Profielwerkstuk

Machine Learning, Neural Networks and the evolution of Neural Networks through Augmenting Topologies

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describing the underlying theory, methods and the particular application of these principles to making a computer teach itself how to play a video game

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3^{rd} of February 2017

Abstract

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Contents

1 Introduction

- Discuss why we chose the subject
Do not be scared by the title, all of the expressions used will be explained throughout this PWS. For now the knowledge that is needed is that we are going to make a computer learn how to complete level 1-1 of Super Mario Bros 3.(SMB3)

To complete this task we will make use of *machine learning*(ML) which is a subfield of *computer science*. ML gives computers the capability to

"...adapt to new circumstances and to detect and extrapolate patterns." [1]

Any knowledge of ML will not be required to fully understand this PWS. However, a basic understanding of programming syntax and a minimum of 6VWO wisA mathematics knowledge is expected to fully understand this PWS.

To explore the world of ML we wanted to set a goal for ourselves, something to prove that we understand what we have learnt and something to apply our newly acquired knowledge on. This meant that it needed to be complex enough to warrant the use of ML and at the same time still be feasible enough to make in a restricted timeframe. It also needed to be interesting, maybe something that we can compare ourselves to or something that we find an impressive example of the power of ML.

After some discussion we quickly settled on the following goal for ourselves to accomplish and formulated it in the form of a question. *How can a machine learning algorithm be made to learn how to finish level 1-1 of Super Mario Bros. 3 for the Nintendo Entertainment System.* To be able to answer this question we divided it into sub-questions.

Firstly, *how does a machine learning algorithm learn?* For our algorithm to complete level 1-1 of SMB3 without any previous knowledge of the environment it will need to learn how to solve the problems that the obstacles of the level pose to it. Before we are able to make a learning algorithm we need to know how they work.

Secondly we will ask ourselves *how does an artificial neural network learn?* Because the technique of *artificial neural networks* (ANNs) seemed the most promising to us we decided to use this ML technique in our ML algorithm and to be able to do that we need to know how ANNs work.

Thirdly we will need to know how we are going to use the ANN, for this we will need to ask ourselves *how do you decide upon the best possible topology of the artificial neural network for the algorithm to be able to finish level 1-1 of Super Mario Bros. 3 for the Nintendo Entertainment System.*

Finally the knowledge gathered from the answers to previous questions has to be applied to SMB3 and thus we will ask ourselves *how do you implement Evolving Neural Networks through Augmenting Topologies to finish level 1-1 of Super Mario Bros. 3 for the Nintendo Entertainment System*

Each subquestion corresponds to a chapter, subquestion 1 corresponds to chapter 3, subquestion 2 corresponds to chapter 4, subquestion 3 corresponds to chapter 5 and sub-

[1] Russell and Norvig (2009).

question 4 corresponds to chapter 6. In chapter 2 we will provide some useful background information on ML and in chapter 7 we will answer the main question of this PWS.

2 Background information

2.1 The history of the automation of algorithmic problem solving

Before giving some background information on the subjects which will be described in this report, it is useful to gain some knowledge about the historical context in this field of research. Therefore, some of the most significant advancements will be described in the following paragraphs, in addition to which their importance to the subject of this report will be discussed.

2.1.1 Bayes' Theorem

The history of machine learning begins not just decades but centuries ago. It begins with the posthumous publication of *An Essay towards solving a Problem in the Doctrine of Chances*, a work by the Reverend Thomas Bayes regarding the mathematical theory of probability. In the *Essay*, Bayes lays out a number of statistical propositions, the fifth of which delineates his seminal theorem. The *Essay* describes the following:

> *If there be two subsequent events, the probability of the* 2^{nd} $\frac{b}{N}$ *and the probability of both together* $\frac{P}{N}$*, and it being* 1^{st} *discovered that the* 2^{nd} *event has also happened, the probability I am right is* $\frac{P}{b}$.[2]

This symbolically implies the following[3]:

$$P(B|A) = \frac{P(A \cap B)}{P(A)}, \text{ if } P(A) \neq 0,$$

which leads to Bayes' Theorem for conditional probabilities:

$$\Rightarrow P(A|B) = \frac{P(B|A)P(A)}{P(B)}, \text{ if } P(B) \neq 0.$$

The theorem describes the relation between a prior probability $P(A)$ and a posterior probability $P(A|B)$ given $P(B|A)$, the probability of observing B when given that A is true:

$$P(A|B) \propto P(B|A)P(A).$$

A is called a conditional probability since the occurrence of event B influences the probability of A's occurrence. An intuitive example is the classification of fruit. When given a random fruit and asked to determine whether it is an apple or an orange, the probabilities for either class is 50%. When given the additional evidence that the fruit is red, probabilities obviously shift in favour of the apple. The conditional probability of the fruit being an apple increases, given the evidence that the fruit is red.

This theorem is used in machine learning to create Naive Bayes classifiers. These are models that assign class labels to problem instances (sets of features $x_1, x_2, \ldots, X_n$), class

[2] Bayes (1763).
[3] Stigler (1982).

labels drawn from a finite set, based on conditional probabilities.

Abstractly, a classifier based on conditional probability assigns instance probabilities

$$P(C_k|x_1,\ldots,x_n)$$

for each class C_k. It is, however, infeasible to base such a model on probability tables when the number of features n is large, or if a feature can take on a large number of values. We can use Bayes' Theorem to decompose the probability as follows:

$$P(C_k|x) = \frac{P(C_k)P(x|C_k)}{P(x)}$$

The numerator is equivalent to the joint probability $P(C_k, x_1, \ldots, x_n)$, which can be rewritten as follows:

$$\begin{aligned}
P(C_k, x_1, \ldots, x_n) &= P(x_1, \ldots, x_n, C_k) && (1)\\
&= P(x_1|x_2, \ldots, x_n, C_k)P(x_2, \ldots, x_n, C_k) && (2)\\
&= P(x_1|x_2, \ldots, x_n, C_k)P(x_2|x_3, \ldots, x_n, C_k)P(x_3, \ldots, x_n, C_k) && (3)\\
&= \ldots && (4)\\
&= P(x_1|x_2, \ldots, x_n, C_k)P(x_2|x_3, \ldots, x_n, C_k)\ldots P(x_{n-1}|x_n, C_k)\\
&\quad P(x_n, C_k)P(C_k) && (5)
\end{aligned}$$

Now, the "naive" part of Naive Bayes comes into play. The algorithm assumes each feature F_i is conditionally independent of every other feature F_j for $j \neq i$, given C. This means that

$$P(x_i|x_{i+1}, \ldots, x_n, C_k) = P(x_i|C_k)$$

And the joint probabilities above can be written as

$$\begin{aligned}
P(C_k|x_1,\ldots,x_n) &\propto P(C_k, x_1, \ldots, x_n) && (6)\\
&\propto P(C_k)P(x_1|C_k)P(x_2|C_k)\ldots && (7)\\
&\propto P(C_k)\prod_{i=1}^{n} P(x_i|C_k) && (8)
\end{aligned}$$

Under the above independence assumptions, the initial instance probability equation can be simplified to:

$$P(C_k|x_1,\ldots,x_n) = \frac{1}{P(x)}P(C_k)\prod_{i=1}^{n} P(x_i|C_k)$$

This probability model is then combined with a decision rule, a common one being choosing the hypothesis that is most probable, the *maximum a posteriori* decision rule. The corresponding classifier is the function that assigns a class $\hat{y} = C_k$ as follows:

$$\hat{y} = \underset{k\in\{1,\ldots,K\}}{\operatorname{argmax}}\ p(C_k)\prod_{i=1}^{n} p(x_i|C_k).$$

2.1.2 Turing Test

In the year 1950, computer scientist Alan Turing published a seminal paper in the philosophical magazine *Mind*.[4] This publication proved an important step in the development of Machine Learning algorithms and Artificial Intelligence. In this paper Turing ponders the question whether machines are able to think. He does this by trying to rephrase the question, for a question such as *"Can a machine think?"* contains vague concepts. Concepts such as *'think'* and *'machine'*, which are not clearly and universally definable.

Turing proposes that, instead of asking this question, one should seek to find out whether a machine is able to play the so called **Imitation Game**. In Turing's version of this game, more commonly know as the **Turing Test**, there are three participants: a machine, a human and a judge (also a human). Let us call these A, B and C respectively. Each of the participants are held in isolated rooms and participant C is only able to communicate with participants A and B with a terminal, through which he is able to ask both of them questions. The aim of the game is for participant C to correctly identify whether participants A and B are human or machine. Participants A and B however, both try to convince participant C they are in fact human. Thus *'think'* has been redefined as being able to act indistinguishably from an entity that, without a doubt, is able to think: a human.

Now, Turing has only solved half of the problem; he still has to come up with a way to unambiguously define the word *'machine'*. This is vital for there are a number of objects which could classify as a machine but would not be suitable to take this test. Turing has an answer to this however, for he thinks this theory should only apply to binary machines. According to him there are two important reasons for using these kinds of machines. For one, they are already available; their existence is not debatable. The second reason is based on one of his theories, which states that any binary or digital machine can simulate any other digital machine. This means that, if *any* digital machine is able to pass the **Turing Test**, *all* of these machine should—in theory—be able to pass the test.

Thus Turing is able to ask the following, more specific question:

> *Is there a conceivable computer D, one with the adequate amount of computing power and the right program, that is able to play the Imitation Game as participant A against participant B—who is human—in such a way that judge C is unable to correctly determine whether participant A or B is the real human?*

In this way, the Turing Test has been used for decades to test the *'intelligence'* of certain Machine Learning algorithms and Artificial Intelligences.

2.1.3 SNARC

One year after Turing's publication, Marvin Minsky finished building his Stochastic Neural Analogue Reinforcement Calculator, also known as SNARC. SNARC was a network of 40 randomly connected Hebb synapses. The SNARC was based on a model created by Warren McCulloch and Walter Pitts in 1943 wherein they proposed a model of artificial neurons where each neuron is characterized as being *on* or *off*, with a switch to *on occurring in response to stimulation by a sufficient number of neighbouring neurons. With

[4] Turing (1950).

the addition of a rule that modifies the connection strength between neurons the network gains the ability to improve it's performance.[5] This rule is now called *Hebbian Learning.*

The SNARC consisted of 40 neurons connected randomly and each neuron consisted of a long term memory and a short term memory. The long term memory is the probability that if a signal comes into on of the inputs that then a signal will come out of the output. This probability varies from 0—if the potentiometer is turned down—to 1—if the potentiometer is turned all the way up. If a signal gets through then the short term memory activates which consist of a capacitor and if the operator of the SNARC liked the outcome it could reward the neurons that fired by pressing a button that changed the probability of a neuron firing based on the state of the short term memory. The network achieves this by running a chain powered by a motor along all the potentiometers which turns the shaft of the potentiometers when the electric clutch is engaged. This only happens when the neuron has received a signal and thus the capacitor holds a charge.[6] In essence the SNARC was a really rudimentary ANN.

2.1.4 Perceptron

Hebb's learning methods were improved upon by Frank Rosenblatt with his perceptron. The perceptron was a machine designed for image recognition with 400 photocells randomly connected to artificial neurons. The weights of the connections were stored in potentiometers and these could be adjusted by electric motors to "learn". The perceptron convergence theorem says that the learning algorithm can adjust the connection strengths of a perceptron to match any input data, provided such a match exists.[7][8]

The early AI developments initially seemed promising, however Marvin Minsky and Seymour Papert book proved in their book *Perceptrons* (1969) that, although perceptrons (a simple form of neural network) could be shown to learn anything they were capable of representing, they could represent very little. In particular, a two-input perceptron (restricted to be simpler than the form Rosenblatt originally studied) could not be trained to recognize when its two inputs were different (XOR)[9]. Although their results did not apply to more complex, multilayer networks, research funding for neural-networks research soon diminished as the optimism for the capabilities of neural-networks vanished.

2.1.5 Backpropagation

In the 1980s the rediscovery of an algorithm to adjust the weights of the connections in the network so as to minimize a measure of the difference between the actual output vector of the net and the desired output vector caused a resurgence in machine learning research. It was applied to many learning problems in computer science and psychology which cause great excitement. The most important feature of backpropagation is that it organizes neurons in the hidden layers to learn to recognize different characteristics of the input. This means that if the network is presented with incomplete or noisy data it will still be able to recognise a pattern if it is present.[10]

[5] Russell and Norvig (2009).
[6] Sykes (2011).
[7] Block (1962).
[8] Russell and Norvig (2009).
[9] Minsky and Papert (1969).
[10] Russell and Norvig (2009).

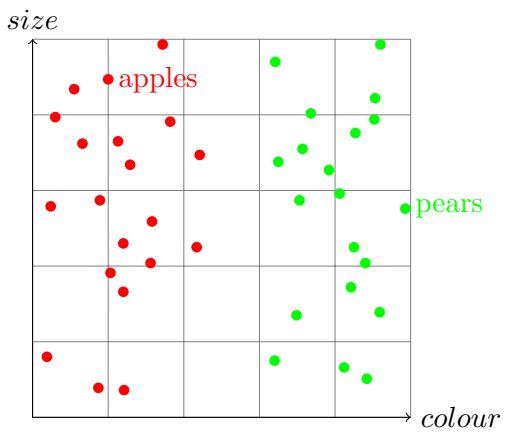
2.2 The basics of Machine Learning

2.2.1 The basic idea of Machine Learning

Fundamentally machine learning is not a difficult concept. Machine learning algorithms are concerned with drawing lines through data. The line that an algorithm draws describes a pattern, whether it is drawing a line through data to separate it(*classification*) or to describe it(*regression*).

2.2.2 Classification and regression

Classification and regression can also be classified in a different way, if the output of the algorithm is a discrete set of values(such as apple, pear or orange) then it is a classification problem. If the output of the algorithm is a continuous value(such as the price of a house) then it is a regression problem. For example we might have a dataset of apples and pears with their corresponding size and colour, this dataset is plotted in figure 2.1.



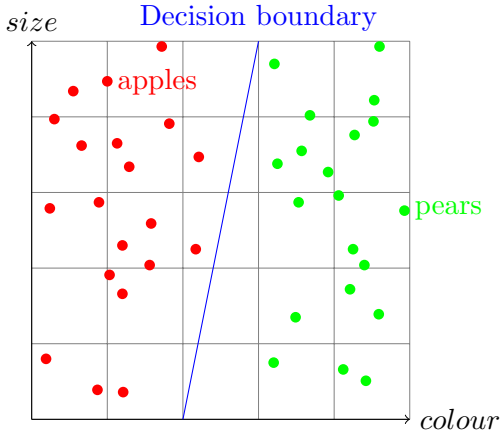
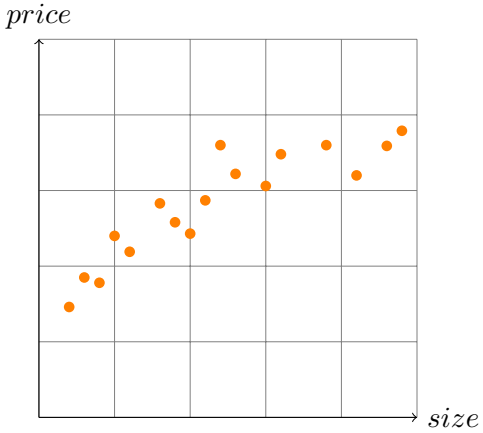


Figure 2.1, 2.2: An example of a labelled dataset of apples and pears and a possible decision boundary.

The red dots are labelled apples and the green dots are labelled pears. We can see that apples are mostly clustered on the left side and pears are mostly clustered on the right side. The learning algorithm might draw a linear decision boundary to separate the two clusters like shown in figure 2.2. After the training we can give the algorithm a new fruit and it's size and colour and it will be able to tell us if it is a pear or an apple.



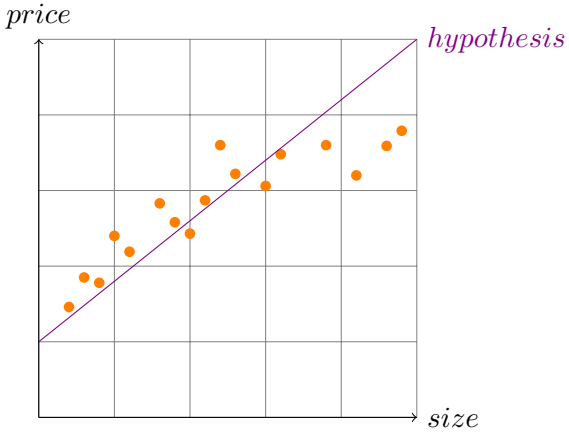


Figure 2.3, 2.4: An example of a labelled dataset of houses and a possible hypothesis.

For example we might have another dataset, this time it contains the size of the house and the price of the house, this dataset is plotted in figure 2.3. Each violet dot represents

a house and we can see that there is a relationship between the size of the house and the price of the house. The algorithm draws a line through the data, as close as possible to each data point. The line that this produces is the hypothesis function and is shown in figure 2.4.
Using this hypothesis function we can predict the price of a house based on its size. In this case the hypothesis is a linear function. However it is possible to choose any function and some will work better than others.

2.2.3 Supervised, unsupervised and reinforcement learning

> *"Well-posed Learning Problem: A computer program is said to learn from experience E with respect to some task T and some performance measure P, if its performance on T, as measured by P, improves with experience E."* [11]

For an algorithm to be capable of improving its performance from experience with respect to some task it needs to have feedback. This feedback comes in three forms that determine the type of learning supervised, unsupervised and reinforcement learning.

