scaled according to the attraction of the bacteria.

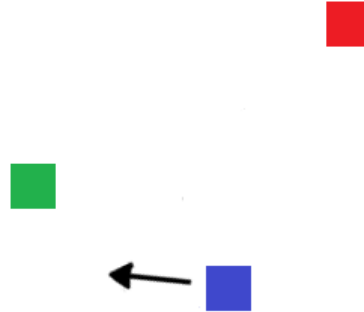


Figure 2e: The resulting vectors are then summed, giving the direction in which the bacteria will ultimately move.

One of the reasons behind our choices is that the simple model we have implemented lets us control and parse the behaviour of the bacteria more easily. For example if a bacteria evolves to have reduced amounts of carnivore attraction, we can easily observe in the simulation that it will avoid carnivores. Furthermore this system of having the genes directly affect behaviour makes it far easier to inspect genetic similarities and differences which will be very important for the results of our experiments. There is no obfuscation of the decision making process, the genes can directly explain which behaviour the bacteria have exhibited.

5.2 Rules of the simulation

For our simulation we need a number of rules to determine how bacteria will behave according to the state of the simulation. How they gain and lose energy, how they reproduce and how they die are all parts of these rules. These rules have been specifically adapted for our simulation with the hope of achieving our goal of observing coevolution.

Something which we decided early in the project was to try to get meaningful results, e.g. that we would make sure that we would give the bacteria viable choices regarding their evolutionary paths and then observe whether they chose those paths or not based on the environment. This would require implementing rules which give each bacteria flexibility to evolve in several different directions. The most important question is perhaps not what happened, but rather how.

5.2.1 Energy

All bacteria have energy, energy determines how healthy they are. Energy is lost constantly over time and is gained by eating other bacteria or plants. Bacteria have a maximum energy threshold which they can not exceed, and when their current energy is more than 90 percent of the maximum they will be able to eat anything as they are full. If a bacteria can not find any sources of food, their energy will decrease. When the energy of a bacteria falls under 25 percent of their maximum value, they will enter a dying state and be unable to perform any actions.

5.2.2 Aging

Each bacteria has an age which increases each tick of the simulation, this value is mostly useful for determine whether a bacteria has reached sexual maturity and can reproduce. If the age of a bacteria exceeds a certain value, it will enter a dying state. It is however not very likely to occur as it requires the bacteria to have gathered enough energy to live to max age, but not enough energy to have been able to reproduce through cell division.

5.2.3 Genetic weights

These are the genetic weights that all bacteria will have. Each of these weights can mutate during reproduction and change the behaviour of the bacteria. All genes have values between 0 and 1 inclusive, or between -1 and 1 inclusive.

Aggression [-1, 1]

The aggression gene determines whether the organism is regarded as a herbivore, carnivore or an omnivore. This gene determines how much energy the bacteria gets from various sources of food and how prone the creature is to attack another organism. Aggression also determines the colour of the bacteria in

our simulation program making herbivores blue, carnivores red and omnivores purple. This helps bacteria visually determine how to act towards each other.

An aggression value of 1 signifies that the creature is a complete carnivore which only eats other creatures, a value of -1 signifies that the creature is a complete herbivore and will only eat plants. A value of 0 signifies that the creature is an omnivore and will eat both plants and other creatures, but it receives less energy from either compared to complete herbivore or carnivore for their respective types of food. All values between -1 and 1 are possible, for example a creature with a value of 0.3 will primarily eat other creatures and get more energy from it, but can also eat plants and get a small amount of energy from them.

Attraction values:

Herbivore attraction [-1, 1]

Omnivore attraction [-1, 1]

Carnivore attraction [-1, 1]

Plant attraction [-1, 1]

Dying attraction [-1, 1]

The attraction gene determines movement. A positive value means a creature is attracted to the object and will move towards it, a negative value means it is repelled from it and will move away from it. The larger the value is, the more the object is considered when it comes to movement. There will generally be multiple creatures and plants in sight, these weights will help determine how much importance is placed to each object when determining movement.

5.2.4 Behavioural weights

Hunger [0, 1]

Hunger is calculated as the fraction of current energy a bacteria has compared to its total energy, and determines how desperate the bacteria is for food. A hungry bacteria will be more concerned about finding food rather than fleeing from predators or other attractions, and will even in some cases take risks in attempt to attack other bacteria. When a bacteria is full it will be unable to eat more food.

5.2.5 Movement

The movement of the bacteria is based on vectors, for each bacteria the simulation will calculate a vector relative to all nearby objects, both plants and other creatures, within the vision range of the bacteria and give it a weight depending on the bacterias genetic attraction to those objects. All vectors are summed, and the resulting vector determines the direction the bacteria moves in. This is how the bacteria makes decisions how to move.

5.2.6 Eating plants

If a bacteria is next to a plant, it is not full on energy it will eat the plant and gain energy. The plant in turn will lose energy, and when it has reached zero energy it is removed from the simulation. Bacteria can are not able to eat an entire plant in one tick, but rather they attempt to take a small bite each tick which will prolong the eating process. If a carnivore with high aggression eats a plant, they will lose energy from doing so since they have not specialized in eating plants. The threshold for this is set at an aggression level of 0.5 or higher.

5.2.7 Eating bacteria

Whether a bacteria is successful in eating another bacteria is controlled by its aggression. A bacteria must be have a minimum value of 0.6 higher aggression than its prey to safely eat it, the result will be that the aggressor will each tick take a bite of its prey (if it is within eating range) and receive more energy the higher aggression it has. One bite will often not be enough to kill a bacteria, but rather the aggressor must chase its prey and perform new attempts over several ticks.

The willingness to attack is controlled by hunger, a bacteria can become desperate enough to attack at only a 0.3 aggression advantage. At a 0.3 advantage in aggression, the bacteria has a 50 percent chance of succeeding which scales linearly up to 100 percent chance at 0.6 advantage in aggression. A bacteria will not be able to eat any other bacteria if the difference in aggression is less than 0.3.

5.2.8 Dying and death

Each organism has a dying threshold. When either their energy reaches drops low enough or when the age of the organism becomes exceeds a certain value it will enter a dying state. In this dying state, the organism will be unable to perform any actions and each turn it will lose energy. This makes the organism very susceptible to be eaten by omnivores and carnivores since it can not defend itself, run away or eat anything. Dying organisms are intended to be a source of food for primarily omnivores. If a dying creature has not been eaten after a certain amount of time, it will die, at the start of each tick of the simulation all dead bacteria are fully removed from the simulation.

5.2.9 Reproduction

Our preliminary idea is to have a cell division as the means of reproduction, when the bacteria are ready to reproduce they split into two offspring where both have the opposite mutation of each other. For example if one offspring has an increase in one gene, the other offspring will have a decrease in the same gene of exactly the same magnitude.

