

Implementation and Evaluation of Recent Neuroevolution Algorithms

Master Thesis



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June, 2023

By
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Cover photo: Vibeke Hempler, 2012

Published by: DTU, Department of Applied Mathematics and Computer Science, Richard Petersens Plads, Building 324, 2800 Kgs. Lyngby Denmark
www.compute.dtu.dk

ISSN: [0000-0000] (electronic version)

ISBN: [000-00-0000-000-0] (electronic version)

ISSN: [0000-0000] (printed version)

ISBN: [000-00-0000-000-0] (printed version)

Approval

This thesis has been prepared over five months at the Department of Applied Mathematics and Computer Science at the Technical University of Denmark, DTU, in partial fulfilment for the degree Master of Computer Science & Engineering. The project has been supervised by Prof. Carsten Witt and corresponds to 30 ECTS points.

It is assumed that the reader has fundamental knowledge of computer science.

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Signature

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Date

Abstract

Neuroevolution is a method for optimizing the topology or parameters of neural networks by means of evolutionary algorithms. This technique is more general than white-box approaches, such as supervised learning, and can therefore be applied to a wider range of problems. It has been studied in research for decades and has been successfully applied to problems such as artificial life, evolutionary robotics and continuous domains of reinforcement learning. In this thesis, we present a framework that implements neuroevolution algorithms and that is used to evaluate these algorithms on a selection of benchmark problems. Algorithms and benchmarks were collected from the state of the art in applied and theoretical research in the field of neuroevolution. The framework, implemented in Rust, allows for a visualization of key problem characteristics and the evolution process through a graphical user interface. Selected algorithms and benchmarks are presented in detail. Results collected from the conducted experiments are analyzed, discussed and used to provide a series of guidelines for the choice of algorithms and parameters with respect to problem classes.

TODO Discuss results, guidelines...

Acknowledgements

TODO

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Chapter 1

Introduction

Neuroevolution is a subfield of artificial intelligence which consists in the evolution of ANNs (artificial neural networks). ANNs are traditionally trained using gradient-based methods, such as stochastic gradient descent. Over the years, these methods have been successfully applied to a variety of problems, such as image classification, speech recognition and natural language processing. Such problems allow for supervised learning, where ANNs are trained on a dataset of input-output pairs. However, there is a class of problems for which supervised learning is not applicable, where instead of input-output pairs, only a measure of performance is available. In addition, the performance of ANNs is also heavily impacted by their architectures. The design of ANNs architecture is a complex and time-consuming task, which is typically done by hand, based on experience.

Neuroevolution, on the other hand, as a more general approach, can in particular be applied to this other class of problems, as well as to the design of ANNs architectures. This method is based on evolutionary algorithms, which are inspired by the process of natural selection. These algorithms maintain a population of individuals, which are mutated and recombined to evolve towards optimal solutions. They have shown success for black-box problems and have successfully been applied to a wide range of engineering problems.

The field of neuroevolution has been researched for over 40 years, hence many different algorithms, benchmarks and applications have been proposed. As a matter of fact, neuroevolution encapsulates algorithms with different goals, such as the optimization of the weights of a fixed topology, the evolution of a network topology alongside the use of gradient-based methods for optimizing weights, the evolution of both the topology and weights, as well as the evolution of hyperparameters or reinforcement learning policies. In this thesis, we are interested in approaches relying entirely on neuroevolution, without the need for gradient-based methods, for evolving neural network parameters, using evolved or fixed topologies. In addition to these approaches, Various benchmark problems covering different problem classes such as classification, continuous control or game planning, have also been proposed in the literature for evaluating and comparing the different algorithms.

The focus of this thesis is the development of a framework that implements a selection of neuroevolution algorithms. The framework is used to evaluate and compare the algorithms on a selection of benchmarks. The framework is implemented in Rust. It allows for the visualization of the problems and the solution process through a graphical user interface. The algorithms can be run and tested through a command line interface, in order to allow for the execution of experiments and the collection of results.

Algorithms and benchmarks implemented in the framework were selected from the state-of-the

art in the theoretical and applied research in the field of neuroevolution, with a particular focus on recent algorithms and benchmarks proposed in 2023 and 2024 in the neuroevolution theory literature. In addition to these proposals, NEAT (NeuroEvolution of Augmenting Topologies), a classic algorithm in the field, and the use of evolution strategies with CMA-ES (Covariance Matrix Adaptation Evolution Strategy), achieving state-of-the-art results, were also considered. Regarding the benchmarks, in addition to the simple two dimensional binary classification benchmarks from the considered theory literature, the classic double pole balancing problem and the CANCER1 classification problem were also implemented.

1.0.1 Overview

The ordering of chapters in this report follows the chronological order of work performed for this project.

Chapter Chapter 2 gives the results of a literature review conducted on neuroevolution algorithms and benchmarks. It presents the state-of-the-art in the field, with a particular focus on recent algorithms and benchmarks proposed in the neuroevolution theory literature from 2023 and 2024. Moreover, it also presents the selection of algorithms and benchmarks that were considered in this thesis and implemented in the framework, motivating the choices and discussing the selected algorithms and benchmarks in further detail.

Furthermore, chapter Chapter 3 describes the process of designing and implementing the framework for running neuroevolution algorithms on benchmark problems, gathering statistics on these runs, and allowing for a visualization of the problems and solution process through a graphical user interface. This is done by first specifying the goals and requirements of the framework, followed by a walkthrough of the main design and implementation points of the framework.