In supervised learning the algorithm knows what the correct output is for an input and thus can learn how to map a function from input to output. The examples for the classification and regression problems are examples of supervised learning. The classification algorithm knew what sizes and colours corresponded to an apple or a pear. The regression algorithm knew the price that corresponded to the size of each house.

In unsupervised learning the algorithm learns the pattern in the data even though no explicit feedback is given. The most common unsupervised task is clustering: detecting potentially useful clusters of input examples.

In reinforcement learning the algorithm learns from a series of reinforcements in the form of reward and punishment. For example a win at the end of a chess game can be a reward. The algorithm knows that the events that the events that led up to this moment were good. However it has to decide which actions were most responsible for the reward.

2.3 Examples of applications of Machine Learning

- Examples of neural network implementation and what they have achieved

3 Machine learning

3.1 Mathematical theory and model

3.1.1 Introduction and overview

As discussed previously, machine learning refers to the study and construction of mathematical algorithms with the goal of learning from and making predictions on data. There are two main basic types of machine learning models, of which other more complex algorithms are often based, and each with their own applications: linear regression and logistic regression. Both are conceptually and in terms of implementation very similar, and a good understanding of linear regression will also provide the knowledge to successfully grasp the

[11] Mitchell (1997).

concepts of logistic regression.

The basic function of linear regression is to model the relationship between one or more explanatory or independent values, more often referred to as input values and x-values, and a dependent variable, frequently referred to as the output value and y-value. A simple example for this would be the amount of rooms and the surface area of a house as x-values, and the price of this house as the y-value. These values serve as a training data for the algorithm, and are used to teach the program to make accurate predictions. These x-values and the y-value together are referred to as a data- or training set or simply 'the example data'. In order for the algorithm to work properly, the application of a great amount of data and thus a large dataset is crucial. The data corresponding to a single y-value will be referred to as a single training example.

Amount of rooms x-value 1	**Surface Area in m^2 x-value 2**	**House price in € y-value**
8	20	4000

Table 3.1: An example of a single training example

The algorithm will use this data to compute a hypothesis function using a process called gradient descent, which will attempt to minimize a cost function. What this means is that the linear regression algorithm will calculate a fit to the data set which is accurate to the data and not excessively complex, in order to be able to correctly predict a y-value for new, unlabelled x-values (x-values without a y-value). For example, considering this data set, which consists of one x-value and the y-value, the linear regression algorithm will compute the following graph:

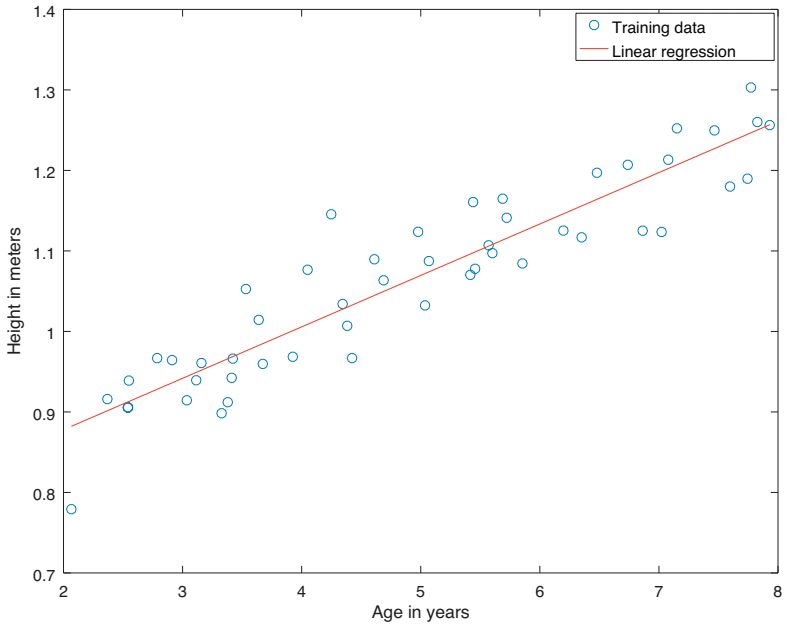


Figure 3.1: show graph with the added line

Note how the vector is a simplified average of the training data and can therefore be used to predict new y-values given unlabelled x-values.

In contrary to linear regression, were the dependent variable (or y-value) is a scaler,

in logistic regression this variable is categorical, meaning it can only be one of a limited and usually fixed number of possible values. The most common application of this model is for binary dependent variables, were it can only take on a value of 0 or 1, or 'true' or 'false'. This concept is essential in the implementation of neural networks, and a more in depth explanation is provided in chapter 3.

3.1.2 Linear regression

3.1.2.1 Datasets

In order to gain an understanding of the mathematics of linear regression, it is useful to make use of an example dataset. For this example the relation between the age and height of various boys between the ages of two an eight.

Example m	**Age in years x-value**	**Height in meters y-value**
1	2.066	0.779
2	2.368	0.916
3	2.540	0.905
4	2.542	0.906
5	2.549	0.939
...	...	...
50	7.9306	1.2562

Table 3.1: A data set with 1 feature and 50 trainings examples

The x- and y-values will be denoted as $x^{(i)}$ and $y^{(i)}$ respectively, where i represents the number of the training example in the data set, ranging from 1 to m. A dataset accordingly can be seen as a list of m training examples $\{(x^{(i)}, y^{(i)}); i = 1, 2, \ldots, m\}$.[12] The variable i represents an index into the training set and is not an exponentiation.

This example considers only one x-value per dataset, coupled with one y-value. This is strictly for the explanation and demonstration of the basic machine learning concepts in this paper. Generally, there will always be more than one x-value, called **features** in this context, used, in order to encompass more complex data and compute more accurate and therefore useful predictions. In such scenarios the x-values are considered vectors in $\mathbb{R}^n$, where n is the number of x-values per training example. This, however, results in calculations and data of higher dimension, which are impossible to display in a clear and concise manner and are thus disadvantageous for the goals of this chapter. Keeping this in mind, the data of the example can be displayed more effectively and concise in a graph.

3.1.2.2 The Hypothesis function

The goal of the algorithm will be to learn a function h that takes the given x-values in a training example to calculate a prediction for the y-value, where $h(x^{(i)}) \approx y^{(i)}$, meaning $h(x^{(i)})$ is a good as possible predictor of $y^{(i)}$. Traditionally, this function is called the hypothesis. Because the y-value is continuous, the learning problem of the example is

[12] Ng (n.d.).

called a regression problem.

The next step is defining the function h. The algorithm needs to factor in all the x-values for the prediction, while learning how to weigh each feature independently. Each x-value is therefore assigned to different variable, which the program will gradually adjust in order to increase the accuracy of the prediction. These parameters are noted as θ_a , where a is the number of the x-value it corresponds to. One extra parameter, θ_0, is also necessary to define h, as it functions as the starting position for the graph. The general function h will subsequently resemble:

$$h_\theta(x) = \theta_0 + \theta_1 x_1 + \theta_2 x_2 + \ldots + \theta_n x_n$$

Where n is the amount of features.

Note that this function, when plotted with the x-values, will result in a linear graph (even in higher dimensions). Often, data will follow a different pattern, such as an exponential curve or a logistic curve. For this, the function can be altered accordingly to fit a specific relationship between the x-value and the y-value. For example, a term for an exponential relation might be $\theta_n(x_n)^2$, and a term for square root relation might be $\theta_n\sqrt{(x_n)}$. It is possible for the program to recognize these patterns itself, but the complex algorithms this requires extends beyond the scope of this paper.

When the first term, θ_0 , is considered to be $\theta_0 x_0$,with $x_0 = 1$, function h can be rewritten as:

$$h_\theta(x) = \sum_{i=0}^{n} \theta_i x_1$$

Where n is the amount of features.

The function for the example will simply be:

$$h_\theta(x) = \theta_0 x_0 + \theta_1 x_1 = \sum_{i=0}^{1} \theta_i x_i$$

3.1.2.3 The Cost function

In order for the program to update the parameters and increase the accuracy of the prediction, it needs to know the margin of error of its previous prediction. For this a square error term is used, which is defined as the difference between the two values squared. In this algorithm this function is referred to as the **cost function**. For a single training set it defines the cost function J:

$$J(\theta)^{(i)} = (h_\theta(x^{(i)}) - y^{(i)})^2$$

The cost function J for the whole training set can be defined as an average of the examples 1 through m. In addition, to simplify a forthcoming partial derivative, it is useful to multiply the function by $\frac{1}{2}$, for minimizing half of the error term will ultimately have the same result as minimizing the full error term:

$$J(\theta) = \frac{1}{2} \cdot \frac{1}{m} \cdot \sum_{i=0}^{m} (h_\theta(x^{(i)}) - y^{(i)})^2$$

The goal of the algorithm will be to minimize this function, through modification of the variables θ; more specifically in the case of the example, the variables θ_0 and θ_1. Relation between the h function and the θ variables can be analysed with help of the following graphs. Notice how different values of θ affect the hypothesis function and subsequently the cost function. The values of θ in graph 3.5 result in the lowest value of function J, indicating the function h to be a reasonable fit to the data.

3.1.2.4 Gradient descent

To achieve the goal of minimizing the cost function, a process called **gradient descent** is used. In principle, this entails that the parameters θ are updated in order to improve the hypothesis function. An important attribute of this process is that it is repeated a considerable number of times, wherein the parameters are updated only to a small extend each iteration. This step as well as other similar algorithms which serve the same objective are the reason why the great computational speeds computers provide are essential for all machine learning algorithms.

For reasons of this explanation, it is useful to visualize the cost function in a graph. The dependent variables of the function are the parameters θ. Because in the example these are comprised of θ_0 and θ_1, the figure is three dimensional.

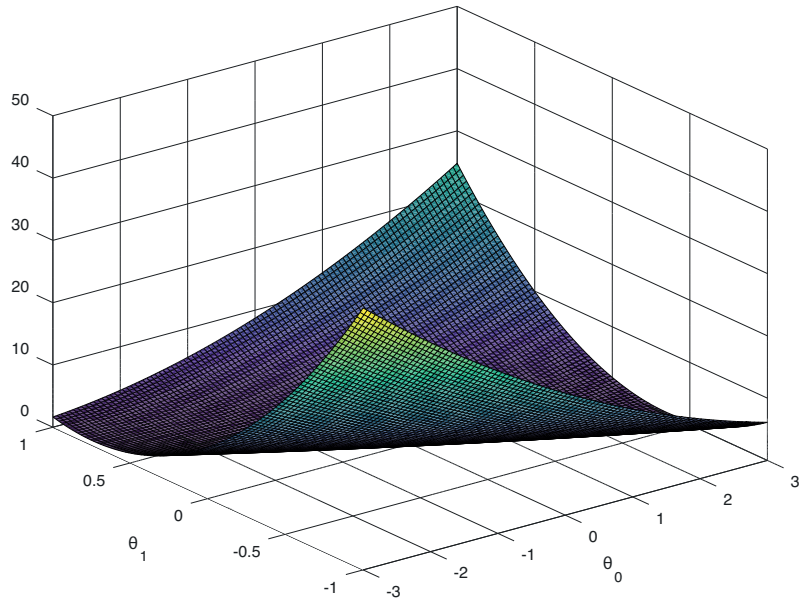


Figure 3.6:

As discussed previously, the goal of the algorithm is to minimize the cost function, which translates to finding a minimum in the plotted figure. As can be seen in figure 3.8, there won't always be just one minimum, but many different **local minima** can be present, while normally only one **global minimum** exists. The simple version of gradient descent in this introduction won't be able to distinguish between these. For now, however, this won't present any substantial problems. Additionally, a schematic rendering of the

direction of the parameters and the cost function through the gradient descent algorithm is shown. Notice how each iteration reduces the outcome of the cost function, although in reality, the amount of iterations will be much larger instead of the 7 shown here.

Furthermore, to make finding the minimum for the example data set - which happens to only have one minimum - more apparent, it is beneficial to display the figure in a top-down view. From this figure, the "route" the parameters will elapse can be determined easily.

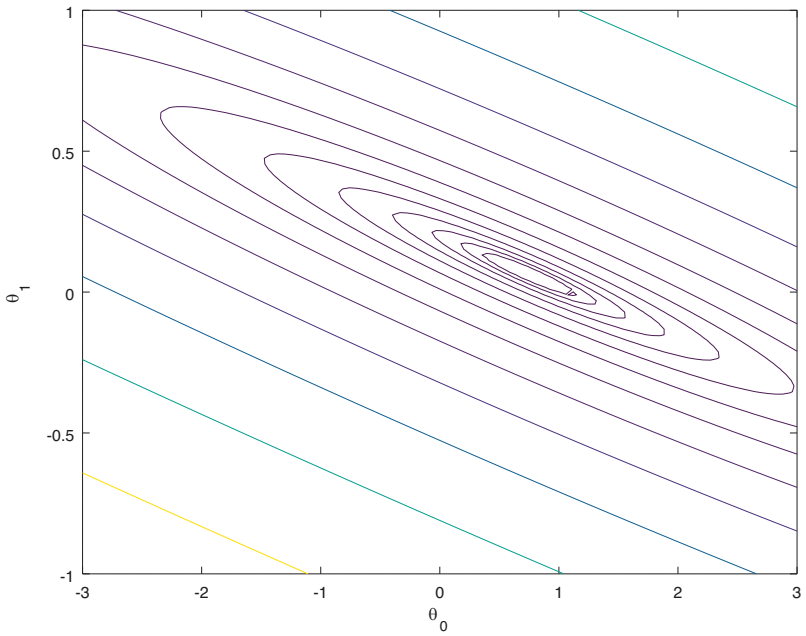


Figure 3.8: show graph with the added line

In order for the program to know which direction is towards a minimum, a **partial derivative** of the cost function is used. With this, the slope of the graph is calculated, in order for the program to know which direction is "uphill" and which direction is "downhill". Additionally, this will cause the parameters to gradually slow down their descent as they get closer to the minimum, where the slope is equal to zero. Note that in this process all features are computed separately. With this, the update function for each separate parameter θ for one iteration can be defined:

$$\theta_j := \theta_j - \alpha \cdot \frac{\partial}{(\partial \cdot \theta_j)} \cdot J(\theta) \quad (for\ all\ j)$$

Where j is the number of the feature, from 0 to the total amount of features
Where $\frac{\partial}{(\partial \cdot \theta_j)}$ indicates a partial derivative over $theta_j$
Where α is parameter indicating the learning rate.

The := symbol indicates an assignment computation. Because θ_j is used in the definition as well, this means the original value of θ_j will be updated in accordance to this original value.

Choosing a desirable learning rate α is an important part in this process, as it defines to which degree the parameters are updated each iteration. When it is too small, the program will take too long to compute, and when it is too large, the program might have trouble converging to a minimum, as the parameter will continually go over the it.

Because all features are computed separately, it is possible to visualize this process.

The next step is to define $\frac{\partial}{(\partial \cdot \theta_j)} \cdot J(\theta)$. The inclusion of the previously defined cost function J gives:

$$\frac{\partial}{(\partial \cdot \theta_j)} \cdot \frac{1}{m} \cdot \frac{a}{m} \cdot \sum_{i=0}^{m} (h_\theta(x^{(i)}) - y^{(i)})^2$$

After differentiation, this formula becomes:

$$\frac{1}{m} \cdot \sum_{i=0}^{m} (h_\theta(x^{(i)}) - y^{(i)}) \cdot x_j^{(i)}$$

With these and as a final step, we can redefine the update formula:

$$\theta_j := \theta_j - \alpha \cdot \frac{1}{m} \cdot \sum_{i=0}^{m} (h_\theta(x^{(i)}) - y^{(i)}) \cdot x_j^{(i)} \quad (for\ each\ j)$$

3.1.2.5 Abridgement

In practice, the program first initializes the parameters θ to random values (often 0). Following this, it will compute the hypothesis function and update the parameters for i amount of iterations using the gradient descend algorithm with learning rate α, using the following formulas, until convergence. The outcome will be a hypothesis function which accurately predicts the y-value for new x-values.

$$h_\theta(x) = \sum_{i=0}^{n} \theta_i \cdot x_i$$

$$\theta_j := \theta_j - \alpha \cdot \frac{1}{m} \cdot \sum_{i=0}^{m} (h_\theta(x^{(i)}) - y^{(i)}) \cdot x_j^{(i)} \quad (for\ each\ j)$$

3.1.2.6 Vectorized implementation

For the machine learning to be as efficient as possible, the amount of calculations required for each iteration should be minimized. Especially for increasingly complex and large datasets, only a tiny decrease in the duration of a single iterations can lead to huge improvement for the whole process. An important aspect for essentially all machine learning algorithms is the vectorized implementation. Making use of a heavily optimized linear algebra library and matrix multiplications, an vectorized implementation creates a significant performance increase in any of the machine learning algorithms. For most programming languages, such a linear algebra library is readily available.