The standard practice when it comes to genetic algorithms is to rank all algorithms by a specific criteria for fitness, and then the algorithms with higher

fitness are more likely to be chosen to reproduce with another bacteria in the pool. The genetics of the offspring are determined by gene splicing which randomly splits up the genes of both parents and then each offspring receives one part from each parents so their genetics are mutually exclusive. Then each offspring has their genes mutated slightly. This is standard practice for efficiently evolving the genes towards more effective solutions. (4)

Instead of a top-down approach where we determine which bacteria are allowed to mate together we follow a more individual and biologically correct version of bacterial asexual reproduction. Whether an organism can reproduce is determined by two factors, the first is whether it has reached sexual maturity and the second is whether it has enough energy to reproduce. If both criteria are met the bacteria will asexually reproduce into two offspring with slightly mutated genetic material as the parent. The mutation will only effect one property (selected randomly), and that property will be increased by a random value between 0 and 0.2 for one of the offspring, and decreased by the same amount for the other offspring. That way both genes will have a similar chance at continuing on. The two offspring will start with a default energy value, and will immediately start searching for food. The parent dies and is removed immediately as it reproduces.

Relying on mutation rather than mating for forming new gene combinations is known to produce particularly poor results combined to traditional methods (14). However even though it yields worse solutions, we have decided to implement that asexual reproduction is the more interesting choice due to that it closer to how bacteria reproduce in nature. (11)

5.2.10 Speed

The speed of a bacteria is controlled by how much energy a bacteria has, each tick each bacteria has a chance to move depending on how much energy it has. The bacteria which have not been able to gather enough energy will move slower, which increases the chance they will perish. When a bacteria reproduces, the two resulting offspring will have low starting energy and thus a low speed which make them more at risk. Furthermore, we added a bonus so all bacteria will move slightly faster if their aggression is lower. This is a necessary addition to ensure survival of herbivores, which have lower aggression than carnivores. Without this bonus the carnivores can easily hunt all herbivores into extinction.

6 Method

In order to conduct our study we developed a program to run our simulations, and determined rules as described previously in our "rules of the simulation". We constantly reworked the rules to ensure a balanced and stable population. We developed the simulation with initial testing with only herbivores and carnivores and spent several weeks trying to balance the simulation so we could be certain of that a simulation of these could coexist.

6.1 First experiment: Heterogeneous bacteria

The first experiment involves a simulation which starts with a pre-determined population of both herbivores and carnivores. There are 80 herbivores, 40 omnivores and 20 carnivores. All the initial bacteria have had their genetic material adjusted by us to initially behave according to our expectations.

This was also our first simulation test, to have a pre-determined population of herbivores and carnivores and give them initial genetics to ensure initial survival and hope to observe long term survival. A large part of our development consisted of various changes to achieve a balance where we tried to make changes to ensure a balance, and this experiment served as a calibration for our later experiments.

6.2 Second experiment: Homogeneous bacteria

The second experiment involved simulating whether an omnivore population would evolve towards the same herbivore and carnivore balance. In this simulation there are initially 80 bacteria, all of them start as omnivores with all genes being set to random values between -0.2 and 0.2, which leaves them very open to easily be influenced by mutations to effect their behaviour early on.

6.3 Third experiment: Random bacteria

The third experiment involved a simulation where all genetic material of the initial bacteria have been set to random values. The purpose of this experiment is to observe how increasing the randomness of the initial starting conditions would affect the coevolution and populations of the bacteria.

6.4 Methods of enforcing behaviour

Early in our development process we had a simulation with only herbivores and plants, we realized that with every run of the simulation the population would always converge to a certain point depending on the amount of plants. If we increased the amount of plants then the amount of bacteria would also increase since there would be more food available. The initial amounts, as long as they were reasonable enough to not cause immediate extinction seemed to not have a large impact. At this point in time, the simulation was very stable with very little variation between the results.

As we added carnivores to the simulation, we disappointingly observed very volatile results as the simulations would converge to one of two different results. The first result consisted of that very shortly into the simulation the carnivores would fail to hunt herbivores, and thus become extinct with the herbivore population continuing to grow unthreatened as a result. The second result consisted of that a few carnivores would successfully hunt herbivores in the beginning of the simulation and reproduce, which gave them the ability to hunt in packs which would lead them to eventually eat the entire herbivore population. With the herbivore population hunted to extinction, the carnivores would also become extinct as they had no sources of food left. Even though these bacteria were manually created by us, it was still evident that the results of our simulation were far too volatile and that there were little possibility for the bacteria to coexist with the existing rules of the simulation. With only omnivores we also initially noticed volatile results, all omnivores would evolve exclusively towards either herbivores or carnivores with no diversity, depending on the implemented rules for that specific run.

One of the first changes we introduced was implementing the dying state of bacteria to help achieving this balance as it would give small benefits to higher values of aggression even for bacteria who mainly feed on plants. Another very important factor in the simulation was to control population growth from an early stage. We encountered scenarios where groups of carnivores would chase groups of herbivores, and what would happen was that as soon as a carnivore ate one of the herbivores it would reproduce and the offspring would continue chasing the herbivores at the same speed. As soon as a few herbivores were eaten it would lead towards them all becoming extinct shortly after. Our solution to this was twofold, first of all to make herbivores slower and carnivores faster than our default movement speed which would require a larger number of carnivores to outnumber a herbivores. Secondly, we implemented a system where the speed of a bacteria is directly related to how much energy it currently has. This ensured not only that bacteria can be hunted into exhaustion, but also that as a bacteria reproduces the offspring will not have enough energy to flee or hunt at higher speeds which slows down the population growth.

Still the results were not satisfactory, and as mentioned earlier we wanted to do our best to ensure a meaningful result. A large part of our work consisted of tweaking the rules to achieve a working model which allows for balance between organisms instead of a volatile environment which only allows for one single type

of behaviour, and many of the simulation rules were tested back and forth. As we found out, handling the aggression rules of the bacteria was critical to ensuring a satisfactory result for the simulation. During our tries how to implement aggression we realized that we needed more refined ways of classifying bacteria rather than just a midpoint of the between the extremes between herbivore and carnivore. For example omnivores would classify their fellow bacteria as a mix between food, friend and enemy, which lead to odd behaviours. Because of this we implemented omnivore attraction, which functions as a buffer variable which lets bacteria make more refined decisions regarding their attraction to potential predators or prey.

Our methods of deciding whether a bacteria can attack another bacteria involves calculating the difference between the aggression of the bacteria and comparing it to a predefined threshold. If the aggression threshold was set too low, it encouraged evolution towards carnivorism because otherwise the bacteria would get immediately eaten by other bacteria with slightly higher aggression. On the other hand, if the threshold was set too high then our bacteria would always converge towards herbivorism since a bacteria would have to spend a lot of time in a sub-optimal state before it could hunt other bacteria. With a too low threshold we also experienced a problem where bacteria would be able to cannibalize each other regardless of their type. Having a situational threshold based on hunger seemed to solve a lot of the problems we encountered.