Moreover, chapter ?? lays out the results collected from running experiments using the implemented framework. Results are presented for the selection of algorithms and benchmarks, and are discussed and compared in detail. Based on these results, a collection of observations, hypotheses and guidelines for algorithms and parameters selection, given the problem at hand, are presented. These observations are backed up by statistical tests compiled from additional experiments, which are also summarized in the chapter.

Finally, chapter ?? identifies the limitations of the project and discusses the potential lines of future work for refining and expanding on the results previously presented. The main work and contributions of this project are finally summed up in chapter ?? which concludes the report and reflects on its results.

Chapter 2

Literature Review

This chapter covers the first task of this thesis project, which is the review of the literature on neuroevolution algorithms and benchmarks. The first goal of this review is to identify the state of the art algorithms and benchmarks which were proposed in the neuroevolution literature, with a particular focus on the recent theory literature from 2023 and 2024. Following this, a selection of algorithms and benchmarks from the ones which were identified is made. This selection consists in the algorithms and benchmarks which are presented in detail in this section and which are implemented in the framework.

2.1 Methodology

Given the large amount of literature on this well-established field, the review was conducted in a systematic manner, following the guidelines of Indeed, using a rigid methodology is important in order to ensure that the review is impartial and precise.

2.1.1 Research Questions

The research goals are summarized in the following research questions:

- **RQ1:** What are the state of the art neuroevolution algorithms?
- **RQ2:** What are the different kinds of neuroevolution algorithms?
- **RQ3:** Which benchmarks are used to evaluate neuroevolution algorithms?
- **RQ4:** What are the key characteristics of these benchmarks?

RQ1 and **RQ3** are concerned with the identification of the state of the art algorithms and benchmarks, while **RQ2** and **RQ4** are concerned with the selection process.

2.1.2 Search Strategy

The search for papers was performed using Google Scholar and the DTU Findit database, which should provide an accurate representation fo the research that has been conducted on the topic. The keywords used for designing the search queries are:

"Neuroevolution", "Neural Networks", "Evolution Algorithm", "Evaluation"

2.1.3 Study Selection

Following the queries on the databases, the results are then filtered based on the title, abstract and full-text reading (in this order). An iteration of forward and backward snowballing were then conducted to include other studies which were missed in the initial search.

The following inclusion criteria were applied to the abstracts:

- **IC1:** The paper is published after 2002.
- **IC2:** It is clear that the work is proposing a new neuroevolution algorithm or performing an evaluation of existing algorithms.
- **IC3:** The considered algorithm(s) rely solely on evolutionary algorithms

And the following exclusion criteria were used:

- **EC1:** The paper is not available in English.
- **EC2:** The full-text of the paper is not accessible
- **EC3:** The study is a duplicate of a previously included study.

The cut-off date of 2002 is motivated by the release year of the .. paper, proposing the NEAT algorithm, which is the most well-known neuroevolution algorithm is still the subject of many studies today.

2.2 Neuroevolution algorithms

A variety of neuroevolution algorithms have been proposed in the literature. These algorithms can be classified into different categories based on their main characteristics. The following three main distinctions have been identified during the review:

- **Conventional neuroevolution algorithms vs. TWEANNs** Conventional neuroevolution algorithms are those which only evolve the connection weights, considering a fixed topology, while TWEANNs (Topology and Weight Evolving Artificial Neural Networks) are those which also evolve the topology of the neural network.
- **The category of the evolutionary algorithm** such as genetic algorithms, evolutionary strategies, genetic programming, etc.
- **The encoding strategy** This refers to the way the neural network is encoded as a genotype, which is then evolved by the algorithm. The most common encoding strategies are direct encoding, indirect encoding and generative encoding.

2.2.1 Algorithms selection

The following algorithms were selected for the implementation in the framework:

- The (1 + 1) NA algorithm and its variants
- The Bias-Invariant (1+1) NA (BNA) algorithm
- The CMA-ES Evolutionary Strategy
- The NEAT algorithm

Given the duration of the project, the choice was made to limit the number of algorithms to four, in order to allow for a thorough implementation and evaluation of each of them, thus various criteria were used for the selection of the algorithm, to allow for a good coverage of the different categories of algorithms and interesting comparisons between them.

Therefore, the (1 + 1) NA and bias-invariant (1+1) NA algorithms were selected as the two theory paper proposals this thesis is particularly interested in. The CMA-ES algorithm, which is the representative of the evolutionary strategies category was selected because of its popularity in the modern neuroevolution literature and applications, and because of its status as a state-of-the-art algorithm for continuous optimization problems. Finally, the NEAT algorithm, the representative of the TWEANN category, was selected because of its status as the most

well-known neuroevolution algorithm, making it a subject of most comparison studies in the literature.

2.2.2 (1 + 1) NA

The (1 + 1) NA algorithm and its variants were introduced in Fischer, Larsen, and Witt 2023. In this work, the authors consider a simple neuroevolution setting where these algorithms are used to optimize the weights and activation function of a simple artificial neural network.