In basic terms, a vectorized implementation simply refers to an implementation where the computer calculates all learning examples 'at once', by positioning them in a single matrix. The hypothesis function will therefore be implemented as the product of two matrices, x^T and θ, instead of the sum of the products of two integers, θ_i and x_i, for all features and subsequently all training examples. Because of the exploitation of the matrix functionality, these computations are effectively identical. The matrix multiplication, however, is many times faster than a relatively slow for-loop and more compact in the

programme as well. Furthermore, by arranging the data as a matrix, data sorting and storing can be done much more efficiently and orderly.

$$h_\theta(x) = \sum_{i=0}^{n} \theta_i \cdot x_i \quad (for\ all\ training\ examples) = x \cdot \theta$$

Note that the $\sum$ will be represented in code as a for-loop.It is important for the two matrices to be the appropriate proportion, in order to allow for the matrix multiplication.

The matrix x consists of all x-values of the training examples, and will be of $\mathbb{R}^{m \times n}$ dimensions, where m is the number of training examples and n the number of features (including x_0). Note the multiplication symbol expresses dimensionality, and does not indicate actual multiplication. The values for the weight values θ have just one value for each iteration, and are thus constant across the multiplications with all training examples in each iteration. θ will accordingly be of $\mathbb{R}^{n \times 1}$ dimensions. Following the multiplication, this computation will result in a matrix of dimensions $\mathbb{R}^{m \times 1}$ as well, containing the hypothesis value for all training examples.

$$\begin{array}{c|c} & \begin{bmatrix} \theta_0 \\ \theta_1 \\ \theta_2 \end{bmatrix} \\ \hline \begin{bmatrix} x_0^{(1)} & x_1^{(1)} & x_2^{(1)} \\ x_0^{(2)} & x_1^{(2)} & x_2^{(2)} \\ \vdots & \vdots & \vdots \\ x_0^{(m)} & x_1^{(m)} & x_2^{(m)} \end{bmatrix} & \begin{bmatrix} x_0^{(1)} \cdot \theta_0 + x_1^{(1)} \cdot \theta_1 + x_2^{(1)} \cdot \theta_2 \\ x_0^{(2)} \cdot \theta_0 + x_1^{(2)} \cdot \theta_1 + x_2^{(2)} \cdot \theta_2 \\ \vdots \\ x_0^{(m)} \cdot \theta_0 + x_1^{(m)} \cdot \theta_1 + x_2^{(m)} \cdot \theta_2 \end{bmatrix} \end{array} = \begin{bmatrix} h_\theta^{(1)}(x) \\ h_\theta^{(2)}(x) \\ \vdots \\ h_\theta^{(m)}(x) \end{bmatrix}$$

Figure 3.10: The matrix multiplication table of the matrices x and θ, wherein the hypothesis values for all training examples are calculated. Following the standard rules for matrix multiplication, the first element of each row of the bottom left matrix is multiplied with the first element of each column of top right matrix, after which the product of the next elements of the respective row and column is added, until all each row has been included. In the bottom right matrix the result of this multiplication can be seen. This result is equal to the hypothesis function, confirming the validity of the use of the matrix multiplications of a vectorized implementation.

Accordingly, the cost function J can be updated for use of the the matrix h_θ, and a matrix y of the y-values of the training examples. Because, instead of with a one-by-one approach, all h-values are used simultaneously the sum can once again be omitted. The function can be rewritten as follows.

$$J(\theta) = \frac{1}{m} \cdot \sum_{i=0}^{m} (h_\theta(x^{(i)}) - y^{(i)})^2 = \frac{1}{m} \cdot (h_\theta - y)^2$$

Note the exponent 2 illustrates an element-wise exponentiation.

Lastly, since the the weight values, θ_0 to θ_n, have been converted to a matrix form as well, the weight update function must be updated similarly. It is once again possible to exploit the functionality of matrix multiplication for a more efficient computation, as the x-value present in the update function can be used to conveniently create a matrix with the corresponding dimensions.

$$\left[\begin{array}{cccc} x_0^{(1)} & x_0^{(2)} & \dots & x_0^{(m)} \\ x_1^{(1)} & x_1^{(2)} & \dots & x_1^{(m)} \\ x_2^{(1)} & x_2^{(2)} & \dots & x_2^{(m)} \end{array}\right] \left| \begin{array}{c} \left[\begin{array}{c} h_\theta^{(1)}(x) \\ h_\theta^{(2)}(x) \\ \vdots \\ h_\theta^{(m)}(x) \end{array}\right] \\ \hline \left[\begin{array}{c} \Delta\theta_0 \\ \Delta\theta_1 \\ \Delta\theta_2 \end{array}\right] \end{array}\right.$$

$$\theta_j := \theta_j - \alpha \cdot \frac{1}{m} \cdot \sum_{i=0}^{m} (h_\theta(x^{(i)}) - y^{(i)}) \cdot x_j^{(i)} \quad (for\ each\ j) \longrightarrow \theta =: \theta - \alpha \cdot (\frac{1}{m} \cdot x^T \cdot h_\theta)$$

One dimensional integers α and $frac1m$ are multiplied element-wise with the according matrices. The T in this formula represents the transpose of the matrix x. Because of standard matrix multiplication notation, the transposed matrix x^T is positioned before the h_θ term in the formula. With this, the complete learning algorithm can be represented with the following formula:

$$\theta := \theta - \alpha \cdot (\frac{1}{m} \cdot x^T \cdot ((x * \theta) - y)^T)$$

3.1.2.7 Sidenotes

While more data usually means more accuracy, because it is often possible that no correlation between the x and y values exists, all x-values should always be carefully considered and analyzed however. Even when no correlation exists, the algorithm will still factor the data in the calculations, which will result in less accurate results.

This paper won't go into detail of many other, more complex aspects of linear regression, on account of space constraints. If a more in depth understanding is required, it is recommended to read up on these concepts, such as feature scaling and the selection of a good learning rate to name a few, from other sources.

Furthermore, it is important to realize these forms of machine learning, linear and logistic regression, are relatively basic and are not used a lot nowadays in their original form. Many more complex and efficient algorithms have since taken their place. These algorithms are still based on the same concept however, and basic understanding of these concepts is crucial in the field. Neural networks are an example of this, since they are essentially a variation on logistic regression.

3.2 Implementation in the programming language Octave

3.2.1 Introduction and overview

The implementation of the linear regression algorithm is relatively simple, and only consists of a few lines. This will be a step by step commentation for a basic implementation as described in chapter 3.1 of this paper. As mentioned previously, the used programming

language is GNU octave, but any programming language is of course suitable, provided it has an linear algebra library available. Octave comes pre installed with a greatly optimized linear algebra library and provides build-in functionality for graphs and other useful figures as well. For this programme the previously described example of chapter 3.1 is used once again.

3.2.2 Non-vectorized implementation in Octave

Before examining vectorized implementation, it is important to understand a basic implementation. Keep in mind a non-vectorized implementation is rarely used anymore and can make for a somewhat disconcerting programme.

The first step is loading the training examples and defining variables. The dataset contains 50 examples, meaning the x and y values, which are defined as an array, will have a length of 50. This example considers the data to be available as an array in a *.dat* file, although the initiating of this data depends on the manner in which it is stored on the computer. The x_0 is defined as 1.

Next, the learning rate α (alpha) and the amount of iterations i (max_iterations) are given the values 0.07 and 1500 respectively. Both values are changeable, and optimal values differ per situation. Unfortunately, the techniques for choosing the best values for these will not be discussed in this paper. For now, realize a smaller value of α will give the algorithm more accuracy, at the cost of speed. The amount of iterations is the amount of times gradient descend will run, and a higher value ensures the hypothesis function has converged to an optimal value, at the cost of the programme running for a greater amount of time.

The starting values for the weights θ are initiated as well, and are given a value of 0, although any value could be used. As a reminder, the example dataset contains only one feature, meaning 2 different θ values need to be initiated, θ_0 (theta0) and θ_1 (theta1).

```
%Inport Training Examples
x0 = 1;
x1 = load('x.dat');
y = load('y.dat');

%Set variables
m = length(y);
alpha = 0.07;
max_iterations = 1500;
theta0 = 0;
theta1 = 0;
```

The next step is defining the hypothesis function. From the general formula, $h_\theta(x) = \theta_0 \cdot x_0 + \theta_1 \cdot x_1 \ldots \theta_n \cdot x_n$, follows for the example the formula $h_\theta(x) = \theta_0 \cdot x_0 + \theta_1 \cdot x_1$. Because each training example has a hypothesis value, the function must be computed m amount of times. This is achieved by use of a for-loop, in which the hypothesis function is defined as the array h[i].

```
%The hypothesis function
for i = 1:m
  h[i] = theta0 * x0 + theta1 * x1[i];
```

```
end
```

The cost function will be defined as the already partially differentiated formula $\frac{1}{m} \cdot \sum_{i=0}^{m}(h_\theta(x^{(i)}) - y^{(i)}) \cdot x_j^{(i)}$. For the sum, a for loop can be used, which goes over all the index values of $h[i]$ and adds them together. The $\frac{1}{m}$ is added in the next step, in order to correctly calculate the outcome. Because the formula has a weight parameter specific term ($x_j^{(i)}$), a separate cost function for each feature is necessary. In the programme, this will be defined as follows.

```
%The cost function
J0 = 0;
J1 = 0;
for i = 1:m
  J0 = J0 + (h[i] - y[i]) * x0;
  J1 = J1 + (h[i] - y[i]) * x1[i];
end
```

Lastly, the weight parameters are updated according to the the update function $\theta_j := \theta_j - \alpha \cdot \frac{1}{m} \cdot \sum_{i=0}^{m}(h_\theta(x^{(i)}) - y^{(i)}) \cdot x_j^{(i)} \quad (for\ each\ j)$, in which $\sum_{i=0}^{m}(h_\theta(x^{(i)}) - y^{(i)}) \cdot x_j^{(i)}$ is replaced with the in the programme defined J. Keep in mind this variable is different than the in section 3.1 defined cost function J. The parameters theta0 and theta1 will be updated as follows.

```
%The update function
theta0 = theta0 - alpha * 1/m * J0;
theta1 = theta1 - alpha * 1/m * J1;
```

The described programme functions as a single iteration of the gradient descend algorithm. In order to finish the full linear regression algorithm, a for-loop is added which encompasses the defined functions. Because for each iteration a new error term is necessary, the variables J0 and J1 need to be reset. The full programme will look as follows.

```
%Inport Training Examples
x0 = 1;
x1 = load('x.dat');
y = load('y.dat');

%Set variables
m = length(y);
alpha = 0.07;
max_iterations = 1500;
theta0 = 0;
theta1 = 0;

%Linear Regression
for i = 0:max_iterations
  for i = 1:m
    h[i] = theta0 * x0 + theta1 * x1[i];
  end

  J0 = 0;
  J1 = 0;
  for i = 1:m
    J0 = J0 + (h[i] - y[i]) * x0;
```

```
    J1 = J1 + (h[i] - y[i]) * x1[i];
  end

  theta0 = theta0 - alpha * 1/m * J0;
  theta1 = theta1 - alpha * 1/m * J1;
end
```

3.2.3 Vectorized implementation in Octave

This basic implementation presents a number of problems. For instance, a high number of features can lead to an incredible amount of theta variables, resulting in a high number of functions or, alternatively, nested for-loops, both of which decrease the clarity and increase inefficiency of the code. A vectorized implementation will solve these problems as well as improve performance significantly, as has been described in section 3.1. Additionally, because of the nature of this implementation, the programme is compatible with all possible number of features.

To start, the x, y and h values previously defined as arrays, can be converted to matrices. The variables y and h both contain one value for each training example, resulting in matrices dimensions $\mathbb{R}^{m\times 1}$, and $\mathbb{R}^{50\times 1}$ for the example. The matrix x includes all x values, and will accordingly have a width of $n+1$ (all features and x_0), resulting in a matrix of $\mathbb{R}^{m\times n}$, and $\mathbb{R}^{50\times 2}$ for the example. The first column is made up of the x_0 values, and all its elements equal one. This column won't be part of any dataset, and needs to be added to the matrix. This can be achieved with an Octave function *ones*(), which will return an matrix of ones of the specified dimensions.

```
%Inport Training Examples
x = load('x.dat');
y = load('y.dat');

%Set variables vectorized
m = length(y);
x = [ones(m, 1), x];
```

For each feature, one weight parameter θ_n needs to be defined. As described in section 3.1, this is achieved in a matrix of dimensions $\mathbb{R}^{n\times 1}$, and $\mathbb{R}^{2\times 1}$ for the example. Once again, the values of θ (theta) are initiated as zero. Because the height of the matrix needs to equal the width of the matrix x, the Octave function *width*() (which, as expected, returns the width of a matrix) is used followed by a transpose. This gives a matrix of the right dimensions. With the Octave function *zeros*(), all elements of the matrix are set to zero.

```
theta = zeros(size(x(1,:)))';
```

Next, the hypothesis function can be defined. All h values are computed at once, and no for-loop is necessary.

```
%The hypothesis function
h = x * theta;
```

The cost function is adjusted in a similar manner, and computes all values at once. Additionally, the different values for J can be represented in one function. A matrix multiplication with x^T will result in a matrix of the same dimension as the matrix theta,

namely $\mathbb{R}^{n\times 1}$, and $\mathbb{R}^{2\times 1}$ for the example. In order to correctly execute this multiplication, the matrix x^T needs to be positioned before the matrix h. In Octave, a transpose is implemented with use of an apostrophe, resulting in x^T being represented as x' in the programme. For consistency, the $\frac{1}{m}$ term is again moved to the update function.

```
%The cost function
J = x' * (h - y)
```

Subsequently, the update function updates all weight parameters θ, present in different rows of the matrix theta, at once. The integers α (alpha) and $\frac{1}{m}$ are multiplied element-wise with the matrix.

```
%The update function
theta = theta - alpha * (1/m) * J;
```

Once again a for-loop is added to finish the linear regression algorithm.

```
%Linear regression vectorized implementation
for i = 1:max_iterations
  h = x * theta;
  J = x' * (h - y);
  theta = theta - alpha * (1/m) * J;
end
```

As a final step, the functions can be combined to shorten the whole algorithm to a single line.

```
%Inport Training Examples
x = load('x.dat');
y = load('y.dat');

%Set variables vectorized
m = length(y);
x = [ones(m, 1), x];
alpha = 0.07;
max_iterations = 1500;
theta = zeros(size(x(1,:)))';

%Linear regression vectorized and shortened implementation
for i = 1:max_iterations
  theta = theta - alpha * ((1/m) * x' * ((x * theta) - y));
end
```

Even for a linear regression algorithm with only two features, the vectorized implementation manages to shorten and optimize the programme by a considerable amount. This example served only as an easy introduction to the idea. The concepts of vectorized implementation play a big role in the implementation of neural networks and will return in the following chapter.

4 Artificial Neural Networks

4.1 Architectural model and mathematical theory

4.1.1 Introduction and overview

Using the aforementioned methods, finding a linear relation among certain data points can be easily achieved. What should one do however, if there is no such linear relation? In that case, other forms of regressional analysis, such as *polynomial regression* can be used. Even then, the analysed data points ought to adhere to a relation which can be described using a polynomial equation or any other type of equation prescribed by the form of regression. Furthermore, what if the data points are defined by an excessive amount of independent variables? Using ordinary regression, this results in a multi-dimensional relation which would become exponentially more difficult to calculate.

There is, however, an alternative method for solving these kinds of problems. Using *Artificial Neural Networks*, complex relations in large amounts of data can be found. Artificial neural networks are currently a popular and effective form of machine learning. Artificial Neural Networks (*ANN*) mimic *Biological Neural Networks* (*BNN*) in their basic functioning. A BNN consists of many neurons [13], the neurons have dendrites and axons. When a neuron fires it sends a signal along its axon which connects to the dendrite of another neuron. A neuron fires if the sum of the input signals is high enough to surpass a certain threshold or in the case of a sensory neuron if it is stimulated by a physical stimulus such as light, temperature or pressure. motor neurons control muscles and function as the output of a BNN. This biological analogy can be used to describe the form and function of the components of an Artificial Neural Network.

Whereas a BNN has sensory neurons, an ANN has so called input nodes. These nodes, just as their biological counterparts, also require a certain amount of stimulation in order for them to relay a signal. The links between nodes in an ANN are handled by *weighted connections*, as opposed axons and dendrites connecting neurons in a BNN. The function of the biological motor neuron

4.1.2 The network architecture

When trying to build an ANN to solve a supervised learning task - let us say a value y has to be predicted based on a value x - there are a few important aspects that need consideration.

First of all, these aspects are comprised of the fundamental building blocks of a ANN. As mentioned earlier, these components are the nodes and weighted connections but also crucial are the layers in which they are arranged. Second of all, the properties of these components should be considered.

To get a clear picture of Artificial Neural Networks, its components, their properties and functions will be explained using the example network shown in figure 4.1.

[13] Skaggs (2013).

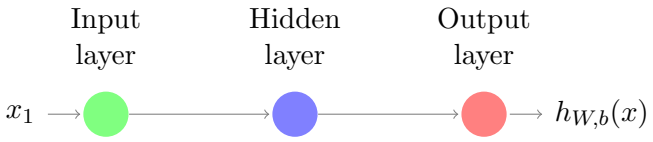


Figure 4.1: A three layered model of an ANN with in each layer one node.

While this might seem like a rather simple network, which can not really be disputed. It does employ the previously specified components in the various forms they can assume.

4.1.2.1 Layers

One of the first noticeable properties of an ANN, as is demonstrated in the aforementioned example, is the composition of the assorted layers in the network. While there are only three layers present in this example, it is not uncommon for a network to have a vast amount of them. The amount of layers needed is determined by the task the ANN has to perform and thus has to be decided with the networks function in mind. For too little layers would limit the networks function. Too many layers however, is not desired either considering it will make computation of the network slower and exceedingly more difficult. Finding a correct balance is imperative and this balance should also be achieved when considering the number of nodes in each layer and the inter-node connections.

