**Czech Technical University in Prague**
**Faculty of Electrical Engineering**

**Department of Cybernetics**

# BACHELOR PROJECT ASSIGNMENT

**Student:** Jan Dvorský

**Study programme:** Cybernetics and Robotics

**Specialisation:** Robotics

**Title of Bachelor Project:** Neuroevolutionary Design of Control Strategy of a Multi-Legged Robot

**Guidelines:**

1. Get acquainted with the robotic simulator SIM (http://lynx1.felk.cvut.cz/~danfis/sim-doc/) and learn to use it.
2. Design a neuroevolutionary system as a combination of a hypercube-based indirect encoding (used in HyperNEAT) and a genetic programming for learning effective motion patterns of multi-legged robots with symmetry properties.
3. Implement the proposed neuroevolutionary algorithm in the SIM simulator.
4. Design proof-of-concept experiments and experimentally evaluate the performance of the neuroevolutionary system, the hexapod robot creature being the goal experiment.
5. Analyse the achieved results.

**Bibliography/Sources:** Will be provided by the supervisor.

**Bachelor Project Supervisor:** Ing. Jiří Kubalík, Ph.D.

**Valid until:** the end of the winter semester of academic year 2013/2014

L.S.

prof. Ing. Vladimír Mařík, DrSc.
**Head of Department**

prof. Ing. Pavel Ripka, CSc.
**Dean**

Prague, January 10, 2013

České vysoké učení technické v Praze
Fakulta elektrotechnická

Katedra kybernetiky

# ZADÁNÍ BAKALÁŘSKÉ PRÁCE

**Student:** Jan Dvorský

**Studijní program:** Kybernetika a robotika (bakalářský)

**Obor:** Robotika

**Název tématu:** Neuroevoluční návrh strategie řídící pohyb vícenohého robotu

**Pokyny pro vypracování:**

1. Seznamte se s robotickým simulátorem SIM (http://lynx1.felk.cvut.cz/~danfis/sim-doc/) a naučte se s ním pracovat.
2. Navrhněte neuroevoluční algoritmus, založený na hyperkubickém nepřímém kódování a genetickém programování, pro učení efektivních pohybových vzorů vícenohého robotu.
3. Implementujte navržený neuroevoluční algoritmus v prostředí simulátoru SIM.
4. Navrhněte experimenty s šestinohým robotem pro empirické ověření funkčnosti neuroevolučního algoritmu.
5. Dosažené výsledky vyhodnoťte.

**Seznam odborné literatury:** Dodá vedoucí práce.

**Vedoucí bakalářské práce:** Ing. Jiří Kubalík, Ph.D.

**Platnost zadání:** do konce zimního semestru 2013/2014

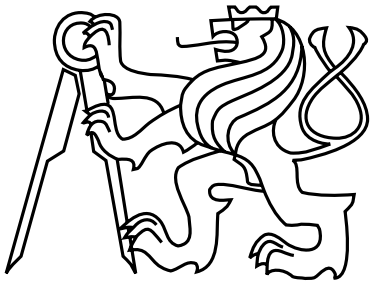
prof. Ing. Vladimír Mařík, DrSc.
**vedoucí katedry**

L.S.

prof. Ing. Pavel Ripka, CSc.
**děkan**

V Praze dne 10. 1. 2013

Czech Technical University in Prague
Faculty of Electrical Engineering
Department of Cybernetics



Bachelor's Thesis

# Neuroevolutionary design of control strategy of a multi-legged robot

*Jan Dvorský*

Supervisor: Ing. Jiří Kubalík, Ph.D.