Something which also created a lot of problems were our incentives for making sure the bacteria would not eat food from sources which they should not be able to eat. The system we implemented had the rules that at the optimal aggression values they would receive twice the energy, and at the least optimal aggression values they would receive no energy at all. This however created situations where herbivores were able to eat dying bacteria without much consequence. As one of the important food sources of the carnivores and omnivores would disappear, those populations would be reduced which would lead to herbivores having an increased chance of survival. Furthermore carnivores would often clump up and due to the low thresholds for attacking they would clump up in large groups where they could feed on each other and gain energy, while hunting bacteria. To rectify these situations we had to implement more severe penalties for eating the "wrong" food sources and less extra energy for eating the "right" food sources.

7 Results

We have performed simulations of each experiment several times, and observed the results of each individual simulation. The simulations will progress differently, but for the vast majority end up with very similar end results. For that purpose, we have specifically chosen one set of data from each experiment which we believe to be representative of the results of the experiment as a whole. The simulations were left to run for between 30-100 minutes of in-simulation time where the longest simulation ran for close to three hours in real time.

All our graphs and heatmaps found in the following sections were generated with MATLAB, the heatmaps were generated with a modified version of the cloudPlot library written by Daniel Armyr. A darker blue colour means fewer occurrences, the lighter colours indicate a moderate amount of occurrences, while the red and dark red colours indicate many occurrences. Something to note for all our heatmaps is that the graphs extend beyond our available data points, which does not indicate that there were no data points at that time in the simulation.

7.1 Heterogeneous bacteria

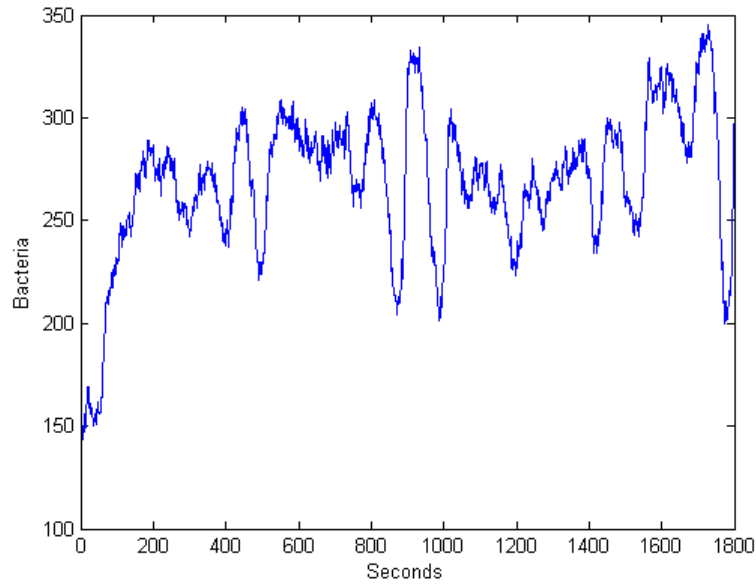


Figure 3a: The number of bacteria in the heterogeneous experiment.

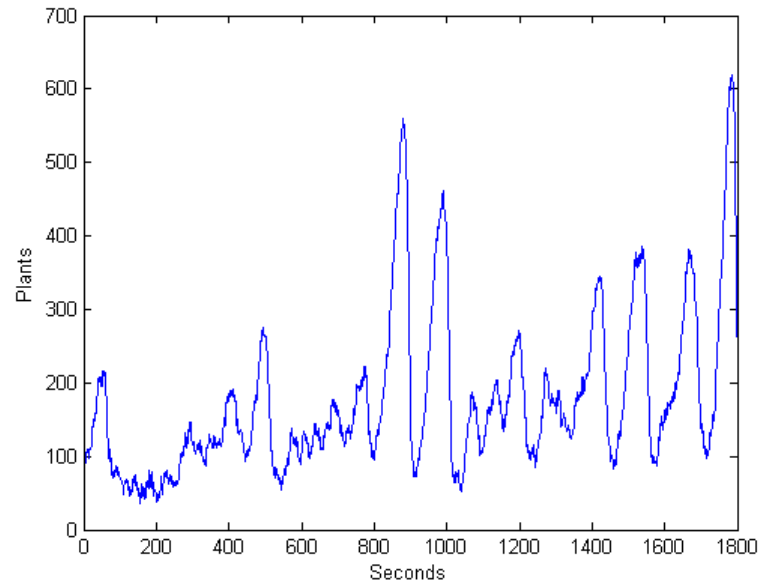


Figure 3b: The number of plants in the heterogeneous experiment.

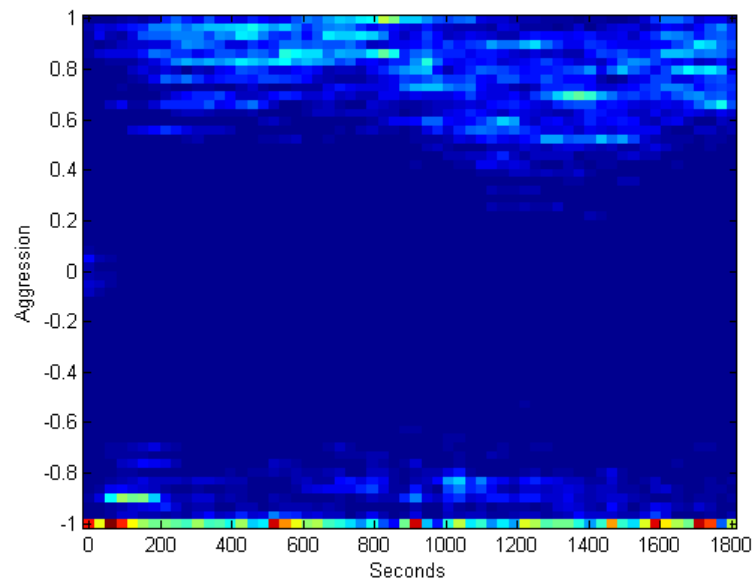


Figure 3c: The aggression values of the heterogeneous bacteria.

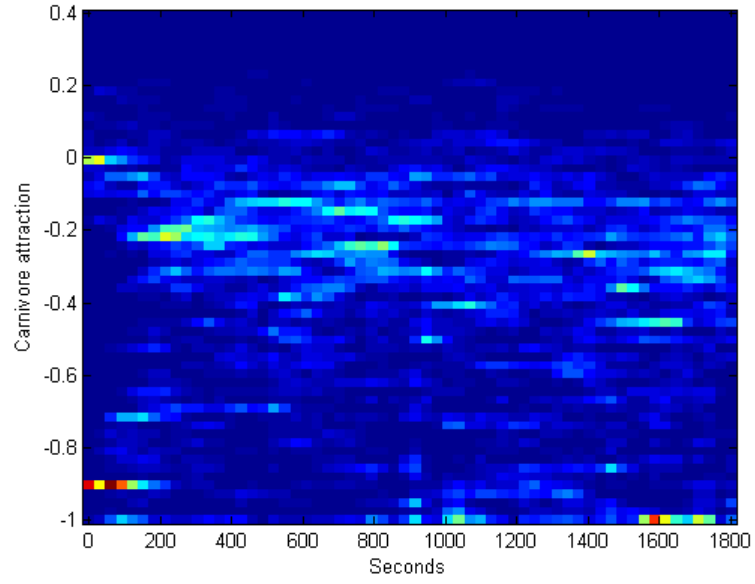


Figure 3d: The carnivore attraction values of the heterogeneous bacteria.