The artificial neural network topology

Artificial neurons with D inputs and a binary threshold activation function are considered. These neurons have D parameters, the input weights w_1, \dots, w_D and the threshold t . Let $x = (x_1, \dots, x_D) \in \mathbb{R}^D$ be the input of the neuron. The neuron outputs 1 if $\sum_{i=1}^D w_i x_i \geq t$ and 0 otherwise. This can be interpreted geometrically as the neuron outputting 1 if the input vector x is above or on the hyperplane with normal vector $w = (w_1, \dots, w_D)$ and bias t . Furthermore, an alternative representation of the decision hyperplane can be used by considering spherical coordinates. The normal vector to the decision hyperplane is described by $D - 1$ angles and the bias, where the bias corresponds to the distance from the origin measured in the opposite direction of that of the normal vector. As a matter of fact, for $D = 2$, the normal vector can be represented by its cartesian coordinates (x_1, x_2) or by its polar coordinates (r, θ) , where r is the distance from the origin and θ is the angle with the x_1 axis. Similarly, for $D = 3$, the normal vector can be represented by its cartesian coordinates (x_1, x_2, x_3) or by its spherical coordinates (r, θ, ϕ) , where r is the distance from the origin, θ is the angle with the x_1 axis and ϕ is the angle with the x_3 axis. It is easy to convert between these two representations. In addition, the spherical representation uses one less parameter than the cartesian representation, and hence, allows for the reduction of the number of inputs to the neurons to $D - 1$.

The ANNs which are considered in the study contain two layers, a hidden layer with $N > 1$ neurons and an output layer with a single neuron. Each of the hidden neurons are connected to the D inputs and output a binary value. The output neuron is connected to the N hidden neurons and computes the Boolean OR function of their outputs. This architecture is motivated by the problems which are considered in the study, described in ???. Geometrically, these ANNs output the union of a number of N -dimensional hyperplanes.

The (1 + 1) NA algorithm

Let's consider an ANN with N neurons in the hidden layer and D inputs, with parameters $(\phi_{1,1}, \dots, \phi_{1,D-1}, b_1, \dots, \phi_{N,1}, \dots, \phi_{N,D-1}, b_N)$. In the paper Fischer, Larsen, and Witt 2023, the search space $[0, \dots, n]^{ND}$ is considered, where r is the resolution of the continuous $[0, 1]$ domain. This discretisation allows for the values $\{0, 1/r, 2/r, \dots, 1\}$. Setting the parameters of ANNs is typically a continuous optimization problem, but rigorous runtime analysis is much less developed for continuous optimization than for discrete optimization, which motivates this choice. Let $f : \{0, \dots, r\}^{ND} \rightarrow [0, 1]$ be the fitness function which measures the performance of the ANN and is to be maximized.

The (1 + 1) NA algorithm is given in Algorithm 1. It maintains a single individual and mutates all angles and biases independently, based on a global search operator using the harmonic distribution $\text{Harm}(r)$ on $\{1, \dots, r\}$: For $l \sim \text{Harm}(r)$,

$$\text{Prob}(l = i) = \frac{1}{H_r} \text{ for } i = 1, \dots, r, \text{ where } H_r = \sum_{i=1}^r \frac{1}{i}.$$

2.2.3 Bias-Invariant (1+1) NA (BNA)

In **bna**, the authors extend upon the analysis in Fischer, Larsen, and Witt 2023 by considering more realistic ANN settings, presenting the Bias-Invariant (1+1) NA (BNA) algorithm. The

Algorithm 1 $(1 + 1)$ NA

```
 $t \leftarrow 0$ 
Select  $x_0$  uniformly at random from  $\{0, \dots, r\}^{DN}$ .
while termination criterion not met do
  Let  $y = (\varphi_{1,1}, \dots, \varphi_{1,D-1}, b_1, \dots, \varphi_{N,1}, \dots, \varphi_{N,N-1}, b_N) \leftarrow x_t$ ;
  for all  $i \in \{1, \dots, N\}$  do
    Mutate  $\varphi_i$  and  $b_i$  with probability  $\frac{1}{DN}$ , independently of each other and other indices;
    Mutation chooses  $\sigma \in \{-1, 1\}$  uniformly at random and  $l\text{Harm}(r)$  and adds  $\sigma l$  to
    the selected component, the result is then taken modulo  $r$  for angles and modulo  $r + 1$  for
    biases.
    for  $i \in \{1, \dots, N\}$  do
      Set bias  $2b_i/r - 1$  for neuron  $i$ .
      for  $j \in \{1, \dots, D\}$  do
        Set the  $j$ -th polar angle to  $2\pi\varphi_{i,j}/r$  for neuron  $i$ .
      end for
    end for
  Evaluate  $f(y)$ 
  if  $f(y) \geq f(x_t)$  then
     $x_{t+1} \leftarrow y$ 
  else
     $x_{t+1} \leftarrow x_t$ 
  end if
  end for
   $t \leftarrow t + 1$ 
end while
```

considered ANNs uses Rectified-Linear-Unit (ReLU) activation functions, commonly used in real-world ANNs. This allows for the construction of bended hyperplanes, resulting in solutions to the problems described in ?? which are invariant to the bias.

The artificial neural network topology

The considered ANNs contain three layers, in which each of the neurons uses a ReLU activation function i.e they output $\max(0, \sum_{i=1}^k w_i x_i)$ for k inputs from the previous layer. The weights between the first and second layer and between the second and third layer are fixed. The topology for $D = 2$ is shown in ??. The use of ReLU activation functions results in piecewise linear output. Hence, as described in ?? for the case $D = 2$, these networks compute a V-shaped area of positive classification. Such topologies are considered as a single neuron, referred to as a **V-neuron**, and which can be part of a standard ANN topology.