Study Programme: Cybernetics and Robotics

Field of Study: Robotics

May 21, 2013

# Aknowledgements

My greatest thanks goes to Dr. Jiri Kubalik for guiding me through the uneasy process of writing this paper. He used his experience and wit to help me overcome all the issues I encountered. I would like to thank Mr. Jan Drchal and Mr. Jan Cerny for always having time for my questions when I came by their offices uninvited. A mention goes to Dr. Jeff Clune of University of Wyoming whom I bombarded with questions during the development and he found time to reply. I also appreciate the help of Mr. Vojta Vonasek and Mr. Daniel Fiser, who assisted me with the robotic simulator. In addition, I would like to thank Ms. Lucie Kratochvil for proof-reading and correcting my work, Mr. Vojtech Micka for helping me look at things from different angles, Ms. Marketa Stonova for being so incredibly patient with me and my dearest parents for always listening and supporting my dreams.

**Prohlášení autora práce**

Prohlašuji, že jsem předloženou práci vypracoval samostatně a že jsem uvedl veškeré použité informační zdroje v souladu s Metodickým pokynem o dodržování etických principů při přípravě vysokoškolských závěrečných prací.

V Praze dne 23.05.2013 ..... Jan Dvorský .....

Podpis autora práce

# Abstract

This paper searches for better solutions of the robot locomotion problem. Our method is based on the well established HyperNEAT algorithm, where we exchange NEAT with genetic programming. We present the resulting algorithm, construct proof-of-concept experiments and show experimental results. In the end we offer possible future improvements to HyperGP and share the implemented testing framework with the community.

# Abstrakt

Tato práce se zaměřuje na hledání lepších řešení problému robotické chůze. Naše metoda je založena na známém algoritmu HyperNEAT, kde vyměníme NEAT za genetické programování. Představíme výsledný algoritmus, provedeme experimenty a ukážeme jejich výsledky. Nakonec navrhneme možná vylepšení algoritmu HyperGP a uvolníme náš testovací framework komunitě.

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# Chapter 1

# Introduction

The humans have always been intrigued by the tools their ancestors built. Many of us devote our lives to building upon and improving those tools. When the industrial revolution brought the accelerated rate of inventions, the future seemed bright for the human kind. With the use of light bulbs, electric machines and combustion engines, inventors could speed up their work and many improvements have just kept coming.

The middle of 20th century brought the greatest invention of all - the computer. Under the spotlight pointed at the unbelievably fast processing machine, the average human could start feeling less brilliant, or even insufficient for the modern age. The world's fastest computer can now compute over $10^{15}$ floating point operations per second [34].

Even though computers have been beating us in many tasks, such as playing chess, organizing data and communication, humans and most animals still have been much more successful than the computers in one little ability - coordinated locomotion. Walking is so natural to us that we do not consider it particularly difficult and that is why this one weakness of computers is the major objective of our work.

We will try to develop an automated system which would enable robots to learn and perform forward locomotion. This system should be independent of the robot's size and topology. Additionally, in order to empower the system to solve various problems, the influence of the experimenter should be as low as possible.

Our approach is based on the HyperNEAT algorithm, originally developed by Ken Stanley and his team [32]. HyperNEAT is a neuroevolutionary method for optimizing synaptic weights in a neural network. It uses generative encoding from genotype to phenotype that enables it to encode symmetries, repetitions and other underlying motifs. Our approach uses a modification of HyperNEAT, called HyperGP, which replaces the original neuroevolutionary algorithm NEAT for a simpler one, genetic programming (GP). This exchange has proved to improve results in certain simple tasks [6] and our goal is to apply HyperGP to a more complex problem - robot locomotion.

A proof-of-concept experiment will be performed, necessary frameworks will be implemented from scratch. With the frameworks in place, we hope to find the strengths and weaknesses of HyperGP through thorough testing. Suggested improvements to the HyperGP algorithm will be presented, showing the direction of possible future research.

The first chapter encloses this introduction and explains, what the motivations and the goals of this work are. We discuss the robot locomotion problem and known solutions to it in Chapter 2. The HyperNEAT algorithm is discussed in Chapter 3, together with a quick overview of Genetic Programming. The used robotic simulator is described in Chapter 4. Chapter 5 brings the suggested approach, combining HyperNEAT with Genetic Programming. The actual implementation of the frameworks and experiments is thoroughly presented in Chapter 6, showing off experimental results and encountered problems in the following chapter. The last chapter concludes the paper and presents suggestions for future work, followed by appendices containing important terms and a detailed setup of the experiments.