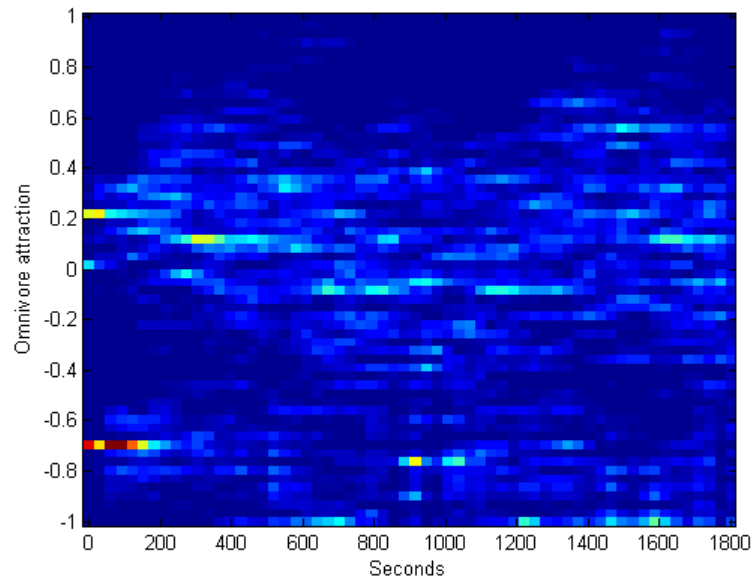


Figure 3e: The omnivore attraction values of the heterogeneous bacteria.

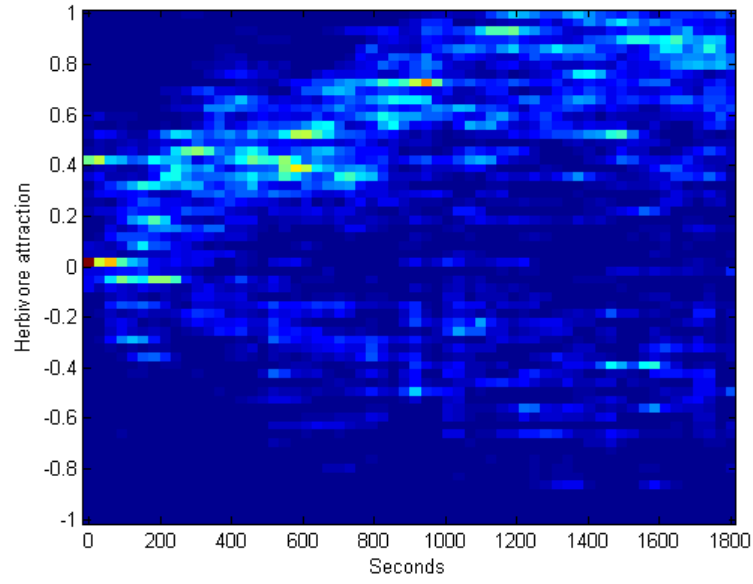


Figure 3f: The herbivore attraction values of the heterogeneous bacteria.

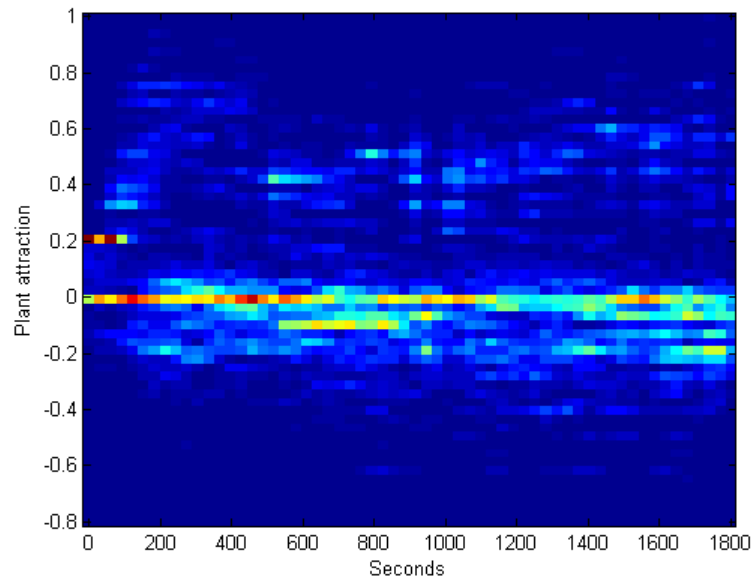


Figure 3g: The plant attraction values of the heterogeneous bacteria.

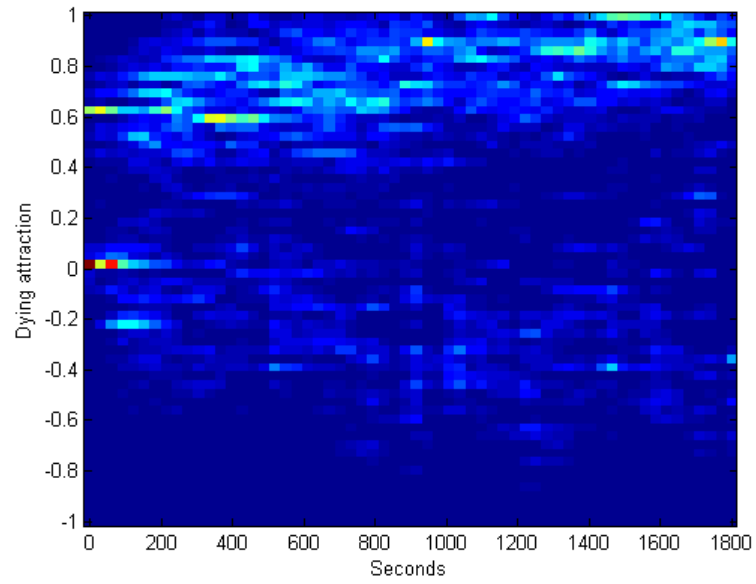


Figure 3h: The dying attraction values of the heterogeneous bacteria.