Therefore, these V-neurons can be described by $D + 1$ parameters:

- The bias b
- The $D - 1$ angles $\varphi_1, \dots, \varphi_{D-1}$.
- The bend angle θ .

The area of positive classification is a (multi-dimensional) cone, all points positively classified correspond to points forming an angle smaller than the bend angle θ with the normal vector to the hyperplane given by the bias b and the $D - 1$ angles $\varphi_1, \dots, \varphi_{D-1}$.

The Bias-Invariant (1+1) NA algorithm

The BNA algorithm is given in Algorithm 2. It is mostly the same as the (1+1) NA algorithm, with the difference that the bend angles are also mutated.

2.2.4 The CMA-ES Evolutionary Strategy

CMA-ES, short for *Covariance Matrix Adaptation Evolution Strategy*, is a kind of evolution strategy (ES). An ES is an optimization technique based on evolution, and belonging to the class of evolutionary algorithms (EA). This kind of black-box optimization algorithms aim at optimizing a function $f : \mathbb{R}^n \rightarrow \mathbb{R}$, for which the analytic form is not known, but for which evaluations of the function are possible. As it is the case for CMA-ES, These algorithms are typically stochastic and are used for the optimization of non-linear or non-convex continuous optimization problems.

ES algorithms maintain a population of candidate solutions. These candidate solutions are sampled from a multivariate normal distribution. Parameters of the distribution are updated at each generation based on the performance of the candidate solutions. As a matter of fact, a simple greedy ES algorithm could consist in updating the mean of the distribution, and using a fixed standard deviation. The mean is updated to the best solution after the evaluation of the fitness of each of the candidate solutions. The next generation is then sampled around this mean. However, this kind of simple greedy algorithms is particularly prone to getting stuck at local optima because of the lack of exploration.

In order to allow for more exploration, rather than exclusively relying on the single best solution, genetic algorithm maintain a proportion of the best solutions from the current generation, and generate the next one through recombinations and mutations. However, this approach is also prone to getting stuck at local optima, as in practice, candidate solutions end up converging to a local optimum.

CMA-ES addresses these issues and allows for the adaption of the search space when needed, reducing it when the confidence in current solutions is high, for fine-tuning, or increasing it when the confidence is low, in order to allow for more exploration. This is done by adapting the covariance matrix of the multivariate normal distribution, which stores pairwise dependencies

Algorithm 2 Bias-Invariant $(1 + 1)$ NA (BNA)

$t \leftarrow 0$
Select x_0 uniformly at random from $\{0, \dots, r\}^{DN}$.
while termination criterion not met **do**
 Let $y = (\theta_1, \varphi_{1,1}, \dots, \varphi_{1,D-1}, b_1, \dots, \theta_N, \varphi_{N,1}, \dots, \varphi_{N,N-1}, b_N) \leftarrow x_t$;
 for all $i \in \{1, \dots, N\}$ **do**
 Mutate φ_i and b_i with probability $\frac{1}{(D+1)N}$, independently of each other and other indices;
 Mutation chooses $\sigma \in \{-1, 1\}$ uniformly at random and $l\text{Harm}(r)$ and adds σl to the selected component, the result is then taken modulo r for angles and modulo $r + 1$ for biases.
 for $j \in \{1, \dots, D\}$ **do**
 Set bias $2b_i/r - 1$ for neuron i .
 Set bend angle $\pi\theta_i/r$ for neuron i .
 for $j \in \{1, \dots, D\}$ **do**
 Set the j -th polar angle to $2\pi\varphi_{i,j}/r$ for neuron i .
 end for
 end for
 Evaluate $f(y)$
 if $f(y) \geq f(x_t)$ **then**
 $x_{t+1} \leftarrow y$
 else
 $x_{t+1} \leftarrow x_t$
 end if
 end for
 $t \leftarrow t + 1$
end while

between the parameters for the sample distribution. This makes CMA-ES a powerful and widely used optimization algorithm. The main drawback of this algorithm is its computational cost, induced by the use of the covariance matrix, which makes it less suitable for high-dimensional problems.

...

CMA-ES can be used for the evolution of fixed-topology neural networks, by considering the weights of the connections as the parameters of the optimization problem, and converting between a vector representation of the network, for the optimization input, and the standard graph representation, for the evaluation.

2.2.5 Neuroevolution of Augmenting Topologies (NEAT)

The NEAT algorithm was introduced in `neat`. It is a TWANN (Topology and Weight Evolving Artificial Neural Network) algorithm, which evolves, simultaneously, both the topology and weights of neural networks. The main idea behind this algorithm is to start from a minimal topology, incrementally adding new neurons and connections to, the networks, which allows for the evolution of complex neural networks while keeping the computational cost low and justifying each new addition to the network topology. The following sections describe the main components of the algorithm.

Genetic Encoding

NEAT uses a direct encoding of the neural networks. The goal of the encoding strategy is to allow crossover among different network topologies. Each genome contains two sets of genes, which specify nodes and connections in the network:

- **Node genes** Each node gene contains an identifier and layer (input, hidden, output or bias, which is an input that is always set to 1.0).
- **Connection genes** Each connection gene specifies an input node identifier, an output node identifier, a weight, whether the connection is enabled or disabled, and an innovation number.

Where node identifiers are shared between the individuals in the population, the enabled flag specifies whether or not the connection is expressed in the phenotype (i.e the network) and the innovation number is used to track the historical origin of the gene.