In ANNs there are three types of layers, all of which are shown in the example of figure 4.1. Each layer contains nodes that fulfil a different function.

The first layer is the *input layer*. This layer contains input nodes and is thus responsible for providing the ANN with data. In an ANN there is only one input layer present.

The final layer present in an ANN is the *output layer*. This layer contains, as one might presume, the output nodes and handles the various outputs of the network. As with the input layer, in each ANN there is only one of these layers present.

The second layer is called the *hidden layer*. Of this layer there are usually more present, situated between the two outside layers. One of which is the input layer and the other one will be discussed hereafter. The hidden layers are comprised of hidden nodes. The layer is called 'hidden', since the user of the network does not directly interact with it, as opposed to the input and output layer, where data is provided or received respectively. The hidden layer is responsible for most of the computation—which depends on its size and the amount of hidden layers.

4.1.2.2 Nodes

Nodes, represented in the model above by the coloured circles, are small and relatively simple computational units. In the example network, three of the four different types of nodes are displayed. The displayed three nodes have been briefly introduced in the preceding paragraphs. Each of these distinct types of nodes has its own functions and treats data in a slightly different way.

The first type of node, represented by the green circle, is the input node. This node acts as the input of the network. By itself, the input node does not perform any computa-

tion; It merely takes the input data given to the network and passes it on to the next layer.

Somewhat similar to the input node is the bias node, a node not included in the example above but not less important. This node however, has a default value of 1. The node solely passes this 1 on to the nodes in the next layer its connected with via weighted connection. The value of a bias node is sometimes given as a separate weight itself, for any number is the solution of its multiplication with 1.

After this, the hidden node is at play, represented by the blue circle. These kinds nodes of receive inputs from the layer that came before it via the connections it has with these previous nodes. The node takes these inputs, sums them up and applies an activation function to this sum. The mathematical nature of the activation function will be discussed following section concerning the mathematical theory of ANNs. The solution of the activation function is passed on to the connected nodes in the next layer.

The final node in the network, represented by the red circle, is the output node. This node, just as the hidden node, takes the sum of its inputs and applies an activation function to this sum. However, it does not pass the result of the activation function on to nodes in the next layer. Instead its result will be given to the user as the final output of the ANN.

4.1.2.3 Weighted connections

The function of nodes having been elaborated upon, just leaves the so called weighted connections between the nodes. These connections are represented in the example by small arrows going from one node to another. The function of these connections is to take the output of a node, multiply it by a certain weight—this is just a number prescribed when constructing a network—and server the result of the multiplication as one op the inputs of the node in the next layer.

4.1.2.4 Network Topology

As has been pointed out in the previous paragraphs briefly, deciding the structure of an ANN to be used for a certain task is essential. When talking about the placement of nodes is various layers and the different connections between nodes this is usually described as the topology of a network. The subject of network topology will be further discussed in chapter 5.

4.1.3 Underlying mathematics

Now that the description of the ANN architecture is out of the way, explaining the mathematical basis is left to be done. For, while an ANN might not look like it, it is just a mathematical algorithm one is able to represent with one single equation. However, for the sake of clarity, this formula will be slit up into simpler and easily digestible parts linked to the various components of the ANN. When discussing these formula's, some symbols will be used to represent certain variables and parameters. These symbols are each introduced in paragraph they are featured in first.

4.1.3.1 Weight computation

While in the structural theory nodes have been discussed before discussing connections, the choice has been made to turn this order around when describing the mathematical theory, for knowledge about weight computation is crucial to understanding node computation.

Each weighted connection is given a weight, represented as $W_{ij}^{(l)}$. Here i represents the target node, j represents the node of origin, (l) the layer of origin and thus $(l+1)$ the destination layer. This $W_{ij}^{(l)}$ is multiplied with the output of node j in layer (l) to get one of the inputs of node i in layer $(l+1)$.

The weight of connections originating from bias nodes is represented by $b_i^{(l)}$ where i represents the destinations node and (l) the layer of the destination node.

4.1.3.2 Node computation

In the above-mentioned description of hidden and output nodes a little bit of light has been shone upon the theory of the activation function. Its algebraical properties have however not been explained yet.

As mentioned, the hidden and output nodes receive multiple weighted values from nodes situated in the previous layer. These inputs are summed by the node. This sum of values is algebraically represented by $z_i^{(l)}$, where i represents the node and (l) the layer. Thus:

$$z_i^{(l)} = \sum_{j=1}^{n} W_{ij}^{(l)} + b_i^{(l)}$$

$f(z)$ is the activation function, also know as the sigmoid function. The equation os the sigmoid function is as follows:

$$f(z) = \frac{1}{1 + e^{(} - z)}$$

This function results in the following graph:

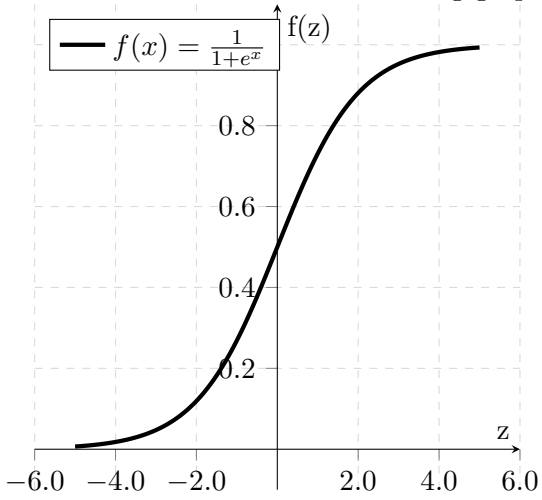


Figure 4.2: A graphical plot of the sigmoid function.

The nature of the sigmoid function, and therefore the node activation, is to return a 0 when the sum of inputs is below a certain value and return a 1 of it is above this value.

Ordinarily this value would be around $z_i^{(l)} = 0$, but by using bias nodes this value can be shifted, due to the bias weight always being added during the nodes summation.

Some implementations of neural networks, like the one used for our experiment, use activation functions derived from the sigmoid functions. The function we use, which will be discussed later is:

$$f(z) = (\frac{2}{1 + e^{(-4.9z)}}) - 1$$

and results in the following graph:

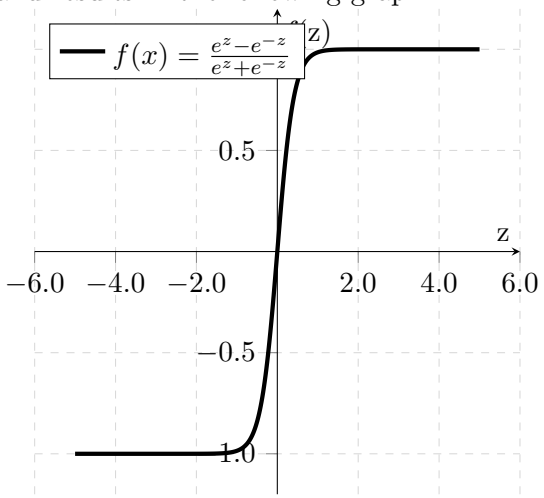


Figure 4.3: A graphical plot of the modified sigmoid function.

In ANN theory the activity of a node—the result of its activation function—is usually represented as $a_i^{(l)}$. i represents the number of the node inside its layer and (l) represents the number of the node's layer in the network. Thus the equation describing a layers activation is as follows:

$$a_i^{(l)} = f(z_i^{(l)})$$

4.1.3.3 The hypothesis

4.1.3.4 Vectorized implementation

4.1.4 Backpropagation

4.2 Implementation in the programming language Octave

Similar to linear regression, it is useful to go through the implementation of a simple neural network in order to fully understand the actual learning process. Once again, the programming language Octave will be used. This chapter will only go over the vectorized implementation. The following neural network, illustrated in figure 4.4, will be trained to act as a simple AND gate.

x_1	x_2	y
0	0	0
0	1	0
1	0	0
1	1	1

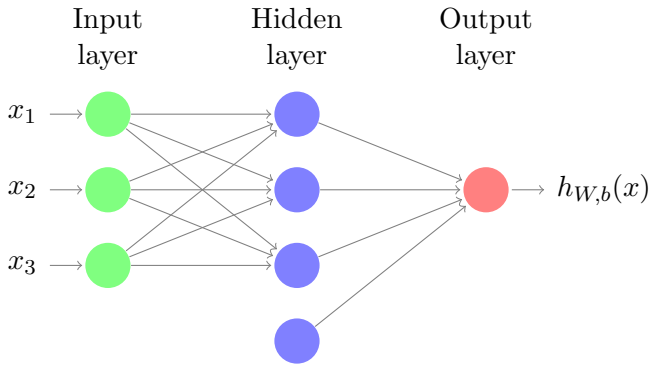


Figure 4.4: A graphical representation of the aforementioned ANN. In this network the bias node in the input layer is represented by x_3 and the bias node in the hidden layer is the bottom most blue node.

4.2.1 Variable initiation

To start, a data set initialized. For a AND gate two x values per training example are required, both of them being boolean. In this example, each value of x is loaded as a separate matrix and added together later. All x matrices have 1 column and m rows. There are $2^2 = 4$ possible combinations of the two x values, meaning $m = 4$. The matrix x_1 and x_2 therefore have a dimensionality of $\mathbb{R}^{4\times1}$. Accordingly, because there is only a single output node, the y matrix has the same dimensionality. The values correspond to a AND gate as follows:

Figure 4.5: A table showing the different x_1 and x_2 values and their result when inserted in an AND gate.

```
%The data set
x1 = [0; 0; 1; 1];
x2 = [0; 1; 0; 1];
y =  [0; 0; 0; 1];
```

The weights are initiated as a matrix of the dimensions corresponding to the amount of connections in a specific layer. The dimensions are equal to the product of the amount of nodes in the layer, excluding the bias node, and the amount of nodes in the next layer, where the weights in each column and row correspond to a single node respectively. For the example, the dimensions of the weights matrix of layer 1, W^1, is $\mathbb{R}^{2\times3}$, according to to the 2 nodes in layer 1 and the 3 nodes in layer 2. Similarly, the weight matrix of layer 2, W^2, is $\mathbb{R}^{3\times1}$. For clarity, the number present in the variable names indicates the layer number, instead of for x_1 and x_2, where it indicates the node number in the input layer. As described, the starting weights need to be initiated to different values for the purpose of symmetry breaking.

Next, the weights of the bias nodes are initiated, for which there is a values for each node in the next layer. The dimensionality of the matrix for the first layer, b_1, is $\mathbb{R}^{1\times3}$ and the matrix for the second layer, b_2, is $\mathbb{R}^{1\times1}$. Because the bias nodes always output a value of 1, these weights equal the complete output of the bias nodes to the next layer.

The matrices are therefore referred to simply as the bias node outputs, and are used in upcoming computations without a multiplication. The Octave function stdnormal_rnd() will generate a matrix of specified dimensions with random elements of normal distribution. The code will look as follows:

```
%Initialisation weights
W1 = stdnormal_rnd(2,3);
W2 = stdnormal_rnd(3,1);
b1 = stdnormal_rnd(1,3);
b2 = stdnormal_rnd(1,1);
```

The variables are initialized afterwards. α (alpha) is initiated to 1 and λ (lambda) is initiated to 0, meaning both won't have any effect on the algorithm. Since this is a simple network, it is not required to contemplate the values of these variables. Like what has been stated in chapter 3, the process of determining these values can be very complicated and will not be discussed in this paper. The amount of iterations the network will run is defined as the variable max_iterations, and is set to 5000, which is more than enough for this simple task. The amount of training examples m is equal to the amount of rows of the x matrices, and it initiated using the Octave functions rows(), which counts the amount of rows of a given matrix.

```
%Initialisation variables
alpha = 1;
labda = 0.01;
max_iterations = 5000;
m = rows(x1);
```

4.2.2 The sigmoid activation function

The sigmoid activation is defined as a function, since the program needs to refer to it multiple times. Because this is a vectorized implementation, the notation ./ is used, indicating a element wise division. exp(-z) means an e exponent, or e^{-z} in this case. Similar to the sigmoid formula, the function is defined as f(z).

```
%sigmoid function
function s = f(z)
  s = 1./(1 + exp(-z));
end
```

4.2.3 Forward propagation

First the forwards propagation is implemented, where each layer is calculated one after the other. First the output of all the nodes except the bias node in layer 1, the input layer, is defined as $a^{(1)}$, where a indicates the output and (1) the layer. Naturally, this value consists of the input values x_1 and x_2, since a vectorized implementation is utilised, $a^{(1)}$ is defined as a matrix, where each column contains the outputs of a single node, either x1 or x2, and each row the data of a single training set. With this matrix and the matrices with the weights of the first layer, W1 and b1, the inputs for the nodes in the next layer are computed. Following the connections in the diagram and the formula $z = [sum](a * w) + b$, the input to each node in layer two equals the sum of the outputs of the nodes in the previous layer and the bias node. This means each node in layer 1 needs to be computed for each node in layer 2, which in the case of this example means the value of x1 and x2 are both necessary 3 times. With another exploitation of matrix

multiplication this can be achieved very efficiently and without use of a for loop. The outputs of the bias node , which in this layer consists of a matrix of the dimensions , is added to the matrix thereafter. a1 will be defined as follows.

```

for i = 1:maxi

    %Forward propagation

    % layer 1 (input)
    a1 = [exx1, exx2];

    % layer 2
    z2 = a1 * W1 + b1;
    a2 = f(z2);

    % layer 3 (output)
    z3 = a2 * W2 + b2;
    h = f(z3);
    a3 = h;

    %Backward propagation

    % Delta values
    delta3 = -(exy - h)   .* (a3 .* (1 - a3));
    delta2 = (delta3 * W2') .* (a2 .* (1 - a2));

    %Update functions
    W2 = W2 - alpha * (a2' * delta3 * 1/m); % + lambda * W2);
```

subsubsectionBackward propagation Next, the δ values are computed. As described in the previous section, the δ values of any specific layer can be seen as an error term for that layer, are are used to update the weights of the connections to that layer. The δ of the last layer, delta3 in the example, is defined first, and is calculated according to the formula delta output layer formula. Subsequent δ values are defined using the δ of the the following layer using the formula de volgende formula. All the δ values are calculated using the derivative of the sigmoid function, which equals the formula de afgeleide van de sigmoid. Because the values of $f'(z^{(l)})$ are already defined as a^l, those can be used instead, in order be as efficient with computational resources as possible.

```
    b2 = b2 - alpha * (sum(delta3) * 1/m);
    b1 = b1 - alpha * (sum(delta2) * 1/m);

end
```

The values of δ are used to update the weights. Because the connections to a layer are defined as weights of the previous layer, the value of delta of any layer is used to update the previous layer, which for the example entails delta3 is used to update $W^{(2)}$ and delta2 is used to update $W^{(1)}$. For the update terms, DeltaW and Deltab, all training examples of the data set need to be added together. For the weight matrices, matrix multiplication can once again help simplify the process. In this calculation, the share each node had in the error of the next layer's node is added to the computation as well, by multiplying the weights with the output values z of the same layer. Because these values equal the input

values of the nodes in the next layer and more divergent values will result in a higher values, the weights will be updated to different lengths accordingly. Since the bias nodes are defined only as weights and always ensue part of the error of the next layer, they are updated with the full delta value. Again a sum of all training examples is calculated. These values are then multiplied element wise with α (alpha) and $\frac{1}{m}$, to lower the update terms to increase accuracy. Lastly, the weights and bias weights are updated. The term including the weight decay parameter λ (lambda) is omitted (only present as comment), since, as has been mentioned before, it won't improve a small network like the one from the example.

```
%Forward propagation

% layer 1 (input)
a1 = [exx1, exx2];
```

As a final step, a for loop is added to complete the algorithm. Additionally, the update term is included directly in the update function.

5 Evolving ANNs and self-learning AI

5.1 TWEANNs and the NEAT Model

5.1.1 Introduction and overview

Neural networks of a fixed topology, as described in the previous chapter, have some limitations. They require a human supervisor to carefully choose the most suitable topology, which is often a difficult or impossible choice. For very complex problems, reasoning about the right topology (one which can find complex relations while being as small and thus as optimized as possible) is practically impossible.

In such a case, the subdomain of neuro-evolution may be of use. In neuro-evolution, the concept of neural networks is combined with the knowledge of biological evolution to produce self-improving neural networks, that learn through a computational version of natural selection. Neuro-evolutionary algorithms use a population of networks and mutate them according to certain rules. Afterwards, they run the networks on the problem and see which network has the highest *fitness*, defined by a *fitness function*, on the basis of which networks get selected to cross over with other networks or mutate to go on to the next generation.

A common distinction between different forms of neuroevolution is whether they merely modify the weights of a neural network (conventional neuro-evolution) or whether they modify the topology of the network along with evolving the weights (TWEANNs). These *Topology and Weight Evolving Artificial Neural Networks* learn in a completely different manner from typical neural networks described in chapter four. Instead of tweaking the weights using a process such as backpropagation, TWEANNs generate a population of networks and mutate the topology and weights randomly. After mutating this population, a fitness value is computed for each network as normal. This cycle repeats until a solution is found.