# Chapter 2

# Robot locomotion problem and existing methods

Today's robots are able to use from tens to hundreds of independent actuators and sensors. The robotic system needs to process the input information in real time and compute the next state for the outputs. This function, transforming the information about the current state of the environment into a new, desired state, thus has many dimensions.

This is the main reason of us using artificial neural networks (ANNs - or just neural networks, for short) for this task. Neural networks are generally capable of solving complicated tasks. The problem faced here is finding the right topology and parameters of the optimal neural network. Many approaches have been suggested and in the rest of this chapter we will discuss some of them.

## 2.1 EANT2 - Evolutionary Acquisition of Neural Topologies, Version 2

This particular method is described in detail in [28], where it is also compared to the NEAT method on a visual servoing task. This approach is different to other methods by its separated evolution of the structure and the parameters of the neural network. Which means that two structures of a network are only compared, when they both have their optimal parameters. The optimization is done by the Covariance Matrix Adaptation Evolution Strategy (CMA-ES) and has yielded better results that NEAT on certain tasks [28]. The reason we could not use this method is the large dependence on a group of preset parameters that have to be found in advance by the designer, clashing with our goal to minimize the human influence.

## 2.2 CPG - Complex motor patter generation (Rodney)

The second approach that also utilizes a separated evolution is called Complex motor Pattern Generation (CPG) [19]. The evolution is separated into two stages. First, a simple

neural network that controls only one leg of a robot (which works like an oscillator) is evolved to some extent. This base oscillator is then copied across the robot to control every single leg. In the second stage, another network controlling the interconnections between all the leg oscillators is evolved to synchronize all the movements into a coordinated gait. A six leg test robot called Rodney was used in [19] to perform testing. The main advantages of this approach are speed and convergence, since the precise goal of the first stage (a decent one-leg oscillator) is clearly specified before the process starts. The purpose of the second stage is to synchronize these oscillators after they are copied into all other legs. Although useful for some purposes, this is a huge disadvantage for us, since a strong hand of a designer is needed to setup the evolution parameters. Thus this approach cannot be used in our case for its lack of generality.

## 2.3 HyperNEAT - Neuro-Evolution of Augmented Topologies employing hypercube-based encoding

Both the approaches mentioned above suffer from one insufficiency: they use *direct* encoding. The problem with direct encoding is that the genotype (genetic material of the robot) and the phenotype (a structure controlling the actual robot) are mapped directly to each other, making the individuals very sensitive to genetic operators such as mutation and crossover. How this problem is approached in HyperNEAT and consequently in HyperGP is explained in the following chapter.

# Chapter 3

# HyperNEAT and Genetic Programming

This chapter describes HyperNEAT in detail, explaining its advantages over methods mentioned in the previous chapter. First we look at the advantage of indirect over direct encoding, providing an example of how genetic operators may act as a destructive, rather than a constructive force on directly-mapped algorithms. Both the genotype and the phenotype of HyperNEAT are described in detail in the second part of the chapter.

## 3.1 Generative encoding

When trying to show why indirect encoding can be more powerful, let's look at an analogy from [9]. Imagine trying to evolve a four-legged table to have some desired properties. If represented by direct encoding, our genotype would have to contain the following piece of information

- leg 1 has a height of 50cm
- leg 2 has a height of 50cm
- leg 3 has a height of 50cm
- leg 4 has a height of 50cm

Thus our table's height is around 50cm. However, what if the genetic operator wanted to try a different height? It could set *leg 1*'s height to 10cm, but that would make the table very unstable. In order to successfully reduce the height of the table, the same modification would have to be applied four times in different places of the genotype. Of course, a stochastic operator such as the genetic programming would take a long time to *discover* that in order to go from one stable solution to another, it is required to apply the same modification four times. With direct encoding, the genotype tells us *what the phenotype looks like.*