Mutations

NEAT uses two types of mutations: weight mutations and structural mutations. Weight mutations are used to perturb the weights of the connections in the network, while structural mutations are used to modify the topology of the network. There are two types of structural mutations:

- **Add connection** This mutation adds a new connection between two unconnected nodes in the network. The connection is assigned a random weight.
- **Add node** This mutation adds a new node in the network, splitting an existing connection into two. The old connection is disabled and two new connections are added to the new node. The connection leading into the new node is assigned a weight of 1, while the connection leading out from the new node is assigned the weight of the old connection. This allows for the minimization of the initial effort of the mutation, as the activation of the output layer node remains the same and the weights of the new connections can be optimized in future generations.

Because of these two types of mutations, inserting new nodes and connection genes, genomes can only grow larger over time, resulting in the evolution of increasingly complex networks.

Crossover

One of the challenges of evolving neural networks is the crossover operator, because of the different topologies of the networks. NEAT addresses this issue by making use of the innovation numbers in connection genes, which allows for the tracking of the historical origin of each gene. This allows for the matching of genes between individuals. Genes are assigned increasing innovation numbers as they appear in the population and innovation numbers are inherited. Hence, the matching of genes is done by comparing the innovation numbers. Thus, the crossover operator consists in inheriting matching genes from one parent at random, and adding the remaining disjoint and excess genes from the fittest parent. This strategy is particularly cost-effective as it requires no topological analysis of the networks.

Speciation

An issue with the current strategy is that the population is unable to protect topological innovation, because of smaller topologies optimizing faster and the addition of new connections usually resulting in an initial drop in fitness. To address this issue, NEAT uses speciation, which groups individuals into species based on their genetic similarity. This strategy allows for the protection of topological innovation by having individuals compete within their specie, rather than the entire population. In addition, as it is the case with the crossover operator, historical matching allows for an efficient solution.

The similarity between two individuals is computed as a weighted sum of the number of excess E genes, the number of disjoint D genes and the average weight difference \bar{W} of matching genes:

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

Where c_1 , c_2 and c_3 are coefficients which control the importance of each term, and N is the number of genes in the larger genome.

At each generation, individuals are sequentially assigned to a specie based on the similarity with the representative of the specie, which is a randomly selected individual from the previous generation which was part of the specie, and a similarity threshold. If no specie is found, a new specie is created.

Each species is given a number of offspring in proportion to the sum of the adjusted fitness of its members. Where the adjusted fitness f'_i of an individual i is given by $f'_i = f_i/n_i$, where f_i is the fitness of the individual and n_i is the number of individuals in the specie. This is done to prevent large species from dominating the population. The offspring are generated using the crossover and mutation operators, on members of the species, after the selection of the fittest individuals. At each generation, the population is replaced by the offspring.

2.3 Neuroevolution benchmarks

2.3.1 Unit hypersphere sphere classification problems

These problems, which can be thought of as a kind of ONEMAX for the $(1 + 1)$ NA algorithm, were introduced in Fischer, Larsen, and Witt 2023. These problems consist in the binary classification of points in the D -dimensional unit hypersphere.

Half The HALF problem consists of all points with non-negative x_D coordinate on the unit hypersphere:

$$\text{HALF} = \{x \in \mathbb{R}^D, \|x\|_2 = 1 \text{ and } \varphi_{D-1} \in [0, \pi]\}.$$

Quarter The QUARTER problem consists of all points with non-negative x_{D-1} and x_D coordinate on the unit hypersphere:

$$\text{QUARTER} = \{x \in \mathbb{R}^D, \|x\|_2 = 1 \text{ and } \varphi_{D-1} \in [0, \pi/2]\}.$$

TwoQuarters The TWOQUARTERS problem consists of all points with either both negative or non-negative x_{D-1} and x_D coordinate on the unit hypersphere:

$$\text{TWOQUARTERS} = \{x \in \mathbb{R}^D, \|x\|_2 = 1 \text{ and } \varphi_{D-1} \in [0, \pi/2] \cup [\pi, 3\pi/2]\}.$$

LocalOpt The LOCALOPT problem consists of all points with polar angle φ_{D-1} between 0 and 60, 120 and 180, 240 and 300 degrees:

$$\text{LOCALOPT} = \{x \in \mathbb{R}^D, \|x\|_2 = 1 \text{ and } \varphi_{D-1} \in [0, \pi/3] \cup [2\pi/3, \pi] \cup [4\pi/3, 5\pi/3]\}.$$

2.3.2 XOR

This classic benchmark problem is a binary classification problem, which consists in the classification of the four points (0, 0), (0, 1), (1, 0) and (1, 1), according to the XOR function. The points (0, 0) and (1, 1) are of class 0, while the points (0, 1) and (1, 0) are of class 1. The popularity of this simple problem comes from its non-linear nature, which makes it impossible to solve with a single-layer perceptron.

2.3.3 Dataset Classification Problems

Classification using datasets is a classical use-case for neural networks. It consists in training a network on labeled data and using it to predict the label of unseen data. Hence, the hypersphere classification problems, presented in Section 2.3.1, from the theory studies, differ from this kind of task, by having algorithms trained and tested on the same data.

Although these problems are not common use-cases for neuroevolution because of the use of labeled data, they are particularly interesting for this study, by allowing to show how neuroevolution can be applied to these common tasks, testing the algorithms on larger state spaces, and potentially observing whether common behaviors which occur when training ANNs using gradient-based methods, such as over-fitting or under-fitting, also apply to neuroevolution.