7.1.1 Analysis

Initially all herbivores and all carnivores would clump together into groups of their own kind, as there was no significant attraction for bacteria of their own kind. This might have been due to herbivores searching for masses of food, and carnivores following the herbivores which naturally leads to these kinds of formations. Later in the simulation we observed very different behaviour, all bacteria had evolved to spread out from each other (figures 3d and 3f). We noticed early on in our development that carnivores would naturally evolve to spread out from each other, as carnivores are a lot slower than the agile herbivores they would perform simultaneous attacks from many different angles rather than trying to chase them herbivores directly which would increase their chances of success.

Something which we also observed was that as the omnivores evolved into herbivores, the lack of plants would lead to peculiar situations. As most new plants already were in the vicinity of several omnivores, the herbivores would take a risky undertaking and begin eating plants which were already being eaten by omnivores. When the omnivores would pursue the herbivore, it would use its superior speed to flee. This behaviour reminded not much of bacteria but rather of typical scavenger behaviour, stealing food and quickly running away.

Something which is interesting is that the dynamics between these bacteria involve very little actual killing. As the herbivores are faster and more nimble than the carnivores, there is a very low chance that the herbivores will catch up to fleeing bacteria. Instead what we observed was that the carnivores will chase the herbivores en masse, the herbivores will temporarily stop at plants to eat and the more carnivores are chasing them the less time they will have to eat the plant before having to flee again. It looks more like the carnivores chasing and nibbling the herbivores away from the plants, and then slowly if the herbivore becomes exhausted enough and slow from the lack of energy, a healthy and fast carnivore will eat it.

Apart from those changes, we observed very few changes from as the bacteria evolved. One major change from the initial state is that the number of bacteria would increase from the initial 140 to between 250 and 300. The swings up and down in bacteria population has a direct negative correlation to the amount of plants as stated in the Lotka-Volterra model (figures 3a and 3b).

7.2 Homogeneous bacteria

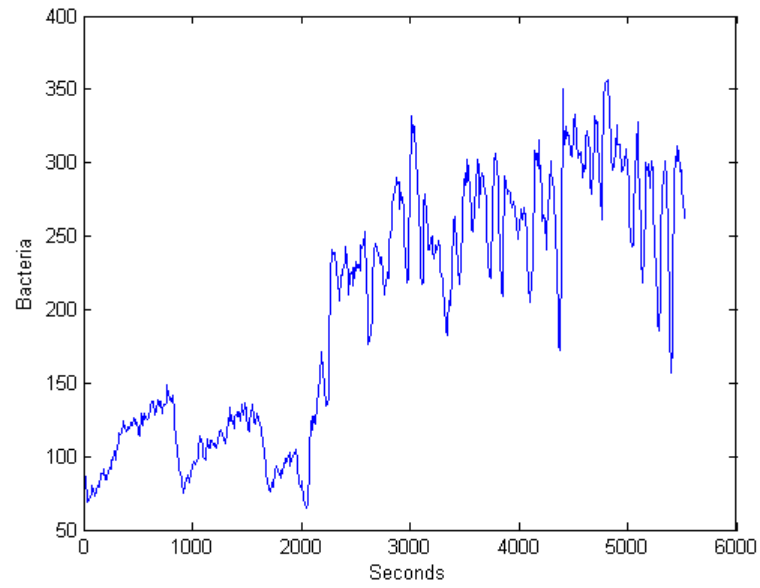


Figure 4a: The number of bacteria in the homogeneous experiment.

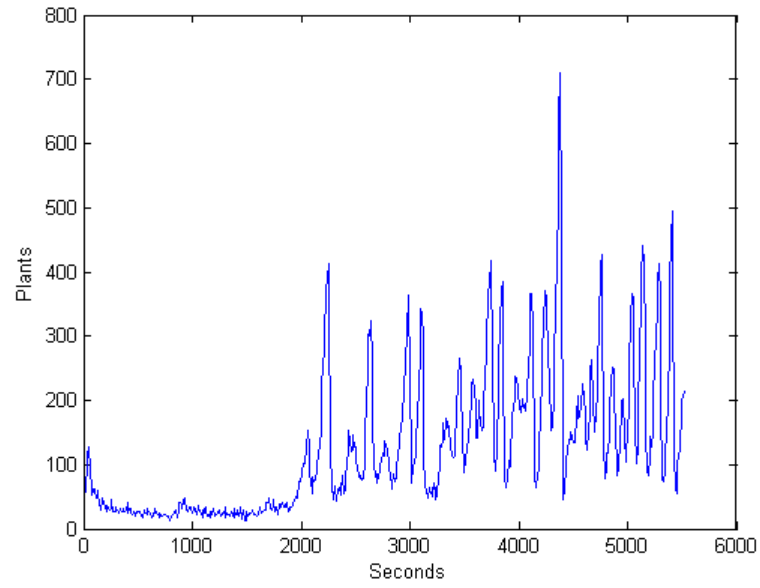


Figure 4b: The number of plants in the homogeneous experiment.

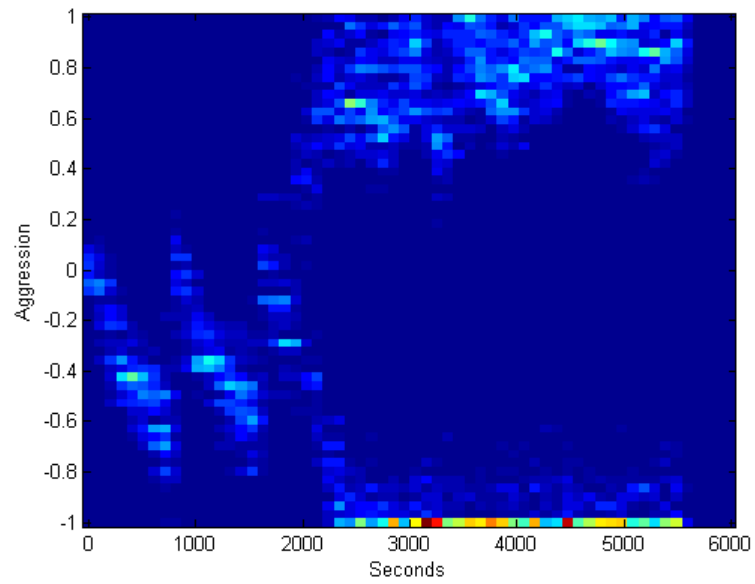


Figure 4c: The aggression values of the homogeneous bacteria.