An attempt to solve this problem with indirect encoding produces better results. With one type of indirect encoding called *generative* encoding, the genotype works like a 'manual'

for us to construct the phenotype. Thus, with our table example, the genotype contains the following information:

- a leg X has a height of 50cm
- leg 1 is the same as leg X
- leg 2 is the same as leg X
- leg 3 is the same as leg X
- leg 4 is the same as leg X

In the case of generative encoding, changing the height of the table is a matter of a single modification: of leg X in this example. Thus the genetic operators can search in the solution space, with the assertion that all the possible tables are stable. With generative encoding, the genotype tells us *how to construct the phenotype*.

All sorts of generative encodings can be found in nature. The human genome contains about 20,000 (20 thousand) genes [27]. However, the human body contains around 50,000,000,000,000 (50 trillion) cells [15]. Just from the numbers, we can see that some kind of generation has to transform the blueprint (the human genome) into an actual human body containing trillions of cells. Another example can be discovered very easily: human fingers and toes. Our DNA does not contain 20 distinct copies of all our slightly altered fingers and toes - that would be very inefficient. In fact, only an original description of a finger is saved and then the modifications of that original model are used to get all fingers found on our hands. In the same matter as with the table, if evolution wanted to strip us of fingers altogether, only one modification to the original would suffice.

This important disadvantage of direct encoding significantly increases the time needed for the evolution to find symmetries and similarities. Crossover and mutation, used with genetic algorithms, can severely damage genotypes that are directly mapped to its phenotype (as with the table example). This might explain why most evolutionary methods (like those mentioned in Section 2) try to somehow overcome this problem by splitting the evolution into stages or not using crossover at all [28].

## 3.2 Genetic operators

The sensitivity of genotypes to genetic operators forced researchers to find a way in which they could keep mutation and crossover in the game and at the same time enable the evolution to explore all the possibilities of solutions without destroying the good ones. A good application of a generative encoding was necessary.

One particular method seems to be able to pass the mentioned restrictions. It was originally developed by Ken Stanley and his team and is called HyperNEAT [32]. It was shown

that this method can have very good results in similar tasks to ours [32, 9]. The main strength of this method is its capability to exploit symmetries, repeating motifs and other underlying principles.

The search for a neural network that could solve the task is approached differently than usual in HyperNEAT. The target neural network is represented by a grid of neurons. Weights between all neurons are not directly encoded in the individual, but instead are computed by a separate neural network-like structure called CPPN (Compositional Pattern Producing Network) (Figure 3.2).

The target neural network with its generated weights is called the *substrate*. In the original HyperNEAT, the CPPN is a neural network-like object - with the difference in neuron activation functions. The individual solution is then represented by both its CPPN (genotype) and its substrate (phenotype). The CPPN is the cause of HyperNEAT's capabilities - finding symmetries and other underlying motifs. Since the CPPN is a multi-input function (multi-dimensional), it in fact encodes a *hyper* cube. Thus the origin of 'hyper' in *Hyper*NEAT.

The NEAT (Neuro-Evolution of Augmented Topologies) part of the method's name is a very sophisticated neuroevolution method that can deal with premature convergence (preserves diversity) and gradual complexity of solutions. In the case of HyperNEAT, the solutions are not the neural networks (substrates) themselves, but the CPPNs that generate them. The NEAT is thus applied on the CPPNs.

## 3.3 Phenotype: substrate

The phenotype in the case of HyperNEAT is a regular neural network. Usually the network is organized as a grid so that the neurons can be uniquely identified by their position in the grid. The relative position of each output neuron in the grid should correspond to the relative position of the actuator in the robot (Figure 3.1).