The proben1 benchmark, presented in ..., introduces various standard benchmark datasets, including the cancer dataset, which contains 699 entries, consisting in cell descriptors gathered by microscopic for tumors being benign or malignant. Each dataset entry contains 9 input features, and a binary output,

The algorithms are evolved using the first 90% of the data, and are tested on the remaining 10%.

2.3.4 Pole Balancing

The pole balancing problem, introduced in ..., is a classical benchmark in control theory, reinforcement learning and neuroevolution literature. It consists in controlling a cart with one degree of freedom, which moves along a one-dimensional track, by applying a horizontal force to it, in order to balance a pole attached to it using a hinge. Some of the reasons for the popularity of this benchmark problem are its simplicity, its relevance to real-world control problems and its unstable and non-linear dynamics.

The difficulty of the problem can be adjusted by changing the number of poles. Indeed, if the poles have different lengths, they will react differently to the forces applied to the cart. As the

single pole variant has become too easy for current techniques, we consider the widely used case of double pole balancing, where two poles are attached to the cart.

The state of the system is described by the cart position x , the cart velocity \dot{x} , the pole angles θ_1 and θ_2 and the angular velocities $\dot{\theta}_1$ and $\dot{\theta}_2$. This task is Markovian, as the state contains all the information needed to determine the future evolution of the system. A more challenging variant of the problem consists in removing the velocity informations from the state, which requires the use of recurrent connections, which were not considered in this project.

The dynamics of the system are described by the following equations:

$$\ddot{x} = \frac{F - \mu_c \text{sgn}(\dot{x}) + \sum_{i=1}^N \tilde{F}_i}{M + \sum_{i=1}^N \tilde{m}_i}$$

$$\forall i \in \{1, N\}, \ddot{\theta}_i = -\frac{3}{4l_i}(\ddot{x} \cos \theta_i + g \sin \theta_i + \frac{\mu_{pi} \dot{\theta}_i}{m_i l_i})$$

$$\forall i \in \{1, N\}, \tilde{F}_i = m_i l_i \dot{\theta}_i^2 \sin \theta_i + \frac{3}{4} m_i \cos \theta_i (\frac{\mu_{pi} \dot{\theta}_i}{m_i l_i} + g \sin \theta_i)$$

$$\tilde{m}_i = m_i (1 - \frac{3}{4} \cos^2 \theta_i).$$

Where:

- F is the magnitude of the force applied to the cart
- μ_c is the cart friction coefficient
- M is the cart mass
- N is the number of poles
- l_i is the length of the i -th pole
- μ_{pi} is the pole friction coefficient
- m_i is the mass of the i -th pole
- g is the gravity constant

The equations for motion are integrated using the Euler method. For a time step Δt :

$$x_{t+1} = x_t + \dot{x}_t \Delta t$$

$$\dot{x}_{t+1} = \dot{x}_t + \ddot{x}_t \Delta t$$

$$\theta_{i,t+1} = \theta_{i,t} + \dot{\theta}_{i,t} \Delta t$$

$$\dot{\theta}_{i,t+1} = \dot{\theta}_{i,t} + \ddot{\theta}_{i,t} \Delta t.$$

The fitness function is defined as the sum of the time steps during which the poles are balanced and the cart is within the allowed bounds, over 1000 time steps. A pole is considered balanced if its angle is within 30 degrees of the vertical position. The evaluated algorithms outputs are mapped to the magnitude of the force $F \in [-10, 10]$ N to be applied to the car at each time step.

Chapter 3

The framework

This chapter presents the design and implementation of the framework which was developed as part of this thesis. It lists the requirements of the framework, goes through its development lifecycle and presents the architecture of the framework.

This framework, which is the main contribution of this thesis, allows for a fair comparison of the considered algorithms by having them implemented in a common environment and language, in order to avoid performance differences induced by the programming language, and running them on the exact same benchmark problem implementations and settings.

The code for the framework is available at <https://github.com/MSc-Thesis-Samy/code> and includes a README file with instructions on how to use it.

3.1 Requirements

3.1.1 Goals and functional requirements

The overarching goal of the framework is to provide a tool for the evaluation of neuroevolution algorithms on benchmark problems, based on the selection presented in Chapter 2. Tests are specified through a command line interface, they consist in an algorithm and problem pair, along with a set of additional parameters. The framework collects the results of the tests as well as the list of passed-in parameters, algorithm and problem. These tests can either be run individually or in batch mode, where the framework runs a set of tests in parallel, and collects statistics on these runs.

Furthermore, the framework also allows for the visualization of the problem, solution process and network structure through a graphical user interface. In addition, it generates graphs for visualizing the test results, plotting the performance of the algorithm on the benchmark problem over the generation count.

3.1.2 Non-functional requirements

Non-functional requirements are the requirements that specify the quality of the system, rather than the features it should have. Apart from the functional requirements that specify the features expected of the framework, a number of non-functional requirements have also been identified.

- Usability and user experience: the framework should be easy to use and provide a good user experience.
- Documentation: The framework should be well documented, providing a clear and concise guide on how to use it.

- Error handling: All errors should be handled gracefully as to not result in runtime errors.
- Performance: The framework should allow for the execution of tests in parallel, making use of multiple CPU cores.
- Extensibility: The framework should be easily extensible, allowing for the addition of algorithms and benchmarks without any major changes to the existing codebase.
- Support: The framework should be able to run on the three major operating systems: Windows, Linux and MacOS.