Research shows, however, that TWEANNs are less efficient than typical artificial neural networks in most scenarios, and often fail to find the necessary structure to solve the problem. An algorithm called NEAT, or *NeuroEvolution of Augmenting Topologies*, has been shown to be able to solve these issues, building upon the concept of TWEANNs and improving its efficacy. NEAT simulates nature to an even higher degree, and has close conceptual ties with actual biological evolution. By encoding networks in genomes

and making use of concepts such as speciation, historical markings and crossover, the NEAT algorithm can arrive much faster at effective networks on simple control tasks than other contemporary neuroevolutionary techniques and reinforcement learning methods[14]. Furthermore, these techniques are essential to evolving an effective algorithm for playing a video games.

5.1.2 Model

The model of neuro-evolution used by NEAT is based on and inspired by the many systems conceived over the last two decades that have implemented both weight and topology evolution. The NEAT model can be separated into a number of different features, outlined below.

5.1.2.1 Genetic Encoding

TWEANNs have to encode the genetic information that can be used to construct a neural network in some way, and can be divided into two groups: TWEANNs that use a direct encoding scheme and TWEANNs that use an indirect encoding scheme.

Direct encoding schemes specify the connections and nodes that will appear in the phenotype directly, whereas indirect encoding schemes merely specify rules for constructing a phenotype without directly specifying the connections and nodes - an example of such a rule could be rules for growing genomes through an equivalent of cell division. This can be more compact because the connections and nodes do not all have to be specified. However, they also require "more detailed knowledge of genetic and neural mechanisms."[15], and when improperly used can lead to a biased search which finds a suboptimal set of topologies. Therefore, NEAT uses a direct encoding scheme.

Direct encoding schemes can also be differentiated into two sets: schemes based on the traditional binary encoding of genetic algorithms (GAs), such as the scheme used in *Structured Genetic Algorithm* (sGA)[16], where a bit string represents the genome of a network, and graph-based schemes, which use encodings that represent the graph structure of a neural network more explicitly, such as the scheme used in the *Parallel Distributed Genetic Programming* system[17]. NEAT uses a version of the traditional binary encoding where the genomes are defined as a linear list of nodes and a linear list of connections between them, as is displayed in figure FIGURE_GENOME. These lists are not of a fixed size, and allow for a technically limitless number of permutations.

5.1.2.2 Mutations

As discussed in the preceding sections, NEAT has the ability both to mutate weights and topology. Connection weights mutate similarly to most other NE systems - connection weights are either perturbed or reassigned from a normal distribution. NEAT has two types of topological mutations: the *add node* mutation and the *add connection* mutation.

The *add node* mutation splits an existing connection in two, and creates a new node. The old connection is disabled, and two connections are added - one from the origin of the new connection (henceforth *source*) to the new node, and one from the new node to the destination of the old connection (henceforth *sink*). The connection between the old source and the new node is given a connection weight of one, and the connection between the new node and the old sink is given the weight of the old connection. This minimizes

[14]Stanley and Miikkulainen (2002).
[15]Braun and Weisbrod (1993).
[16]Dasgupta and McGregor (1992).
[17]Pujol and Poli (1998).

the disturbance of the network due to the mutation, while still giving the network the ability to evolve new behaviors using the new node.

Over multiple generations, these mutations amount to a gradual increase in genome size, and because the mutations are based on chance, genomes of varying sizes will result. Crossover must be able to recombine these different networks, and the next section will explain how NEAT addresses this problem.

5.1.2.3 Historical Markings

One of the largest problems in neuro-evolution is the *Competing Conventions Problem* (CC). The essence of this problem is the fact that there are multiple ways of expressing the same solution to a problem with a neural network. When these ways do not have the same genetic encoding, crossover is likely to produce damaged offspring. (figure FIGURE_COMPETINGCONVENTIONS). This is a fundamental problem with representing different structures and trying to apply crossover - their representations may not match up.

This problem is not new, however, and in this case the NEAT authors decided to look inspect how Mother Nature solved this problem. In nature, genomes also don't have a fixed length, but are still able to cross over successfully, crossing the right genes with each other. Nature solves this using a process called synapsis, which matches up homologous genes between two genomes before crossover. In neuro-evolution, ascertaining the homology of genes using structural analysis proves not to be easy - hence the competing conventions problem - so NEAT tries to solve CC by using historical markings. Genes are marked with an innovation number (see figure FIGURE_GENOME), which indicates its historical origin. When crossing over, genes with the same innovation number are lined up, and these are called *matching* genes. Genes that do not match can be *disjoint* or *excess*. Genes are defined as *disjoint* if they occur within the other parent's range of innovation numbers, *excess* when they do not (figure FIGURE_CROSSOVER). Matching genes are inherited randomly from either parent, while disjoint and excess genes are inherited from the parent genome with the highest fitness.

Historical markings give NEAT the capability to perform crossover while avoiding the competing conventions problem. Genomes differing in size and topology stay compatible throughout evolution, and this methodology allows NEAT to complexify structure while maintaining compatibility. Smaller species, however, optimize more quickly than larger species, and mutating a network usually initially decreases the fitness of a network. To keep these newly augmented networks from disappearing from the population, innovation can be protected by using speciation, as explained in the next section.

5.1.2.4 Speciation

NEAT subdivides the population of genomes into species to protect their topological innovations using their topological similarity. This topological similarity can be computed by using the historical markings described in the section above. The distance δ between two networks can be computed using the following function, where E denotes the number of excess genes, D the number of disjoint genes, and $\overline{W}$ the average weight difference of matching genes:

$$\delta = \frac{c_1 \cdot D}{N} + \frac{c_2 \cdot E}{N} + c_3 \cdot \overline{W}$$

The coefficients c_1, c_2 and c_3 adjust the importance of the three factors, and the factor N, the number of genes in the larger genome, normalizes for genome size.

Genomes are put into species one at a time by checking whether its distance to a randomly chosen member of the species is less than the compatibility threshold δ_t. If no species exists that satisfies the above condition, the genome is placed into a new species.

To determine the amount of offspring for a given species, NEAT uses *explicit fitness sharing*, where organisms in the same species share the fitness of their niche. This means a species cannot afford to become too big, even if many of its organisms perform well, thereby promoting topological diversity. The adjusted fitness f'_i for an organism i is computed according to the distance from every organism j in the population:

$$f'_i = \frac{f_i}{\sum_{i=j}^{n} sh(\delta(i,j))}$$

In the above equation, sh is the sharing function, which is set to 0 if $\delta(i,j) > \delta_t$ and 1 otherwise, reducing $\sum_{i=j}^{n} sh(\delta(i,j))$ to the number of organisms in the same species as i. The offspring for a given species is assigned proportionally to the sum of its members' adjusted fitnesses. This offspring may be produced either through mutation, crossover, or interspecies crossover, the rates of which are supplied in a configuration file.

The final goal is to perform the search for a solution as efficiently as possible, which is achieved through gradual complexification, described in the next section.

5.1.2.5 Initial Population Choice

TWEANNs usually start with an initial random population, in order to immediately introduce diversity. NEAT biases the search towards minimally dimensional spaces by starting with a population without any hidden nodes and introducing structure incrementally. Minimizing dimensionality in this way makes NEAT more performant.

5.2 The application of ANN-based AI to video games

NEAT has been shown to be a capable learning method in many different problems NEAT, and seems to be excellent for solving our research problem. But before NEAT can be applied and the experiment be initiated, some considerations are necessary, concerning a more accurate definition and description of the learning process as applied to video games, as well as a brief commentation on the selected game, Super Mario Bros. 3.

5.2.1 Games as mathematical problems

5.2.1.1

For NEAT, video games present a huge challenge for numerous reasons. Because of the nature of video games, the algorithm, instead of solving only one problem at the time, often has to solve multiple in a row or even at once, while using a single topology. These problems rarely have a similar solution, and scenarios which may be similar with regards to inputs can require entirely different outputs. In addition, a tremendous amount of inputs nodes (the data from the game to the NEAT algorithm) is required in order to accurately represent the screen. Often, a topology will have to decide its outputs basis on multiple inputs, in order to solve a problem. In short, video games are the ultimate test for the NEAT algorithm.

Video games often present a challenge to the (human) player, and force them to improve in some manner, be it motoric proficiency, memory, critical thinking or reflexes. Playing a game requires logic from the player. Certain actions will lead to certain effects. If, for example, a player chooses to press the A button, a character might jump. Successive presses of the A button will always lead to the character jumping. This cause and effect system is a critical aspect of video games and to be able to make any algorithm .

Essentially, playing a game is nothing but problem solving. When the player is a human brain, the problem, especially a simple introductory level, can often be solved quickly. The data from the display of the game can be easily scanned for useful information with use of sensory neurons in the eyes - represented in NEAT as the input nodes - and thereafter processed in the brain - represented as the hidden nodes. These signals continue to motor neurons - the output nodes - in accordance with the topology of the brain. Within the complex human brain however, many complex systems have evolved. When the player sees an obstacle in the way, for example, they, by using logical thinking and memory, will quickly understand to try and jump over it. An artificial neural network, especially one with a relatively small topology, does not have this ability. All outputs are derived directly from the inputs and the structure of the network. [example simplicity of networks] Therefore, NEAT does not learn in a typical sense, but in a manner more resembling how life on earth, through the process of evolution, has 'learned' to become incredibly complex as it is now.

5.2.2 The way of learning and possible limitations

All changes are entirely random, caused by mutations to existing genomes.

Due to the random nature of the learning process, forming a detailed and accurate hypothesis is difficult. If active for a long enough period of time, a correctly implemented NEAT algorithm should always be able to find a solution for most tasks.

In theory, all changes made to the genome need to be justified, as a disadvantageous mutation would lower the fitness score NEAT. In reality, it is unlikely for this to happen, at least at first.

An important attribute is that no individual genomes or species actively tries to improve, the best just continue. There is no will like with animals now

The critical ingenuity NEAT offers over many other learning methods, is the ability to effectively escape local optima, and over time, arrive at the global optimum. A typical level of any game will consist of many local optima. [explain local optima of mario 3 and other games]

5.2.3 What videogames are applicable

-Little inputs -Little outputs -Definable fitness function -Difficulty

5.2.4 NEAT as a model for evolution

The NEAT algorithm illustrates the development of early brains, as they emerged in the ancestral life forms of animals over 500 million years ago een of andere bron. And although current computation speeds are a long way from achieving this, the algorithm could in theory simulate a legitimate brain. Mario 3 can be seen as an extremely simplified version of earth all those years ago, when organisms, or rather their genes, possessing optimal network topology would have a higher fitness and subsequently gain an advantage for reproduction and survival. Each instance of Mario represents a single organism,

In the real world however, there the level is unending, and genomes can be improved infinitely. Even with the extreme low mutation rates, life on earth was able to evolve exceptionally complex brains, with totals of billions of neurons.

By defining a fitness value in the NEAT algorithm, this exact procedure can be replicated. The algorithm can therefore be seen as evidence

5.3 Implementation in the programming language Python

PyNEAT, our Python implementation of the NEAT algorithm, is subdivided into the ten files shown in the figure below. These files, and the code inside them, shall be described in the following few sections.

```
PyNEAT
├─ neat
│  ├─ genome.py - Contains genotypic classes
│  ├─ network.py - Contains phenotypic classes
│  ├─ species.py - Contains the species specification
│  ├─ pool.py - Contains the network pool
│  ├─ loader.py - Contains a loader for saved data
│  ├─ configuration.py - Contains a configuration loader
│  └─ nodetype.py - Contains an enumeration of possible node types
├─ mario.py - Contains Lua ⇔ Python code & model data
├─ Mario.toml - Contains the NEAT configuration
└─ requirements.txt - Contains the dependencies (the TOML module)
```

5.3.1 The genotype implementation, `genome.py`

This file contains the classes that define the genotype of a neural network: `NodeGene`, `ConnectionGene` and `Genome`, but it starts off with a prelude full of imports. The definitions on lines 11, 12 and 14 define global initial values for the connection ID, node ID and genome ID. `GLOBAL_NODES` is initialised to 248 because this happens to be the first non-preinitialised node ID for our experiment.

```
1  import random
2  import math
3  import copy
4  from statistics import mean
5  from . import configuration
6  from collections import defaultdict
7  from .nodetype import NodeType
8  import itertools
9  from pprint import pprint
10
11 GLOBAL_INNOVATION = 1
12 GLOBAL_NODES = 248
13
14 GENOME_ID = 1
```

Subsequently, the activation function used in our experiment is defined.

```
1  def modSigmoid(x):
2      return (2 / (1 + math.exp(-4.9*x)))-1
```

Then, the first proper part of the genotype, the `NodeGene` class, is defined. Nodes have to have a `nodeId`, `nodeType` (either an input, bias, hidden or output node) and an `activationFunction` attached to them. These are set in the initialisation function. Additionally, Python *magic methods* are defined which make sure that nodes with the

same node ID are hashed and compared as equal, and define a textual representation for nodes.

```
class NodeGene():
    def __init__(self, nodeType, nodeId=None, activationFunction = modSigmoid):
        global GLOBAL_NODES
        global GLOBAL_INNOVATION
        self.nodeId = nodeId or GLOBAL_NODES
        if not nodeId:
            GLOBAL_NODES += 1
        self.nodeType = nodeType
        self.activationFunction = activationFunction

    def __eq__(self, other):
        try:
            return self.nodeId == other.nodeId
        except:
            return False

    def __ne__(self, other):
        return not self.__eq__(other)

    def __hash__(self):
        return hash(self.nodeId)

    def __repr__(self):
        if self.nodeType in (NodeType.SENSOR, NodeType.BIAS):
            return "Node(#%r, %r)" % (self.nodeId, self.nodeType)
        return "Node(#%r, %r, %s)" % (self.nodeId, self.nodeType,
            self.activationFunction.__name__)
```

Next, the `ConnectionGene` class is defined. Connections have a `source`, `sink`, `weight` and `connectionId`, and an `enabled` flag, which are defined in its respective initialisation function. The subsequent lines define magic methods akin to those mentioned for `NodeGene`.

```
class ConnectionGene():
    def __init__(self, source, sink, weight = None, connectionId = None, enabled
        = None):
        global GLOBAL_INNOVATION
        self.source = source
        self.sink = sink
        self.weight = weight or random.gauss(0.0, 1.0)
        self.connectionId = connectionId or GLOBAL_INNOVATION
        if not connectionId:
            GLOBAL_INNOVATION += 1
        self.enabled = enabled or True

    def __repr__(self):
        return "Connection(#%d, Node %r => Node %r, Weight %f, %s)" \
            % (self.connectionId, self.source.nodeId, self.sink.nodeId,
                self.weight, "Enabled" if self.enabled else "Disabled")

    def __eq__(self, other):
        return self.connectionId == other.connectionId

```

```
    def __ne__(self, other):
        return not self.__eq__(other)

    def __hash__(self):
        return hash(self.connectionId)
```

Now, we've gotten to the most important class in this file, the `Genome` class. This class defines the way the lists of nodes and connections are stored, as well as the way they are mutated, the way the species difference is computed and the way genomes are crossed over. First, let's look at the data definitions.