During the run of the robot, the input neurons receive values from its sensors and the output neurons compute the values that are sent to its actuators. The grid can be filled with neurons in the same fashion but at a higher resolution again (without modifying the CPPN at all), so that the grid remains the same physical size. This enables easy scaling of the network, since one CPPN can generate a different substrate (with very similar properties) at each resolution. This ability is called *scaling* and is one of the features of HyperNEAT. It is discussed in detail in [32], but is beyond the range of this work.

## 3.4 Genotype: CPPN

The CPPN is a network closely resembling a neural network. If we depict this network as a tree, we see that the nodes can employ any function (sigmoid, sine, absolute value, square,

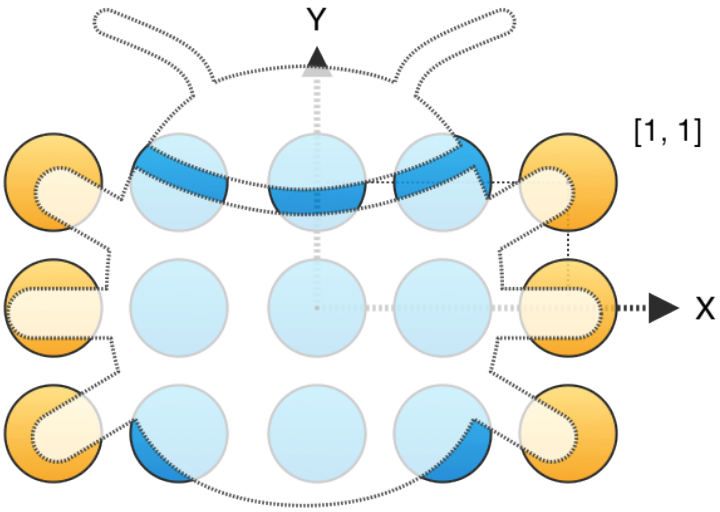



Figure 3.1: Relationship of the substrate and the robot topology

square root etc) and the leaves are input variables into the network. The output node (the root) just carries the result of the computations coming from inside of the tree.

The input variables, in the case of HyperNEAT, are the coordinates of the chosen neurons in the substrate and the output is the synaptic weight value between those neurons. This way, the substrate is constructed by querying its CPPN for weight values between all neurons in the substrate (Figure 3.2). When all the neurons have all the synaptic weights between each other determined, the substrate is ready for use.

The choice of the neuron activation functions enables the CPPN to discover corresponding spatial properties in the robot. For instance, absolute value of $x$ can encode Y-axis symmetry, sine of $x$ can encode repeating parts along the robot etc.

The potential of this encoding has been shown in experiments [32, 9] where the CPPN can in fact encode symmetries and other regularities that could hardly be present if direct encoding was used. This way, through evolution, the discovered symmetries cause the network to realize that it just copies one leg multiple times into the robot body. This is something that in previous methods [28, 19, 14] had to be explicitly enforced on the evolution by separating it into stages [19, 14] or using inner optimization loops [28].

With this approach, the change in the genotype (CPPN) caused by genetic operators such as mutation and crossover does not have to be destructive (like in the case of direct encoding), because a change to one table leg is propagated to all other legs (Section 3.1).