3.2 Architecture

The framework is implemented in Rust. This general-purpose programming language, originally intended to serve as an alternative for system languages such as C and C++, offers a good balance between performance provided by such low-level languages and the safety and ease of use of higher-level languages such as Python. Furthermore, various libraries (referred to as Rust crates) which could be used when implementing aspects of the framework, such as designing the command-line interfaces and graphical-user interfaces, or running CMA-ES are available in Rust. Lastly, the language can target a range of platforms, including Windows, Linux and MacOS.

The framework is divided into three main components:

- The core: This component is responsible for the execution of the tests and the collection of results. It contains the algorithms and benchmark implementations.
- The command-line interface: This component allows the user to specify the tests to be run, as well as the parameters for these tests.
- The graphical user interface: This component allows the user to visualize the problem, solution process and network structure, as well as the test results.

The core is used by both the command line interface and the graphical user interface. And the graphical user interface is used by the command line interface. Indeed, the UI allows for the visualization of the solution process, but interaction with the framework is done when invoking it through the command line interface.

The dependency graph of the framework is shown in ??.

3.2.1 Background on Rust features

This section provides a brief overview of the features of the Rust programming language before going into the details of the framework's implementation.

Object-oriented capabilities

Nowadays, object-oriented languages are considered the norm for the development of large-scale software systems in the industry. Rust is inspired by various programming paradigms, such as functional programming and object-oriented programming. Although there is no consensus on the list of features which define an object-oriented programming language, Rust can be considered object-oriented. Indeed, it allows for the definition of structs and enums which can store data and methods using implementation blocks. It also allows for encapsulation through the use of the `pub` keyword, which specifies the visibility of objects, thus defining the public API for interacting with them. When not using the `pub` keyword, the object is private and can only be accessed by the module it is defined in. Modules are used to organize code and define the visibility of objects, and can be nested to form a hierarchy. However, a major difference with other object-oriented languages such as Java or C# is that Rust does not have a class-based inheritance system. Instead, it takes a different approach which consists in polymorphism,

which is a more general system referring to code that can work with multiple types. In practice, this is achieved through the use of generics in method and object definitions, and the use of traits, which are similar to interfaces in other languages. In fact, traits allow for the definition of a default implementation for a set of methods, which can be overridden by the implementing type.

Library management

Cargo is Rust's build system and package manager. Most projects are managed using this tool which handles the download and building of the dependencies of projects. In Rust, packages are referred to as crates.

Attributes

Attributes are metadata applied to some module, crate or object. They are, for example, used to enable compiler features or mark functions as unit tests. or to define the behavior of the code. They are defined using the `#` symbol and are placed before the object they are associated with.

Testing

In Rust, unit-testing is usually done by defining a test module (with a test attribute) at the end of the file containing the functionalities to be tested. Test functions correspond to functions defined in such modules, which are marked with a specific test attribute. Tests can be run with `cargo test`. They fail when a *panics* occur, and utility macros such as `assert_eq` or `assert` can be used to panic when conditions are not met.

3.2.2 Core

This component contains the core functionality of the framework. Various constants and utility functions, used across the project, are defined in the `utils.rs` and `constants.rs` files.

Algorithms

The algorithms are implemented as structs and are accessed as variants of an `Algorithm` enum, which lists all the implemented algorithms. The algorithm structs and the `Algorithm` enum implement the `NeuroevolutionAlgorithm` trait, which defines the methods that an algorithm must implement. These methods are `optimization_step`, `optimize_cmaes`, `evaluate` and `optimize`, which is implemented as a default method in the trait. The `Algorithm` enum and the `NeuroevolutionAlgorithm` trait are defined in the `neuroevolution_algorithm.rs` file. Each of the different algorithm structs are defined in their own file, such as `vneuron.rs` or `neat.rs`.

Benchmarks

The problems are implemented as variants of a `Benchmark` enum, and are defined in the `benchmarks.rs` file. This enum contains three variants, for each of the implemented benchmark types: `PoleBalancing`, `Classification` and `SphereClassification`. The two classification enums hold an instance of the `LabeledPoints` type, storing the labeled data. The file contains functions to generate the data for each of the classification problems, i.e., parsing it from a text file for the *cancer* problem and generating and iterating other angle values for the sphere classification problems. In particular, the `Benchmark` enum defines a `evaluate` method, taking as input an algorithm (an instance of the `Algorithm` enum) and which returns the fitness of the algorithm on the task.

Classification problems For the sphere classification and dataset classification tasks, the fitness is computed using the `classification` function from the `benchmarks.rs` file, which computes the *MAE* (Mean Absolute Error). For the `bna` and `(1 + 1) NA` algorithm, which output boolean values, this is equivalent to computing the accuracy (i.e., the number of correct predictions divided by the number of total predictions), while also allowing for the evaluation of the CMA-ES and NEAT method, outputting probabilities when using the sigmoid activation on the output neuron.

Pole Balancing The logic for the pole balancing simulation is implemented in the `pole.balancing.rs` file, where the state is defined, along with methods responsible for updating it based on the equations and the Euler method. The `pole.balancing` function in the `benchmarks.rs` file simply updates the state, using the algorithm output as the applied force, and checking whether or not the success conditions for the task are still met.

Testing

Unit-tests were implemented across the core component to test the behavior of the algorithms and benchmarks. These tests were implemented in parallel with the functionalities to avoid and identify potential bugs early in the development process before building up with more functionalities. In addition, they were ran at each new push to github using a workflow responsible for compiling the project and running all the tests. This is to ensure that new changes do not break any past working functionality.