The configuration is fetched using the `configuration.getGlobalConfig()` method described further on in this section, and the node and connection lists are represented using Python's hashmaps (also called key-value maps or dictionaries), mapping nodeId and connectionId to node and connection, respectively. The fitness and global rank are initialised to 0, and will be updated by other methods and classes.

```
class Genome():
    def __init__(self, nodes=None, connections=None):
        global GENOME_ID
        self.config = configuration.getGlobalConfig()
        self.nodes = {node.nodeId:node for node in (nodes or [])}
        self.connections = {connection.connectionId:connection for connection in
            (connections or [])}
        self.fitness = 0
        self.id = GENOME_ID
        GENOME_ID += 1

        self.globalRank = 0
```

A few convenience methods are defined for easily adding nodes and connections.

```
    def addNode(self, nodeId, nodeType):
        node = NodeGene(NodeType(nodeType), nodeId)
        self.nodes[node.nodeId] = node

    def addConnection(self, source, sink, weight=None, connectionId=None,
        enabled=None):
        connection = ConnectionGene(source, sink, weight, connectionId, enabled)
        self.connections[connection.connectionId] = connection
```

We now get to the first of the mutation functions, `mutateNode`. This function performs the add node mutation, adding a new node between an existing connection. It chooses a random connection from the list, disables it, constructs a new hidden node and adds the appropriate connections.

```
    def mutateNode(self):
        if (not self.connections):
            return False

        node = NodeGene(NodeType.HIDDEN)
        # Add a node between an existing connection
        conn = random.choice(list(self.connections.values()))
        conn.enabled = False

        new_connections = (ConnectionGene(conn.source, node, weight = 1),
```

```
            ConnectionGene(node, conn.sink, weight=conn.weight))

        for connection in new_connections:
            self.connections[connection.connectionId] = connection

        self.nodes[node.nodeId] = node
```

The second mutation function, `mutateConnection`, adds a connection between two random nodes. It defines a list of nodes that are eligible to be sources and a list of nodes that are eligible to be sinks (input nodes and bias nodes are not eligible to be sinks, and if the `bias` argument is passed, only bias nodes can be sources), whereafter it creates the Cartesian product of these two lists using the built-in `itertools` module. (The Cartesian product $A \times B$ is the set of all ordered pairs (a, b) where $a \in A$ and $b \in B$). It chooses a random combination from this product where $a \neq b$ and where the connection does not already exist, and adds this connection to the list of connection genes.

```
    def mutateConnection(self, bias=False):
        if not bias:
            source_eligible = [node for node in self.nodes.values() if
                node.nodeType in (NodeType.SENSOR, NodeType.BIAS,
                NodeType.HIDDEN, NodeType.OUTPUT)]
        else:
            source_eligible = [node for node in self.nodes.values() if
                node.nodeType == NodeType.BIAS]
        sink_eligible = [node for node in self.nodes.values() if node.nodeType in
            (NodeType.HIDDEN, NodeType.OUTPUT)]

        existing_connections = {(conn.source, conn.sink):conn for conn in
            self.connections.values()}

        combinations = [combination for combination in
            itertools.product(source_eligible, sink_eligible) if combination[0]
            != combination[1] and combination not in existing_connections]

        if (not combinations):
            return False
        chosen = random.choice(combinations)

        self.addConnection(*chosen)
```

Some more convenience functions for copying the structure and fetching a specific node or connection are defined.

```
    def node(self, nodeId):
        return self.nodes.get(nodeId, False)

    def connection(self, connectionId):
        return self.connections.get(connectionId, False)

    def copy(self):
        return copy.deepcopy(self)
```

The `mutateWeights` function is defined, which either perturbs or resets connection weights.

```
    def mutateWeights(self):
        for connection in self.connections.values():
            if (random.random() < self.config["rates"]["perturbation"]):
                connection.weight += (random.gauss(0.0, 0.5))
            else:
                connection.weight = random.gauss(0.0, 1.0)
```

The `mutate` function is defined, which uses the $[0.0, 1.0)$ output from `random.random()` as a chance comparison to choose whether to perform the mutations provided by the functions above.

```
    def mutate(self):
        if (random.random() < self.config["rates"]["mutation"]):
            self.mutateWeights()

        n = self.config["rates"]["newnode"]
        while (random.random() < n):
            self.mutateNode()
            n -= 1

        n = self.config["rates"]["newlink"]
        while (random.random() < n):
            self.mutateConnection()
            n -= 1

        if (random.random() < self.config["rates"]["biasmut"]):
            self.mutateConnection(True)
```

The function used to determine whether two genomes belong to the same species, `sameSpecies`, is defined. Firstly, it fetches the constants c_1, c_2 and c_3 from the configuration. Then, it computes various values used in the equation $\delta = \frac{c_1 \cdot D}{N} + \frac{c_2 \cdot E}{N} + c_3 \cdot \overline{W}$. The excess threshold is determined by taking the minimum largest connection ID from the species, and is used to determine whether genes are disjoint or excess. The matching genes are determined using a list comprehension that checks whether a connection with the same ID exists in the other genome's connection list, in which case it adds both to the matching gene set. The computation of the other values is fairly self-explanatory. At the end of the function, a boolean value representing its membership in the species is returned.

```
    def sameSpecies(self, other):
        c_1 = self.config["compatibility"]["excess"]
        c_2 = self.config["compatibility"]["disjoint"]
        c_3 = self.config["compatibility"]["weights"]

        # d = c_1*E/N + c_2*D/N + c_3 * W
        nGenes = (len(self.connections), len(other.connections))

        N = max(len(self.nodes), len(other.nodes)) + 1

        # Gene connectionIds below this threshold are disjoint. Uniques higher
            than this threshold are excess.
        if (len(self.connections) == 0) or (len(other.connections) == 0):
            excessThresh = 0
        else:
            excessThresh = min(max(cId for cId in self.connections.keys()),
                max(cId for cId in other.connections.keys()))
```

```
16
17          matchingGenes = {gene: other.connection(gene.connectionId) for gene in
                self.connections.values() if other.connection(gene.connectionId)}
18
19          weightDiff = [abs(a.weight - b.weight) for a,b in matchingGenes.items()]
20          if (weightDiff):
21              avgweightDiff = mean(weightDiff)
22          else:
23              avgweightDiff = 0
24
25          otherGenes   = set(self.connections.values()) ^
                set(other.connections.values())
26
27          disjoints = {gene for gene in otherGenes if gene.connectionId >
                excessThresh}
28          excesses = otherGenes - disjoints
29
30          return ((c_1 * len(excesses) + c_2 * len(disjoints)) / N + c_3 *
                avgweightDiff) < self.config["speciation"]["species_difference"]
```

The `crossover` function, the final piece of the genotype puzzle, is defined last. It computes variables also used in the `sameSpecies` function, and so requires little explanation. The matching and other genes are selected, and are chosen based on the rules described in section 5.1.2.3. At the end, the resulting genome is returned.

```
1       def crossover(self, other):
2           global GENOME_ID
3           offspring = Genome()
4
5           if (len(self.connections) == 0) or (len(other.connections) == 0):
6               excessThresh = 0
7           else:
8               excessThresh = min(max(cId for cId in self.connections.keys()),
                    max(cId for cId in other.connections.keys()))
9
10          matchingGenes = [(gene, other.connection(gene.connectionId)) for gene in
                self.connections.values() if other.connection(gene.connectionId)]
11
12          otherGenes = set(self.connections.values()) ^
                set(other.connections.values())
13
14          matchingChoices = [random.choice(x) for x in matchingGenes]
15
16          if (self.fitness > other.fitness):
17              otherChoices = [choice for choice in otherGenes if choice in
                    self.connections.values()]
18          elif (other.fitness > self.fitness):
19              otherChoices = [choice for choice in otherGenes if choice in
                    other.connections.values()]
20          else:
21              otherChoices = list(otherGenes)
22
23          offspring.connections = {i.connectionId:i for i in (matchingChoices +
                otherChoices)}
24
```

```
        for connection in offspring.connections.values():
            if connection.enabled == False:
                connection.enabled == False if random.random() <
                    self.config["rates"]["disabled_inherit"] else True

        offspring.nodes = {i.nodeId:i for i in (set(self.nodes.values()) |
            set(other.nodes.values()))}

        GENOME_ID += 1
        offspring.id = GENOME_ID

        return offspring
```

5.3.2 The phenotype implementation, `network.py`

This file contains the classes that define the phenotype of a neural network: `Node` and `Network`. We can once again start with the imports:

```
from collections import defaultdict, namedtuple, OrderedDict
from .nodetype import NodeType
from pprint import pprint
import random
import sys
```

No definitions here, so we will continue to describe the `Node` class. In the initialisation function, the node type, ID and activation function are fetched from the passed node gene. The weights leading into this node are fetched from the passed connections, as are the node's dependencies.

```
class Node():
    def __init__(self, nodeGene, connections):
        self.nodeType = nodeGene.nodeType
        self.nodeId = nodeGene.nodeId
        self.weights = {conn.source.nodeId:conn.weight for conn in connections
                        if conn.enabled and conn.sink == self}
        self.activationFunction = nodeGene.activationFunction
        self.connections = connections
        self.dependencies = {conn.source.nodeId for conn in connections
                             if conn.sink == self and conn.enabled}
```

More magic methods describing equality are defined below, just like in the `ConnectionGene` and `NodeGene` classes.

```
    def __eq__(self, other):
        if (self.nodeId == other.nodeId) and (self.nodeType == other.nodeType):
            return True
        return False

    def __ne__(self, other):
        return not self.__eq__(other)

    def __hash__(self):
        return hash(self.nodeId)

    def __repr__(self):
```

```
        if self.nodeType in (NodeType.SENSOR, NodeType.BIAS):
            return "Node(#%r, %r, %r)" % (self.nodeId, self.nodeType,
                    self.weights)
        return "Node(#%r, %r, %s, %r)" % (self.nodeId, self.nodeType,
                self.activationFunction.__name__, self.weights)
```

Finally, the most important function, `__call__`, is defined. This function computes the output of the node based on the passed inputs. First, all of the inputs that the node depends on (from `self.dependencies`) are summed and multiplied by their weights. If the node is a bias node, the input is set to 1. If the node is an input node, the input is fetched directly, because input nodes have no dependencies or weights. If the node is a hidden or output node, the activation function is applied to the input. Finally, the output is added to the necessary lists and returned.

```
    def __call__(self, output, inputs=None, final_out=None):
        if (self.nodeType == NodeType.SENSOR):
            input = inputs.get(self.nodeId)
        else:
            input = 0
            for dependency in self.dependencies:
                val = inputs.get(dependency, 0.0)
                cW = self.weights.get(dependency, 0.0)
                if (val == None):
                    inputs[dependency] = 0.0
                    val = 0.0
                input += val * cW

        if (self.nodeType == NodeType.BIAS):
            input = 1.0

        if (self.nodeType in (NodeType.HIDDEN, NodeType.OUTPUT)):
            input = self.activationFunction(input)

        output[self.nodeId] = input

        if self.nodeType == NodeType.OUTPUT:
            final_out[self.nodeId] = input

        return output
```

The `Network` class is defined. This is the phenotype version of the `Genome` class defined in `genome.py`. In the initialisation function, the nodes are created from the passed genome, and an empty values hashmap is created which stores the output of the network for use with recurrent connections. Additionally, a convenience function is defined to select a node.

```
class Network():
    def __init__(self, genome):
        self.nodes = OrderedDict(sorted(self.createNodes(genome), key=lambda
            x:x[0]))
        self.values = defaultdict(float)

    def node(self, nodeId):
        return self.nodes[nodeId]
```

The `createNodes` function is a generator that yields a list of nodes from a given genome. For every node gene in a genome, it selects its corresponding connections, constructs a `Node` instance and yields a pair of `(nodeId, node)`.

```
    def createNodes(self, genome):
        for nGene in genome.nodes.values():
            connections = [c for c in genome.connections.values()
                   if c.sink == nGene or c.source == nGene]
            node = Node(nGene, list(connections))
            yield (node.nodeId, node)
```

Next, the function to run the network is defined. First, the input and bias nodes are selected and run. Then, the rest of the functions are run. As you may have spotted, the node hashmap has been defined as an `OrderedDict` in the initialisation function, and the nodes already have an ordering. This is used to our advantage when running the pool, because we can run the pool without caring about dependencies for the first frame (making recurrent connections possible), then save the values in `self.values`. These values are used in the computation of the outputs for the other frames, and in spite of the incorrect output for the first frame, still accurately runs the neural network. This is similar to code used in other implementations.[18] The final outputs are collected in `output_data`, which is returned, sorted on nodeId, as the output of the neural network.

```
    def runWith(self, inputdata=None):
        data_pool = defaultdict(float)
        output_data = defaultdict(float)

        # First, run the inputs and bias nodes
        inputs = [node for node in self.nodes.values() if node.nodeType ==
            NodeType.SENSOR or node.nodeType == NodeType.BIAS]
        inputs.sort(key=lambda node:node.nodeId)

        for ip in inputs:
            ip(self.values, dict(zip([node.nodeId for node in inputs],
                inputdata)), output_data)


        # Then the other nodes
        other_nodes = [node for node in self.nodes.values() if node.nodeType in
            (NodeType.OUTPUT, NodeType.HIDDEN)]

        for node in other_nodes:
            node(self.values, self.values, output_data)

        self.values.update(output_data)
        output_data = list(output_data.items())
        output_data.sort(key=lambda node: node[0])

        return [x[1] for x in output_data]
```

5.3.3 The Species class, `species.py`

This file contains a `Species` class, which contains a list of genomes, a species ID, and some fitness measurements (`topFitness`, `averageFitness`, `staleness`), and functions to

[18] CodeReclaimers (2008-2017).

compute average fitness and sort the genomes. The reason the genomes are sorted on fitness reverse is to make sure `genomes[0]` is the species with highest fitness, whereas a normal sort would sort the genomes lowest fitness to highest.

```
import random
from . import configuration

SPECIES_ID = 1

class Species():
    def __init__(self):
        global SPECIES_ID
        self.config = configuration.getGlobalConfig()
        self.id = SPECIES_ID
        self.genomes = []
        self.topFitness = 0.0
        self.averageFitness = 0.0
        self.staleness = 0
        SPECIES_ID += 1

    def calculateAverageFitness(self):
        total = 0

        for genome in self.genomes:
            total = total + genome.globalRank

        self.averageFitness = total / len(self.genomes)

    def sortGenomes(self):
        self.genomes.sort(key=lambda genome: genome.fitness, reverse=True)
```

5.3.4 The network pool, `pool.py`

The network pool, combined with the genotypic and phenotypic classes, forms the meat of the NEAT algorithm. A population of networks described by genomes is divided into multiple species, run using the `Network` class, sorted, and using the algorithms described below, turned into a new generation, and run again, until a genome is generated that is optimized for the problem that is being solved.

The initialisation function starts by initialisating data that applies to the pool, such as the `fitnessFunction`, `maxFitness`, et cetera. If an initial genome is passed, it is used to create an initial generation. If an initial genome is not passed, such as during loading of a previously saved generation as discussed below, the generation has to be created separately. Additionally, a runtime directory is created wherein the genomes are saved.

```
import pprint
import random
import sys
import os
import pdb
import datetime
import json
import traceback
from .species import Species
from .network import Network
from . import configuration
```

```
12
13 class NetworkPool():
14     def __init__(self, initialGenome=None, fitnessFunction=None):
15         print("Constructing pool.")
16         self.fitnessFn = fitnessFunction
17         self.config = configuration.getGlobalConfig()
18         self.species = []
19         if initialGenome:
20             for i in range(self.config["pool"]["population"]):
21                 print("Constructing genome %d" % i)
22                 copy = initialGenome.copy()
23                 copy.mutate()
24                 self.addToSpecies(copy)
25
26         self.maxFitness = 0.0
27         self.maxPrevFitness = 0.0
28         self.maxGenome = None
29         self.evaluatedGenomes = 0
30         self.generation = 1
31
32         self.rtdir = "run-" + datetime.datetime.utcnow().strftime("%Y%m%d-%H%M%S")
33         os.mkdir(self.rtdir)
```

The `addToSpecies` function provides the functionality of adding a genome to a species, which can be either existing or newly created, based on the algorithm described in 5.1.2.4.

```
1     def addToSpecies(self, genome, speciesId=None, staleness=None):
2         for species in self.species:
3             if species.genomes[0].sameSpecies(genome):
4                 species.genomes.append(genome)
5                 return
6
7         newSpecies = Species()
8         newSpecies.genomes.append(genome)
9         newSpecies.staleness = staleness or 0
10        self.species.append(newSpecies)
```

The `rankGlobally` and `totalAverageFitness` functions concern the ranking of genomes and the species they are a member of, which is used to proportionally assign the number of offspring created by species.

```
1     def rankGlobally(self):
2         globalList = [genome for species in self.species for genome in
              species.genomes]
3
4         globalList.sort(key=lambda x: x.fitness)
5
6         for n, genome in enumerate(globalList):
7             genome.globalRank = n
8
9     def totalAverageFitness(self):
10        total = 0
11
12        for species in self.species:
13            total = total + species.averageFitness
14
```

```
15        return total
```

Constructing a new generation is handled by the `nextGeneration` function. First, the species are culled, removing the least fit half of their genomes. Then, the stale species (species that have stagnated for more than `staleness` generations) are removed, whereafter the species are ranked globally. The average fitness is calculated, and with that, the proportional offspring calculated. If the offspring is less than one genome, the species is deleted by the function `removeWeakSpecies`. The species generate their offspring, whereafter they are culled to consist of their single most fit organism, which is then copied verbatim into the next generation. If the number of genomes in the total population is less than the population size, the gap is filled with extra offspring through mutating the best genomes. Subsequently, the generation counter is updated.

```
1     def nextGeneration(self):
2         self.cullSpecies(cutToOne=False)
3         self.removeStaleSpecies()
4         self.rankGlobally()
5         for species in self.species: species.calculateAverageFitness()
6         self.removeWeakSpecies()
7
8         self.totalFitness = self.totalAverageFitness()
9
10        children = []
11
12        for species in self.species:
13            toBreed = (self.config["pool"]["population"] *
                  species.averageFitness) // self.totalFitness
14            toBreed -= 1
15
16            children.append(self.generateOffspring(species))
17
18        self.cullSpecies(cutToOne=True)
19
20        while (len(children) + len(self.species) <
              self.config["pool"]["population"]):
21            species = random.choice(self.species)
22            children.append(self.generateOffspring(species))
23
24        for child in children: self.addToSpecies(child)
25
26        self.generation += 1
```

The `generateOffspring` function constructs a new child from a species based on the crossover and interspecies mating rate described in the configuration file.

```
1     def generateOffspring(self, species):
2         if random.random() < self.config["rates"]["crossover"]:
3             if (random.random() < self.config["rates"]["interspecies"]):
4                 species2 = random.choice(self.species)
5                 genome = random.choice(species2.genomes)
6                 child = genome.crossover(random.choice(species.genomes))
7                 child.mutate()
8                 return child
9             elif len(species.genomes) >= 2:
10                g1, g2 = random.sample(species.genomes, 2)
```

```
            child = g1.crossover(g2)
            child.mutate()
            return child

    child = random.choice(species.genomes).copy()
    child.mutate()
    return child
```