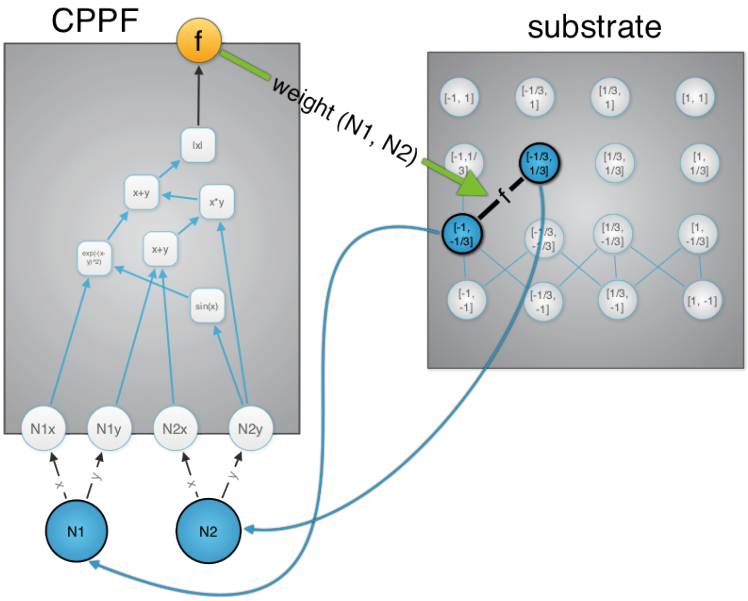



Figure 3.2: Hypercube encoding example

## 3.5 Genetic Programming (GP)

Genetic programming (GP) is an evolutionary algorithm-based method for creating computer programs [16]. It is a special kind of a evolutionary algorithm, where each individual is represented by a tree of functions and terminals.

The genetic operators commonly used in genetic algorithm methods such as mutation and crossover are also present in GP. The *mutation* operator takes a random tree node and replaces it with a newly generated subtree. The crossover (one point crossover), selects a node in each of the two trees coming into the crossover operator and exchanges the subtrees originating from those selected points.

The selection in GP is based on the fitness value (measure of the quality of the solution) and can be done through methods like the Roulette wheel, Stochastic Universal Sampling, Tournament Selection or Remainder Stochastic Sampling.

# Chapter 4

# Robotic simulator Sim

We will use the following robotic simulator for the fitness acquisition and individual robot behavior visualization. This robotic simulator Sim was created at the Czech Technical University by Daniel Fiser and Vojta Vonasek [31]. The Sim combines the physics simulator Open Dynamics Engine [24] with the graphics engine OpenSceneGraph [26].

The Sim can be used in both non-visual and visual mode. The non-visual is practical for fast robot evaluations during the experiment run and the visual one, obviously, for confirmation of desired behavior by the experimenter. Usually this confirmation is undertaken after the experiment is over and the best individual from the evolved population is loaded into the simulator and shown to the experimenter.

Sim comes with a wide variety of input options, although for our purposes, the SSSA modular robot input turned out to be the most frictionless approach. SSSA robots are the robots used with the SYMBRION/REPLICATOR projects, thoroughly described and used in [7]. In our simplified simulator, one SSSA robot consists of a joint connecting the body (cube) and a moving flat connection panel (Figure 4.1). The panel can move in one degree of freedom around the body in the range of $[-\frac{\pi}{2}, \frac{\pi}{2}]$. What we refer to as a *robot* in this work, however, is a set of connected SSSA robots, together forming a structure with many degrees of freedom (Figure 4.2).

Deeper description of the SSSA robots is not included in this work, because they were just used as a tool of evaluating the efectivness of the HyperGP algorithm implemented in our framework.

The *input* of the simulator consists of setting up the simulation parameters (start and stop times, sample time, physics constants) and creating the robot body in the simulator. The creation of the robot body is done through describing the positions and rotations of each SSSA body. The simulator then attaches all the bodies that can be attached (are next to each other). This way we create the robot. Each SSSA body then gets registered to the simulator for updates.