In fact, the `bna` and $(1 + 1)$ NA problems were tested using the sphere classification problems, where optimal solutions are known. These tests consist in checking whether one of these algorithms, with parameters corresponding to an optimal solution, does indeed lead to a maximum fitness value of 1.0. These tests are defined in the `benchmarks.rs` file. For example, the `test_half_network` function checks that a decision line corresponding to the x-axis for the continuous $(1 + 1)$ NA algorithm gives a fitness of 1.0. For the BNA algorithm, where there are infinitely many solutions to the sphere classification problems, different solutions were checked.

Furthermore, two additional tests in the `benchmarks.rs` file are responsible for checking that the data is loaded properly from the `cancer` text file. Tests in the `pole.balancing.rs` file test the physics of the simulation implementation, for example verifying that a pole at the lowest position, with no external force, does not lead to any movement of the cart or the pole.

Lastly, regarding the CMA-ES and NEAT algorithms, the behavior of their core functions was tested. Test functions in the `neat.rs` test the behavior of functions such as the crossover or initialization, using examples from the original paper ... when available. The functions in `neural_network.rs` test the output of the feed-forward method and activation functions.

3.2.3 Command-line interface

The command line interface is implemented using the `clap` crate, which is a widely used command line argument parser in Rust. It allows for the execution of tests, by providing the algorithm, the problem and additional parameters. These additional parameters are optional and have default values, they are used to specify parameters for the algorithms, such as the number of neurons, parameters for the optimization, such as the number of iterations, and toggling the visualization of the solution process and network structure.

Arguments can be of three different types:

- **Positional:** These are required arguments which are specified in the order they are defined in the command line interface.
- **Named:** These are optional arguments which are specified by their name and a value.
- **Flags:** These are optional arguments which are specified by their name and are either present or not.

The `Cli` struct is defined in the `cli.rs` file, it contains members for each of the command line arguments and derives the `Parser` trait. The argument name is set to the member name, a short name, help message, default value and the argument type are specified in an attribute on the member.

```

1 Neuroevolution framework for testing algorithms on benchmark problems.
2
3 Usage: main [OPTIONS] <ALGORITHM> <PROBLEM>
4
5 Arguments:
6   <ALGORITHM> The algorithm to test [possible values: oneplusonena, bna]
7   <PROBLEM>    the benchmark problem [possible values: half, quarter, two-
               quarters]
8
9 Options:
10  -r, --resolution <RESOLUTION> Resolution, when applicable [default:
               1000]
11  -i, --iterations <ITERATIONS> Number of iterations [default: 5000]
12  -c, --continuous          Use the continuous version of the
               algorithm, when applicable
13  -e, --es                  Optimize using cma-es
14  -n, --neurons <NEURONS>   Number of neurons, when applicable [
               default: 1]
15  -g, --gui                 Display visualization
16  -h, --help                Print help
17  -V, --version             Print version

```

Listing 3.1: Command line interface

The arguments are parsed in the `bin/main.rs` file, which is the entry point of the program.

In order to ensure that the passed-in arguments are valid, the rust type system is leveraged, specifying appropriate data types for each of the argument. For example, the iteration number is set to an unsigned integer `u32`, while the algorithm and benchmarks are set to two enums, `AlgorithmType` and `Problem`, with variants for each possible option.

The command line interface is shown in 3.1. Parameters for the BNA and (1+1) NA algorithms are passed in as named arguments. For NEAT and CMA-ES, where more parameters can be specified, the path to `.toml` configuration files are passed-in instead.

3.2.4 Graphical user interface

The UI is implemented using the `ggez` crate, which is intended to be a simple 2D game framework. In particular, it provides a simple interface for creating windows, drawing geometrical shapes and handling user input. This crate relies on the definition of a `State` struct, which holds the parameters of the game state, and which implements the `EventHandler` trait. This trait defines two methods: `update`, which is used for updating the state, and `draw` which is used for rendering the state. These two methods are called by the game loop, which is triggered in the `bin/main.rs` file if the `gui` flag is set when invoking the program.

This game abstraction is particularly suited for the implementation of visualization in the framework. The `State` struct defined in `gui.rs` holds an `algorithm`, a `problem`, and two additional members keeping track of the number of iterations. An instance of this struct is created in the `bin/main.rs` file using the arguments passed in the command line interface. The `update` method updates the `algorithm` by running an optimization step, and the `draw` renders the different visualizations, based on the `problem` and `algorithm` members.

The number of iterations and the best fitness value are shown in the top left corner of the window.

Classification problems

For the sphere classification problem, the unit-sphere is shown, along with its points which are labeled as `true`, which are shown in green, and its points labeled as `false` which are shown in

red. When running the $(1 + 1)$ NA algorithm, the decision line and normal vector are shown. In the case of the BNA algorithm, the normal vector and decision cones are shown. For the CMA-ES and NEAT algorithms, the output of the network is shown.

Pole balancing

The visualization of the pole balancing problem consists in drawing the cart and pole, and updating their position based on the state of the simulation. It is implemented in the `pole_balancing_gui.rs` file. Compared to the classification problems, where the visualization is updated as the algorithm is evolved in the `update` method, the pole balancing visualization does not update the passed-in algorithm, but rather updates the simulation state based on the output of the algorithm.

Bibliography

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Appendix A

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