The functions `cullSpecies`, `removeWeakSpecies` and `removeStaleSpecies` fulfill the functions described above in `nextGeneration`.

```
def cullSpecies(self, cutToOne = False):
    for species in self.species:
        species.sortGenomes()

        remaining = (len(species.genomes) // 2) + 1

        if (cutToOne):
            remaining = 1

        species.genomes = species.genomes[:remaining]

def removeWeakSpecies(self):
    survived = []

    self.totalFitness = self.totalAverageFitness()

    for species in self.species:
        toBreed = (self.config["pool"]["population"] *
            species.averageFitness) // self.totalFitness
        if toBreed >= 1:
            survived.append(species)
        else:
            print("Removing species %d (tB: %d, avF: %f, tF: %f)" %
                (species.id, toBreed, species.averageFitness,
                self.totalFitness))

    self.species = survived

def removeStaleSpecies(self):
    survived = []
    for species in self.species:
        species.sortGenomes()

        if (species.genomes[0].fitness > species.topFitness):
            species.topFitness = species.genomes[0].fitness
            species.staleness = 0
        else:
            species.staleness += 1

        if (species.staleness <
            self.config["speciation"]["stagnation_threshold"]) or
            (species.topFitness >= self.maxFitness):
            survived.append(species)
        else:
            print("Removing stale species %d." % (species.id))
```

```
41
42          self.species = survived
```

The genomes are saved to disk in the runtime directory initialised in the initialisation function, and the `saveGenome` function fulfills this task. The data format used is JSON (*JavaScript Object Notation*), which is a broadly used exchange format both for Python and in the general programming community.

```
1       def saveGenome(self, species, n, genome):
2           dataFile = open(os.path.join(self.rtdir, "gen-%d" % self.generation,
                "spc-%d-gnm-%d" % (species.id, n)), "w")
3           data = {"connections": sorted([(conn.connectionId, conn.source.nodeId,
                conn.sink.nodeId, conn.weight) for conn in genome.connections.values()
4                                   if conn.enabled], key=lambda x: x[0]),
5           "nodes": sorted([(node.nodeId, node.nodeType.value) for node in
                genome.nodes.values()]),
6           "maxFitness": self.maxFitness,
7           "generation": self.generation,
8           "genomeId": n,
9           "staleness": species.staleness,
10          "speciesId": species.id}
11
12          dataFile.write(json.dumps(data))
13          dataFile.close()
```

5.3.5 The Loader class, `loader.py`

This file provides a loader for the files saved to disk by the NetworkPool described in the above section. It simply reconstructs the pool from the saved data.

```
1   # This file has proved instrumental a few times when we have had to reload
        generations from disk
2   # because of errors made both in the Python and Lua scripts, but was really
        fairly simple to write
3
4   # in fact, it was done during a particularly boring chemistry lesson.
5
6   from .genome import NodeGene, ConnectionGene, Genome
7   from .pool import NetworkPool
8   from .nodetype import NodeType
9
10  import json, os
11
12  class Loader():
13      def __init__(self, rundir, gen):
14          self.gendir = os.path.join(rundir, "gen-%s" % gen)
15
16      def getGenomes(self, fitnessFunction):
17          pool = NetworkPool()
18
19          for genome in os.listdir(self.gendir):
20              data = json.load(open(os.path.join(self.gendir, genome)))
21              g = Genome()
22
23              for node in data["nodes"]:
24                  g.addNode(node[0], node[1])
```

```
25
26              for connection in data["connections"]:
27                  g.addConnection(g.node(connection[1]), g.node(connection[2]),
                        connection[-1], connection[0])
```

6 Experiment: The application of ANN based AI to SMB3

6.1 Data allocation and RAM map

6.1.1 Introduction and overview

Before the NEAT algorithm can be applied to the learning problem, it needs to be given a usable set of inputs. For the learning process to be as fair as possible, the neural network needs to 'see' what a normal player would. This means everything displayed on screen must be to converted to a set of numerical data, which has been diminished in size and complexity. Conveniently, all the necessary data can be received directly from memory. For this, the freeware emulator BizHawk is used, as it has functionality to read RAM data, as well as support for lua scripting.

6.1.2 NES Memory Mapping

Super Mario Bros. 3 (SMB3) is a 1988 software title for the 8-bit console, the Nintendo Entertainment System (NES). Although this means the total amount of data is relatively small, the semi-arbitrary nature of the allocation of it still makes finding the right locations difficult and time consuming. For SMB3, however, there are some resources available online to simplify the process a bit [19], although no complete RAM map is currently available. This paper will present an incomplete RAM map as well, wherein all used data locations are given.

Data is stored within the memory in different memory locations, for specific use of a single variable, such as the location of an enemy, or the location of a tile sprite. The ROM (read-only memory) is fixed, and consists of all the game data. Because this does not (directly) correspond to what is displayed on screen, this won't be useful for the experiment. The RAM (random-access memory) contains the instructions for the display, and contain all the data necessary for defining the inputs. All locations have a size of a single byte and their location is defined in hexadecimal notation, for which the prefix $0x$ is used. For example, data location number 1234 will be notated as $0x04D2$.

For early NES games, the maximum amount of memory that could be addressed was 32KB of program ROM, 8KB of 8x8 character graphics tiles and 2 KB of RAM[20]. In order to be able to increase the complexity and size of the games such as SMB3, later NES software developers designed creative solutions to bypass these limitations. Within the cartridge, a chip called a *mapper* was added, which provided access to extended memory. For SMB3, the mapper is known as MMC3 and changed a couple aspects of the RAM and ROM. For now, the only relevant modification is the extension of 8KB additional RAM at the location $0x6000$ until $0x7FFF$. Because of this, SMB3 has access to a total of 10KB of RAM.

Similar to all NES games, level data in SMB3 is stored as an sequence of tiles, each 16x16 pixels in size. A single level is are often around 160 tiles wide and 27 tiles high. This means the tile data for a level consists of $160 \cdot 27 = 4320$ data locations. Because of the large amount of RAM, it was possible for the developers of SMB3 to load an entire level into memory. This was done in sections with a width of 16 horizontal tiles, where

[19] Crystal (n.d.).
[20] Epoch (n.d.).

the top left tile corresponds to the first location ($0x0001 = 1$) and the bottom right tile corresponds to the last location ($16 \cdot 27 = 0x01B0 = 432$). The byte directly after this accordingly corresponds to the top left tile of the next section. It turns out all the tile data is stored in sequential order in the additional RAM, starting from location $0x6000$. The value of each byte determines which tile will be present.

The remainder of the necessary data is located in the original RAM locations, $0x0000$ until $0x07FF$. The data is roughly classified in corresponding groups and assigned in one of eight 256 byte long sections. However, this only results in the data being only a little more organized. A lot of inconsistencies are present, to a point where their layout might seems entirely random. Fortunately, bytes with the same or closely related function are often positioned right next to each other.

Mario's location is stored in a similar manner as the tiles. Because a single byte can only amount to 256 (2^8) different integers, it is not possible to store Mario's x and y coordinates, which must be able to over $256 \cdot 10 = 2560$, in a single byte. This is why both these values have a so called high and low byte. Because 256 pixels is equal to the width of 16 tiles, one byte, the high byte, determines the section Mario is in, while the other byte, the low byte, determines the pixel in the section on which Mario is located. Mario's x coordinate high byte is located in $0x0075$, and the low byte in $0x0090$. Mario's y coordinate high byte is located in $0x0087$, and the low byte in $0x00A2$ [21].

Enemy locations are a bit more complex. For the horizontal position, instead of an absolute coordinate, their location relative to the screen position is defined instead. Unfortunately, we were unable to find a corresponding high byte for their location, resulting in an overflow problem we were unable to resolve. The workaround for this problem will be described in later in this section. The vertical position is defined using an absolute coordinate. SMB3 has support for the presence of up to 5 enemies at once, which are sequentially stored in descending order. Additionally, because the values only get reset when a new enemy has taken its place in the data, it is necessary to make use of an additional byte, in which the display status of the enemy is defined. The corresponding values for different enemy states is available in the RAM map. The horizontal positions are defined in the locations $0x00AB$-$0x00B0$, the vertical positions in the locations $0x00A2$-$0x00A7$, and the status in the locations $0x0660$-$0x0665$. In order to transfer this data to the input data, the horizontal position of the screen is required as well, which is located at $0x00FD$ and $0x0012$.

In the early levels, two types of projectiles are present, both of which two can be present on screen at any given time. The data follows the same rules as the enemies, where the horizontal byte is relative to the screen position, and the vertical is an absolute coordinate. Because the projectiles do not have an assigned status byte, the program computes its speed, by comparing previous frame data with the current frame data, in order to determine whether it should be considered an input. For the first projectile, a fireball, the horizontal position is located in $0x05CB$ and $0x05CC$, and the vertical position in $0x05C1$ and $0x05C2$. For the second projectile, a boomerang, the horizontal position is located in $0x05CD$ and $0x05CE$, and the vertical position in $0x05C3$ and $0x05C4$.

Lastly, we need to compute a fitness value. This will consist of Mario's x coordinate, located in $0x0075$ and $0x0090$, the amount of time left, located in $0x05EE$ to $0x05F0$ [22], and the achieved score, located in $0x0715$ to $0x0717$. The relative significance of these values will be discussed in the following section.

[21] Crystal (n.d.).
[22] Crystal (n.d.).

6.1.3 Converting the data to NN inputs

The retrieved data needs to be modified in order for the neural network to be able to successfully utilize it. The inputs need to be in accordance with the display and what a normal player would observe, as well as be limited in the amount of inputs. This is achieved by defining the inputs as an approximation of the space surrounding Mario, where each input represent a single 16 by 16 pixel tile. Each tile can represent one of three value: a hitbox is present, which is represented by a white square and will output a positive value; an enemy or projectile is present, which is represented by a black square and will output a negative value, or nothing is present, which is represented by the absence of a colour and an output of zero. In accordance with the display, the inputs are 16 tiles wide. The height is 15 tiles. This leads to a total input size of $16 \cdot 15 = 240$, defined as a single array. Each frame, this array is updated to reflect the current status of the game. Before the updated data for the next frame is added to the array, the input array is cleared. This is achieved by setting all values to zero, by means of a simple for loop.

```
1       -- Refresh inputs
2       for c = 1, 16*16, 1 do
3           tiles[c] = 0
4       end
```

Mario's location can be determined directly from memory using the appropriate byte locations. When Mario goes off-screen at the top of the level, the vertical high byte goes from zero to $0-1 = 255$, resulting in misleading y coordinates. Although it is very unlikely this will occur during the experiment, this is circumvented anyway.

```
1       -- Get Mario Coordinates
2       marioX = memory.readbyte(0x00090) + memory.readbyte(0x00075) * 256 + 8
3       if memory.readbyte(0x00087) ~= 255 then
4           marioY = memory.readbyte(0x000A2) + memory.readbyte(0x00087) * 256
5       else
6           -- (The vertical Low byte is equal to 255 on the topmost row of the
                map)
7           marioY = 0
8       end
```

Every frame, the program tests the data location of the tiles around Mario for their values, and determines if a hitbox is present. To achieve this, the x and y coordinates for all 240 tiles are determined, after which those are converted to a tile location. Using the previously described relations, this location is converted to the location within the RAM. By reading this byte and comparing the value to a list of tiles that contain hitboxes, the presence of a hitbox is determined. Because of the limitations of lua, this results in an excessively large if statement, which will be omitted in the following code. The full list of values can be examined in either the included full version of the program, or the RAM map. For each tile, the array is updated to a value of 1 if the presence of a hitbox is detected.

```
1       -- Check all tiles around Mario for hitboxes and update inputs (hitboxes)
2       for i = 1, 241, 1 do
3           tileX = marioX - 128 + (16*(i-1))%256
4           tileY = marioY - 128 + 16*math.floor((i-1)/16)
5
6           tileHorizontalLow = math.floor(tileX/256)
```

```
            tileHorizontalHigh = math.floor((tileX%256)/16)
            if tileY >= 0 then
                tileVertical = math.floor(tileY/16)
            else
                -- Dit is voor dezelfde redenen als bij marioY hierboven
                tileVertical = 0
            end
            tileData = memory.readbyte(0x6000 + tileHorizontalLow*27*16 +
                tileHorizontalHigh + tileVertical*16)
            if tileData == 44 or tileData == 83 or tileData == 85 or tileData ==
                87 or tileData == 95 or tileData == 97 or tileData == 99 or
                tileData == 103 or
```

```
            then
                tiles[i] = 1
            end
        end
```

After this, the array is updated for the locations of all enemies. Since the enemies are located relative to the screen position, their absolute x coordinates can be determined by adding the horizontal position of the screen to their location. Because the coordinates are calculated from the top left of the actual hitbox of the enemy, half the length of their sprite (8) is added as well. The y position can be determined simply by adding 256 to the byte. Next, these two values are converted to a tile position relative to Mario. Note the enemies are calculated in in reverse order. This was done to better reflect their positions in the RAM, but it is not required.

The solution to the overflow problem is also implemented here. The inputs are not updated for enemies positions at the 3 columns at both ends of the screen. The overflow would cause the coordinates to be displayed on the wrong side of the inputs array, but does not continue to within these border, as the enemy despawns before that point is reached. Lastly, if the enemy status is of a correct value as well, the inputs are updated with an value of -1. The horizontal and vertical tile locations are converted to the appropriate location in the array, by multiplying the vertical value by the length of one row (16) and adding the horizontal value.

```
        -- Update frame-dependent Variables
        screenHorizontalPosition = memory.readbyte(0x00FD) +
            memory.readbyte(0x0012)*256

        -- Get enemy data
        for i = 1, 5, 1 do
            enemyAlive[i] = memory.readbyte(0x665 - i + 1)

            enemyX = screenHorizontalPosition + memory.readbyte(176 - i + 1) + 8
            enemyHorizontal[i] = math.floor((enemyX - marioX) / 16) - 7

            enemyY = memory.readbyte(167 - i + 1) + 256
            enemyVertical[i] = math.floor(enemyY / 16) + 9 - math.floor(marioY/16)
        end
        -- Circumvent enemy position overflow - No enemies render outside the two
            lines
        for i = 1, 5, 1 do
            if enemyHorizontal[i] < -12 or enemyHorizontal[i] > -3 then
```

```
            EnableEnemyRender[i] = 0
        else
            EnableEnemyRender[i] = 1
        end
    end
    -- Update inputs (enemies)
    for i = 1, 5, 1 do
        if EnableEnemyRender[i] == 1 then
            if enemyAlive[i] == 2 or enemyAlive[i] == 5 then
                    tiles[(enemyVertical[i])*16 + enemyHorizontal[i]] = -1
            end
        end
    end
```

The projectile locations are calculated differently. It is possible to calculate their position with only the available low byte. By making use of Mario's position and computing either the modulo of 16, for the horizontal position, or an division with 16, for the vertical position, and adding a certain integer, the relative position to Mario can be determined. In order for the programme to know when to stop rendering the projectile, it calculates when it has stopped moving. When active, projectiles are always moving, and only when they have disappeared from screen do their coordinates stop changing. Because the projectile does not always move every single frame, the data of the two previous frames is stored. When the program detects one of the projectiles is moving, it updates the appropriate location of the input array with a value of -1.

```
    -- Get Projectile data (fireball)
    fireballHorizontal1 =
        math.floor((memory.readbyte(0x05CB)+256-marioX)/16)%16 - 6
    fireballHorizontal2 =
        math.floor((memory.readbyte(0x05CC)+256-marioX)/16)%16 - 6
    fireballVertical1 = math.floor((memory.readbyte(0x05C1) + 256 -
        marioY)/16) + 9
    fireballVertical2 = math.floor((memory.readbyte(0x05C2) + 256 -
        marioY)/16) + 9

    fireballDirection1 = fireballSecondPrevious1 - memory.readbyte(0x05CB)
    fireballSecondPrevious1 = fireballPrevious1
    fireballPrevious1 = memory.readbyte(0x05CB)

    fireballDirection2 = fireballSecondPrevious2 - memory.readbyte(0x05CC)
    fireballSecondPrevious2 = fireballPrevious2
    fireballPrevious2 = memory.readbyte(0x05CC)
```

```
    -- Update inputs (projectiles)
    if fireballDirection1 ~= 0 then
        tiles[fireballVertical1*16 + fireballHorizontal1] = -1
    end
    if fireballDirection2 ~= 0 then
    tiles[fireballVertical2*16 + fireballHorizontal2] = -1
    end
```

As a final step, all this data is drawn on screen. First an empty box is drawn, after which the input tiles are drawn over this. Mario's location relative to the inputs is drawn

as well.

```
        -- Draw Input Box - empty
        gui.drawBox(3, 11, 16*4 + 4, 15*4 + 12, 0xff000000 ,0x40000000)
        gui.drawLine(15, 12, 15, 71, 0xff888888)
        gui.drawLine(56, 12, 56, 71, 0xff888888)
```

```
        -- Draw inputs
        for layer = 1, 15, 1 do
            for i = 1, 16, 1 do
                sqX = 4 + (i-1) * 4
                sqY = 12 + (layer-1) * 4
                -- Enemies and projectiles
                if tiles[(layer-1)*16+i] == -1 then
                    gui.drawBox(sqX, sqY, sqX + 3, sqY + 3, 0xFF000000, 0xFF000000)
                else
                -- Hitboxes
                if tiles[(layer-1)*16+i] == 1 then
                    gui.drawBox(sqX, sqY, sqX + 3, sqY + 3, 0xffffffff, 0xffffffff)
                else
                -- Empty space
                    gui.drawBox(sqX, sqY, sqX + 3, sqY + 3, 0x000000, 0x000000)
                end
                end
            end
        end

        -- Draw position Mario
        gui.drawBox(37, 45, 38, 51, 0xFF740858, 0xFF740858)
        gui.drawLine(34, 51, 41, 51, 0xFF740858)
```

6.2 The set-up and time partition of the experiment

6.3 Results

After running the experiment for 92 generations it completed 64% of level 1-1 as indicated by the red line in figure 7.1 it reached a distance of 1792 pixels out of the total distance of 2816 pixels.