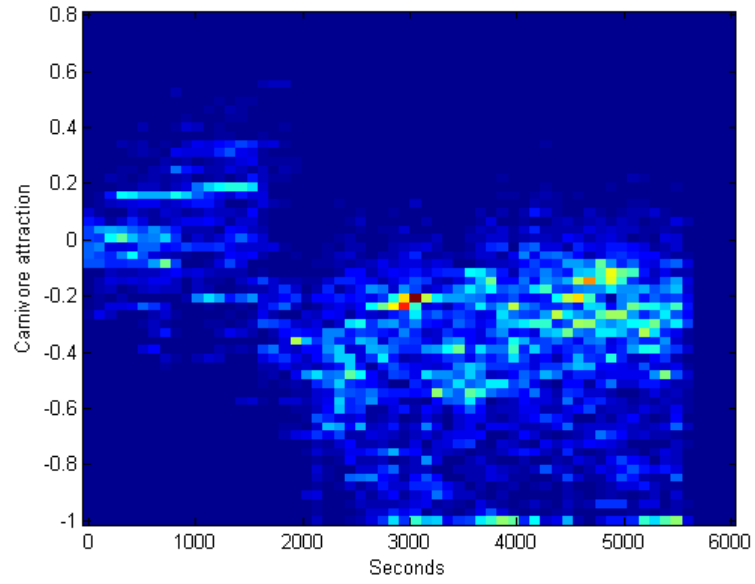


Figure 4d: The carnivore attraction values of the homogeneous bacteria.

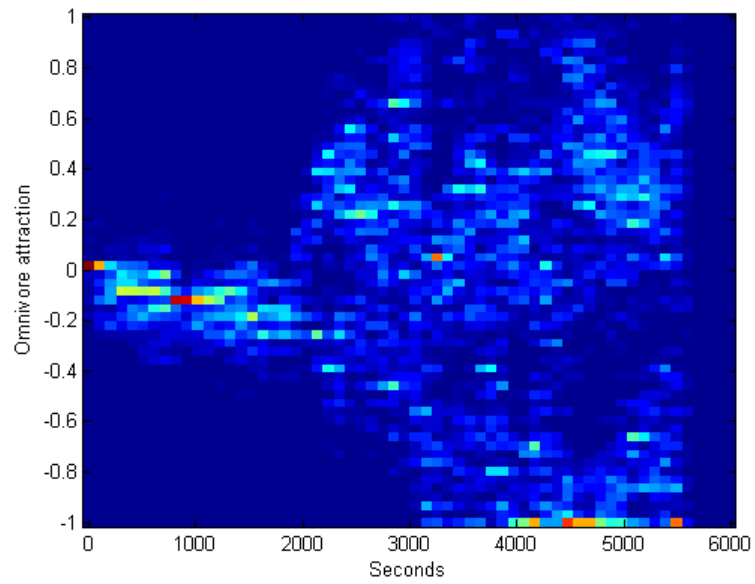


Figure 4e: The omnivore attraction values of the homogeneous bacteria.

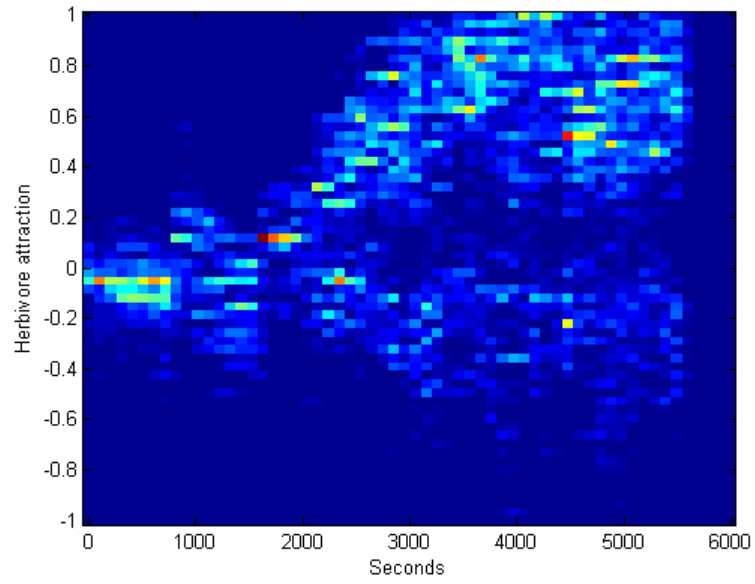


Figure 4f: The herbivore attraction values of the homogeneous bacteria.

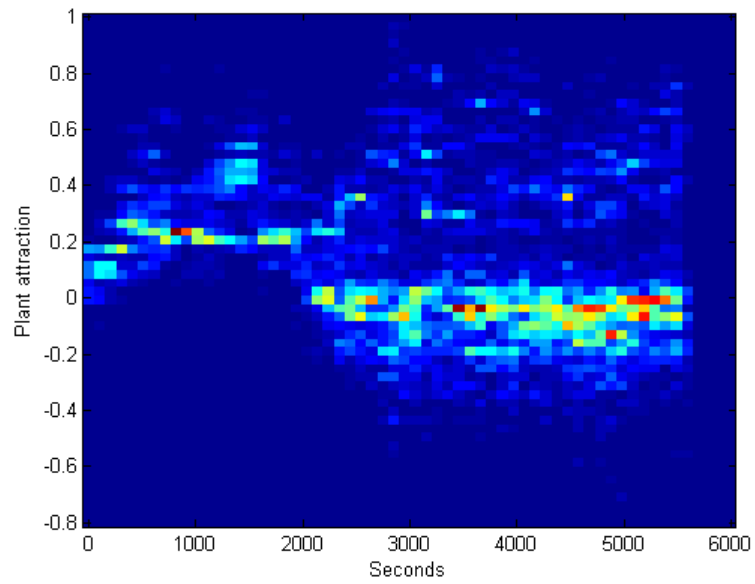


Figure 4g: The plant attraction values of the homogeneous bacteria.

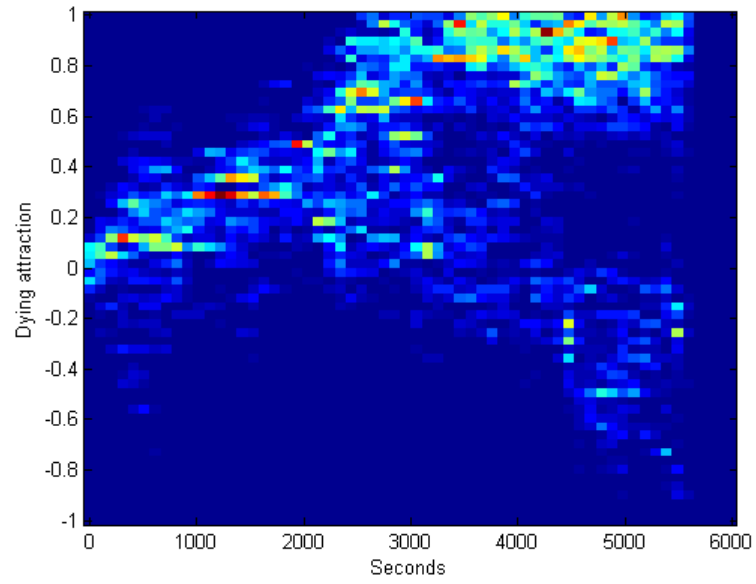


Figure 4h: The dying attraction values of the homogeneous bacteria.