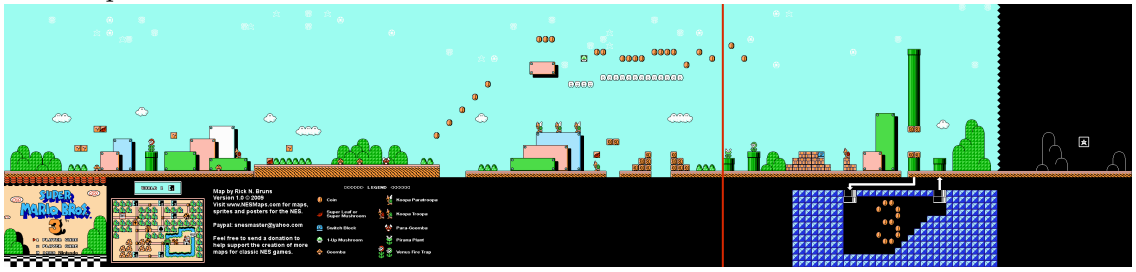


Figure 7.1: A zoomed-out view of level 1-1 with a red line indicating the maximum distance reached.

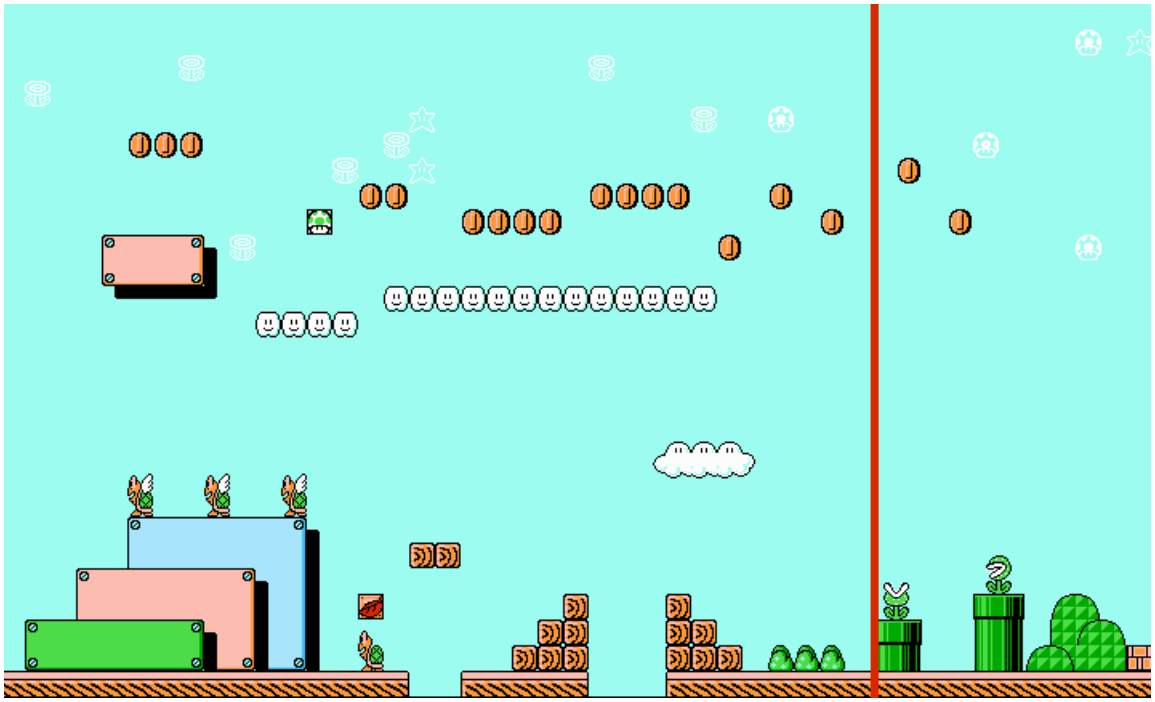


Figure 7.2: A zoomed-in view of level 1-1 with a red line indicating the maximum distance reached.

In figure 7.2 it can be seen that the experiment had trouble passing the green pipes. However, if given more time there would have been a chance that it would have made it past the green pipes because it had previously overcome similar obstacles. The same is true for the other obstacles that follow the green pipes in figure 7.3 where the experiment got stuck.

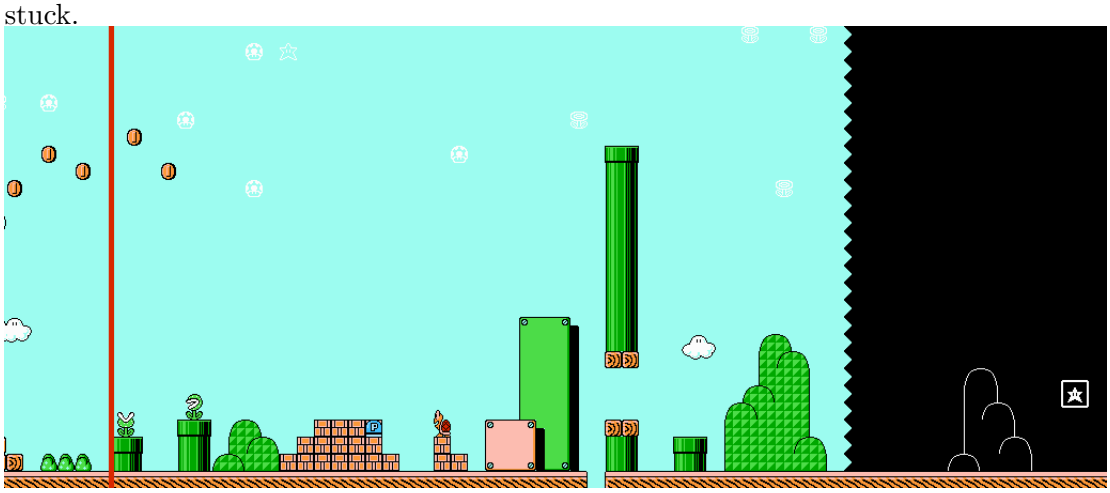


Figure 7.3: A zoomed-in view of level 1-1 with a red line indicating the maximum distance reached showing the final obstacles to be overcome.

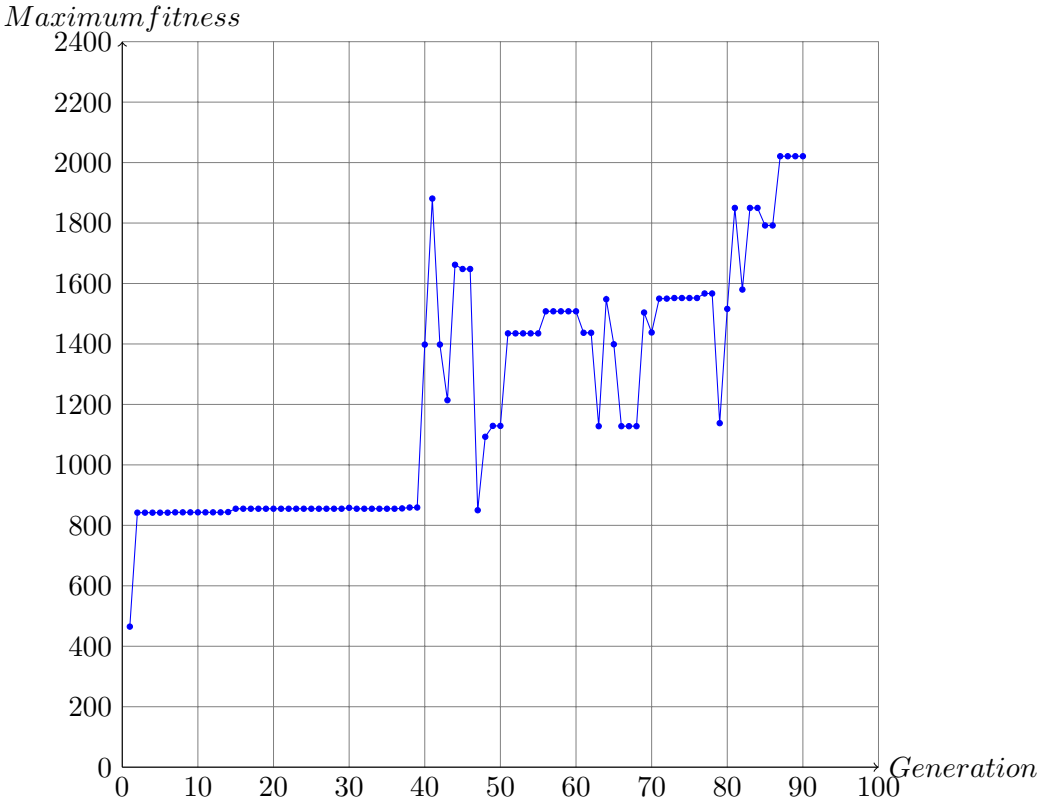


Figure 7.4: The maximum fitness of each generation.

In figure 7.4 can be seen where generations got stuck on an obstacle. When they got stuck the fitness didn't improve and figure 7.4 shows a plateau where this occurred. - How long did it take?

- Application on other levels and games
- How can the program be improved

7 Conclusion

8 (Definitions)

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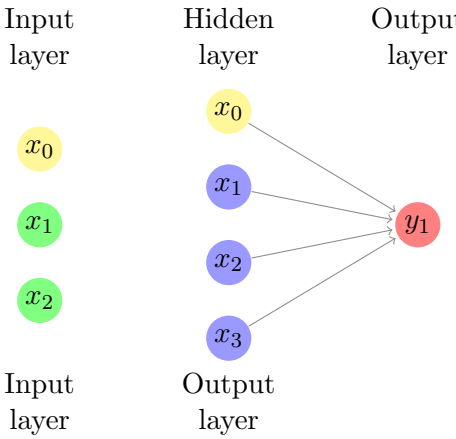
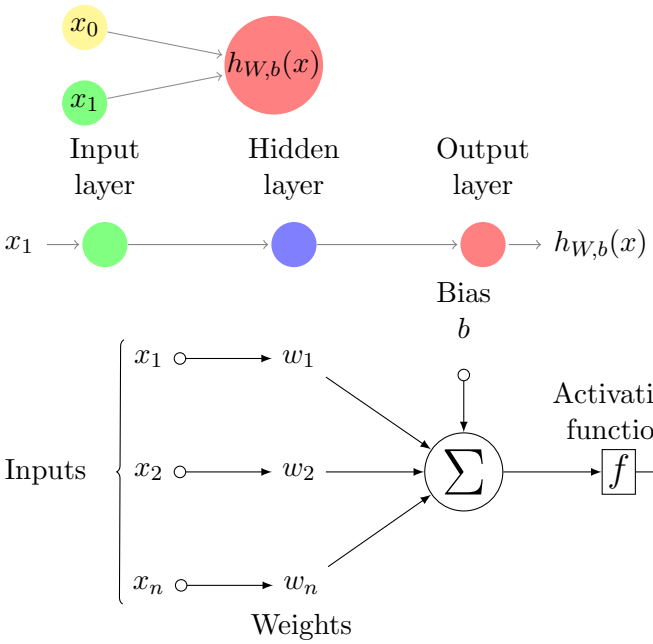
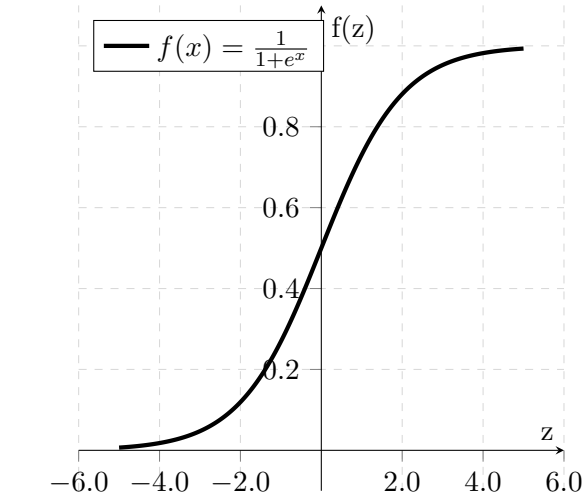
9 Appendices

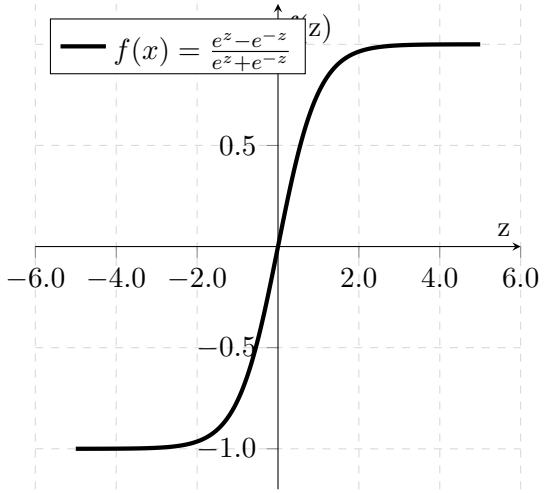

Input layer
Hidden layer
Output layer
x_0
x_1
x_2
x_0
x_1
x_2
x_3
y_1
Input layer
Output layer

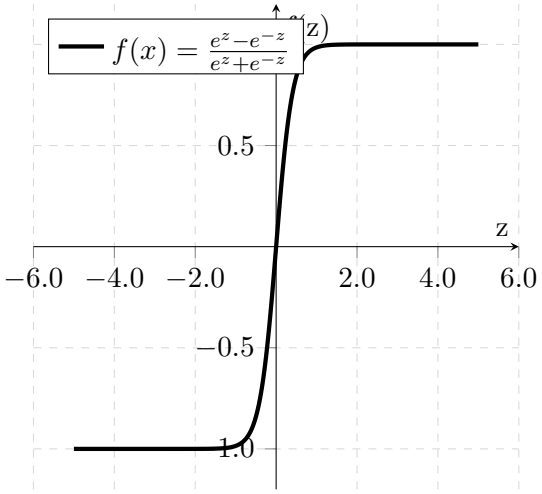

x_0
x_1
$h_{W,b}(x)$
Input layer
Hidden layer
Output layer
x_1
$h_{W,b}(x)$
Bias
b
Inputs
x_1
x_2
x_n
w_1
w_2
w_n
$\sum$
Activation function
f
Output
y
Weights

```
%The data set
x1 = [0; 0; 1; 1];
x2 = [0; 1; 0; 1];
y =  [0; 0; 0; 1];

%Initialisation weights
W1 = stdnormal_rnd(2,3);
W2 = stdnormal_rnd(3,1);
b1 = stdnormal_rnd(1,3);
b2 = stdnormal_rnd(1,1);

%Initialisation variables
alpha = 1;
labda = 0.01;
max_iterations = 5000;
m = rows(x1);

%sigmoid function
function s = f(z)
  s = 1./(1 + exp(-z));
end


for i = 1:maxi

    %Forward propagation

    % layer 1 (input)
    a1 = [exx1, exx2];

    % layer 2
    z2 = a1 * W1 + b1;
    a2 = f(z2);

    % layer 3 (output)
    z3 = a2 * W2 + b2;
    h = f(z3);
    a3 = h;

    %Backward propagation

    % Delta values
    delta3 = -(exy - h)   .* (a3 .* (1 - a3));
    delta2 = (delta3 * W2') .* (a2 .* (1 - a2));

    %Update functions
    W2 = W2 - alpha * (a2' * delta3 * 1/m); % + lambda * W2);
    W1 = W1 - alpha * (a1' * delta2 * 1/m); % + lambda * W1);
    b2 = b2 - alpha * (sum(delta3) * 1/m);
    b1 = b1 - alpha * (sum(delta2) * 1/m);

end
```

```
%Forward propagation

% layer 1 (input)
a1 = [exx1, exx2];

% layer 2
z2 = a1 * W1 + b1;
a2 = f(z2);

% layer 3 (output)
z3 = a2 * W2 + b2;
h = f(z3);
a3 = h;

%Backward propagation

% Delta values
delta3 = -(exy - h)   .* (a3 .* (1 - a3));
delta2 = (delta3 * W2') .* (a2 .* (1 - a2));

%Update terms
deltaW2 = a2' * delta3;
deltaW1 = a1' * delta2;
deltab2 = sum(delta3);
deltab1 = sum(delta2);

%Update functions
W2 = W2 - alpha * (gradW2 * 1/m); % + lambda * W2);
W1 = W1 - alpha * (gradW1 * 1/m); % + lambda * W1);
b2 = b2 - alpha * (gradb2 * 1/m);
b1 = b1 - alpha * (gradb1 * 1/m);
```


$f(x) = \frac{1}{1+e^x}$
f(z)
0.8
0.6
0.4
0.2
z
−6.0 −4.0 −2.0 2.0 4.0 6.0


$f(x) = \frac{e^z - e^{-z}}{e^z + e^{-z}}$
0.5
z
−6.0 −4.0 −2.0 2.0 4.0 6.0
−0.5
−1.0


$f(x) = \frac{e^z - e^{-z}}{e^z + e^{-z}}$
0.5
z
−6.0 −4.0 −2.0 2.0 4.0 6.0
−0.5
1.0