7.2.1 Analysis

In this experiment, we have observed that the omnivores initially converged towards herbivorism with only a few omnivores left which tried to feed on the few food sources they can get hold of (figure 4c). In a simulation filled with herbivores, omnivores have many disadvantages which make their survival very difficult. First of all they are slightly slower than herbivores which makes it harder for them to search for plants, and furthermore they receive far less energy from the plants than herbivores. However there's much that is left up to chance.

As our plants spawn randomly there is a high chance that after time omnivores will be able to eat multiple plants in a row and reproduce, which will lead to small groups of omnivores and larger group of herbivores who had not evolved much fear of omnivores. One of the advantages we noticed omnivores had was that they were able to secure their plants at higher rates than herbivores later in the simulation, if herbivores would try to approach the plant then omnivores would often try to take a bite out of them. Herbivores would as they developed more fear of omnivores be chased away from the plants more. As the number of aggressive bacteria in the simulation increased, we observed less emphasis on how quickly the bacteria could get to the plants but rather whether they could safely eat the plants without being subject to external threats.

As these omnivores became more and more aggressive, they could secure their plants to higher degrees. However this had the disadvantage of that as they became more and more aggressive, they would receive less and less energy from plants which counter-intuitively decreased their chances of survival. After a while as the omnivores evolved towards carnivorism, they would actually lose energy when trying to eat plants which would put pressure on eating bacteria instead of plants.

7.3 Random bacteria

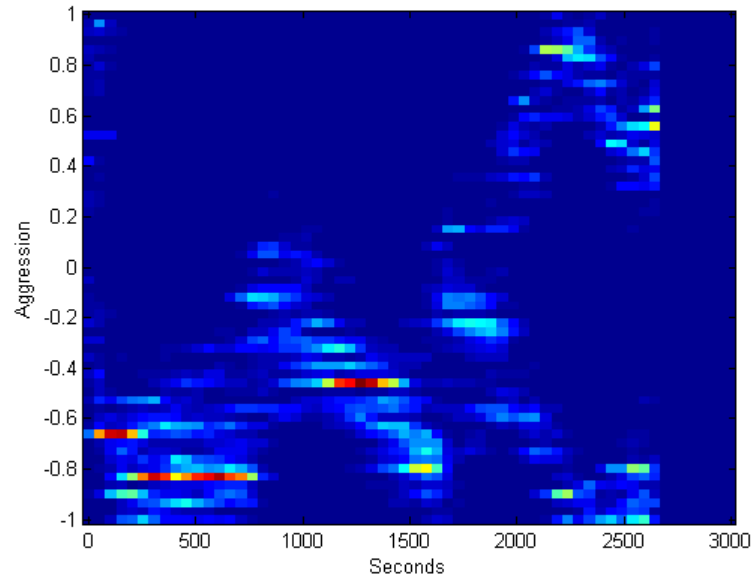


Figure 5a: The aggression values of the bacteria in the random experiment.

7.3.1 Analysis

In the simulation with random bacteria, we observed that the only bacteria which survived the initial minutes were those with positive plant attraction. Herbivores seemed to thrive in this environment, while omnivores would quickly become extinct. Somewhat surprisingly carnivores would outlast the herbivores even though they sought out plants which gave them very little nutrition, our guess is that the carnivores would feed on other bacteria also gathering at the plants as they would have close to no initial fear of these carnivores. Within minutes our experiment with random bacteria would highly resemble our homogeneous experiment (figure 5a and 4c). So in other words, despite completely different starting values, our genetic algorithm has converged to similar results.

We argue the cause may be since the genetic material of the bacteria is entirely decided at random, there can occur many unfavourable combinations. Most of the bacteria which were not attracted to plants died out immediately, and the bacteria which got the most nutrition from plants adapted the best. The plants often outnumber anything else in this simulation, and even very low values of plant attraction will result in bacteria seeking or fleeing from plants. In theory, the minimum required to survive for a bacteria would be a small amount of positive plant attraction and not too much aggression that it does not receive nutrition from plants. Then the bacteria could survive living as a herbivore or omnivore. For a bacteria to survive as a carnivore, the genetic combinations required for hunting other bacteria are much stricter, it would require having positive attraction for both herbivores, omnivores and dying bacteria and most importantly also a have their attraction to plants be a value as close to zero as possible or else seeking or fleeing from plants would interfere with their hunting. This is obviously a much harder requirement to achieve than for herbivores or omnivores.

8 Discussion

Over the course of our different simulations, we have observed relatively similar results, and the end results in all three different simulations are very similar to each other. These results are satisfactory and correspond to our expectations.

As seen in all the graphs representing bacteria population (figures 3a and 4a), there are clear swings up and down in terms of population, this is corresponding in a negative correlation to the amount of plants (figures 3b and 4b). This follows the Lotka-Volterra system, which states that some swings up and down in population will occur, since a lack of plants lead to a reduction in the herbivore population, which in turn leads to a reduction in carnivore population. The lower amount of herbivores will then lead to an upswing in the amount of plants, which gives more food to the herbivores and allows the herbivore population to rise again, with the carnivore population following. And so the cycle repeats. It is also worth noting that in all of our simulations the population amount converged to around 250-300 regardless of initial values, since beyond those values the populations get constrained by the amount of energy we put into the system.

8.1 Omnivore instability

Omnivores gain both the positives and negatives of both herbivores and carnivores. The advantages of specialization are mainly that they can gain energy from multiple sources of food, rather than being limited to just one like herbivores or carnivores. However as we have observed, the disadvantages often have more of an impact than the advantages. For example omnivores only gain a third of the energy from plants compared to herbivores, and combined with their slower speeds they pose little threat to herbivores. We have observed that our predators hunt much more effectively in numbers, but as omnivores are easy prey for carnivores (partly due to their low speed), they are often quickly hunted to extinction by carnivores. Omnivores do not have much of a place in our simulation, and we have not been able to observe a prolonged omnivore population which has not immediately been followed by periods of instability.

8.2 Specialization

One of the most interesting results which we have observed, are the massive and rapid changes of the population which can occur up to several times each simulation for the second and third experiment (figures 4c and 5a). The process of how the bacteria seem to specialize into both herbivores and carnivores can be very rapid and volatile.

We observe in figures 4a and 4b that a growth of herbivores is often followed by a sharp increase in the omnivore population, as predicted by the Lotka-Volterra model. However what follows after that is not easily explained. As the population of predators increases, their capabilities to hunt are vastly increased due to being able to surround their prey. Even a seemingly small increase in

the population of predators can easily lead to a massive increase a few minutes later which would put the predators in a very advantageous position.

However, initially what often happens is that the omnivores reach large numbers and then somehow decide to evolve towards herbivorism again. Our observations point to that a major contributor to this is that because this is the first time there has been a large enough predator population to pose a threat to the herbivores, a lot of them have not been able to evolve any fear of the predators and thus easily become eaten. We can observe in figure 4d and 4e how a large number of the bacteria who die during these periods are bacteria with high omnivore and carnivore attraction. This leads to a large population of omnivores who have been able to feed on prey that have been easy to hunt, and as the herbivores which remain are those who have been able to consistently flee from the predators, the omnivores can no longer sustain their large numbers and their population is reduced.

The second spike in omnivores is far more dramatic, and the population changes far more dramatically. It is still very similar to the first spike, but as we see in figure 4d the bacteria that die during this time are not a small amount of bacteria with positive omnivore attraction, but rather a large amount of bacteria with positive carnivore attraction. As we see in the first spike, there are barely any bacteria which could be classified as carnivores (a bacteria with 0.2 aggression would be classified as 20 percent carnivore and 80 percent omnivore). Thus, bacteria that evolve to have a very high aggression have an element of surprise as many of their prey have not have been exposed enough to be able to adapt to this new kind of threat.

This essentially leads to a threshold for the aggression of the omnivores for the specialization to occur, if their aggression is too low then the population will return back to normal and we see something similar to the first spike. However if the aggression of the omnivores reaches high enough values, there is a lot of potential for growth in the omnivore population as the higher the aggression values evolve, the less defenses the herbivores will have against potential attacks.

We have observed that in these situations, if the omnivores overcome this initial threshold they will evolve towards higher and higher values of aggression to take advantage of these specific situations, and the population of the omnivores will heavily increase. What happens with the surviving herbivores is that the population will also evolve to adapt to the situation, namely the herbivores will evolve towards even lower and lower values of aggression. This not only has the benefit of increased nutrition from plants, but also an increase in speed and when the amount of predators heavily increase the ability to flee from them becomes vital. We have observed that aggression of bacteria are similar, it can be beneficial to evolve higher values of aggression even as a herbivore as it might decrease the chance of being attacked but as the aggression levels of the predators increase this tactic becomes far less useful.

One thing to note is that multiple spikes are not necessary for the bacteria to specialize, and we have been able to observe the bacteria specializing after the first spike of omnivores. However in the event that this diversification occurs after the first spike, it has generally taken an exceptionally long time for that

spike to occur. We believe that the longer it takes for this event to happen, the more likely it is to result in specialization as the random mutations will ensure that the amount of bacteria with very high carnivore attraction increases over time. As the simulation progresses, if the carnivore attraction gene does not impact reproduction then the genetic values will spread over time due to the mutations which would favour predators.

8.3 Population imbalance

A very surprising phenomenon we have observed is that this specialization increases the population of bacteria almost threefold. As the bacteria specialize they will make better use of the energy which we put into the system, and thus the population can sustain larger numbers of bacteria. In our simulations we often end up with far more carnivores than herbivores, around a factor of five more. In real life as energy travels up the food chain it diminishes, so creatures higher up are always dependent on the creatures lower in the food chain. (6). According to our rules, when a bacteria eats something it will receive extra energy if it is specialized in eating a specific food source, and lose energy when it tries to eat something it is not specialized in eating. This inadvertently creates so that as the energy travels up the food chain it increases which goes against a basic principle of physics, that energy can not be created from nothing. (15)

For our herbivores, this has very little effect as the nutrition they get from plants is an arbitrary number with no real significance. However for omnivores and carnivores, this feedback loop leads to a heavily inflated population. When for example carnivores feed on herbivores, they not only receive the total energy of the herbivore (including any extra from plants) but also they get extra energy from eating the herbivores. Then when the carnivore enters a dying state, if it is then eaten by a bacteria it will receive further extra energy. With each step in the food chain, we add energy instead of subtract and thus as bacteria eat other bacteria it leads to a feedback loop where the energy we put into the system multiplies every time a bacteria receives energy. This however is not a major disaster since our simulation despite this supports stable and diverse populations, as it stands our carnivores are not effective hunters and need strength in numbers in order to thrive.

8.4 End state

The homogeneous and random experiments can be very volatile, and while in most of our simulations the end states are stable we have at times been able to observe far more volatile end states. What happens is that the carnivore population will rapidly increase, and as carnivores are much more effective at hunting the larger their number are this can have devastating effects. Normally if the amount of carnivores in an environment increase, they would overhunt their prey and there would be less food available for them which would lead to a reduction in the carnivore population. In our simulation, a full carnivore can hunt for over a minute without succumbing to complete exhaustion and in

this time the carnivore population can sometimes hunt their prey to exhaustion. The typical case we saw in our simulations was that the population of carnivores would increase much more slowly, and thus they would not be able to hunt all the herbivores to extinction.

However, in the rare case that carnivores manage to hunt the herbivores into extinction there are generally two different scenarios that can occur. As there are no herbivores to eat the plants, the number of plants will explode dramatically which would provide a lot of nutrition for bacteria that can receive nutrition from plants. The problem is that from 0.5 to 1.0 aggression a carnivore will lose energy from eating plants as a means of enforcing carnivorism, so there will be no available sources of energy and all the bacteria die of extinction. This is a perfect example of bacteria evolving for short term gains, even when that has very negative consequences when it comes to long term gains. In the event that a carnivore with less than 0.5 aggression survives, it would receive nutrition from the plants and repopulate the simulation due to the massive amount of plants available and the simulation would move towards omnivorism. One major reason why this is not that prevalent is that because bacteria at such low values of aggression are at risk to become eaten by more aggressive carnivores.

9 Conclusion

In conclusion, we can determine that our attempt to simulate basic evolution through artificial means was largely successful. All creatures had the opportunity to evolve their genes in different directions, yet some mutations were significantly more common and dominant while bacteria with less suitable genes did not survive long enough to successfully reproduce. This is evidence of how our simulation has been able to imitate nature.

In all three experiments the end result was a largely heterogeneous population, no matter if the initial population was heterogeneous, homogeneous or random. Our results were generally accurate according to the Lotka-Volterra model, and the populations would remain stable, but with small variations following the model. This further confirms that we were successful with developing rules of the simulation which would allow for stable and diverse populations.

In our second and third experiments, we were able to observe coevolution as all bacteria initially evolved in the same direction responding to each other, but when the bacteria specialized (fig. 4c) into herbivores and carnivores, only those who quickly adjusted to the evolutionary arms race would survive and others quickly perish.

Since the simulation is non-deterministic, it did not always develop in the same way each time, however, the end results were very similar even though the exact time or path it took to get there was not necessarily the same. The genetic algorithm pushed our bacteria towards near-optimal states, and in the vast majority cases it succeeded in finding states of far greater prosperity than the initial conditions. Even though there might have been other ways to evolve the bacteria, using genetic algorithms in order to imitate nature has yielded very successful results for this study.

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12 Appendix

12.1 Source code

GitHub:

<https://github.com/adrianblp/SimulatedEvolution>

12.2 Libraries

Cloudplot:

<http://www.mathworks.com/matlabcentral/fileexchange/23238-cloudplot>

12.3 Simulation footage

Comparison of the initial and evolved bacteria in the heterogeneous experiment:

<https://www.youtube.com/watch?v=FKgIaPood08>