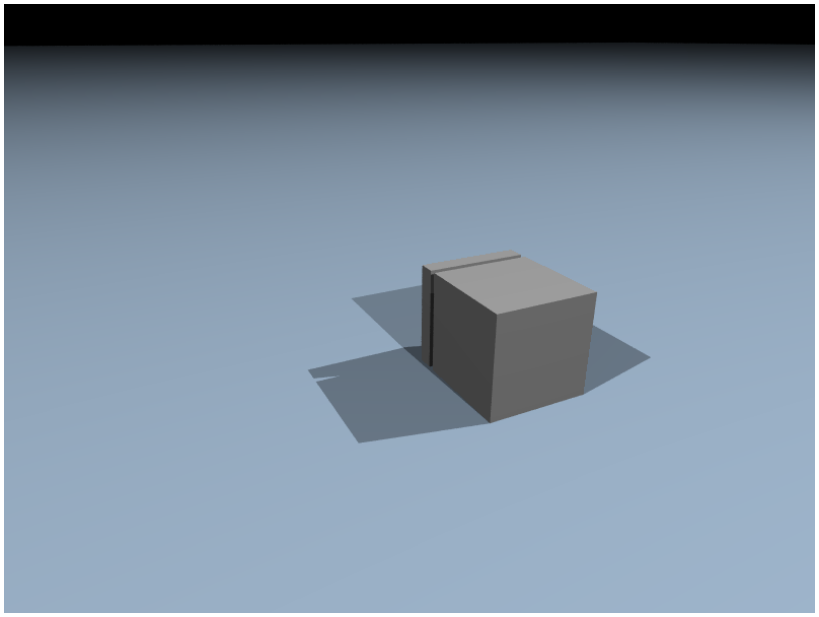


Figure 4.1: One SSSA robot

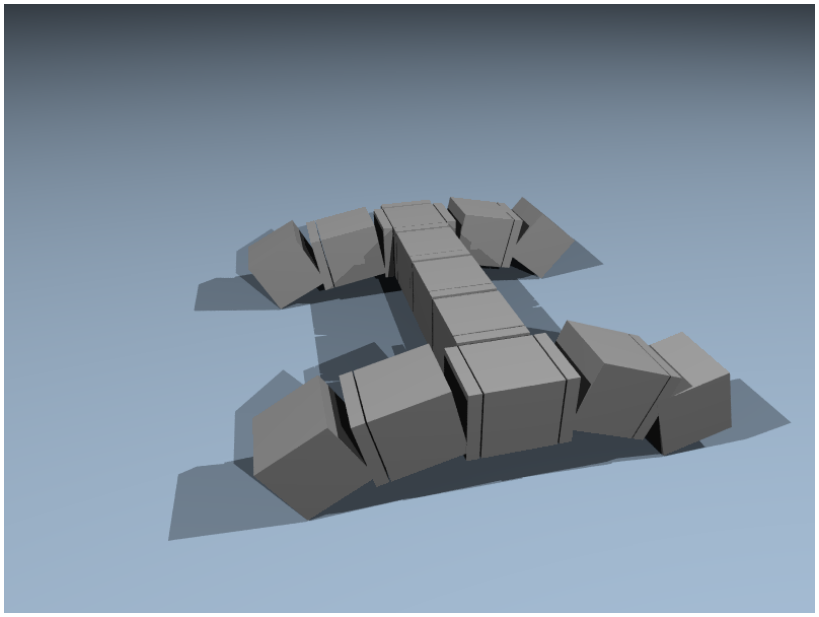


Figure 4.2: Many SSSA pieces forming what we refer to as a *robot*

Later, during the simulation, an object containing the phenotype outputs for all time steps is queried for these values. Each of the SSSA bodies queries our object independently. We answer these queries by identifying the source SSSA body by its relative position in the whole robot and looking up the value (desired rotation angle) which is set as the desired

rotation of the SSSA body.

The simulator takes care of moving the SSSA body into the desired rotation over time. It does so by taking the difference between the current and desired rotations and multiplying it by a *gain* constant to get the desired angular velocity. The default of the simulator was $gain = -0.5$, for our experiments we increased it to $gain = -1.0$ to get speedier movements.

The position of the center SSSA body is computed at the end of the simulation. The difference of the end position and the start position (or position at some delayed time) is considered the output of the simulator. We later compute fitness from this translation vector.

# Chapter 5

# Proposed HyperGP approach

Our approach consists of modifying the HyperNEAT algorithm into HyperGP and adding a bloat control method. Both changes are described in this chapter.

## 5.1 HyperGP

After researching multiple neuroevolution methods, the HyperNEAT approach seemed best suited for our task. The ability to encode symmetries and spacial motifs of the robot could be a great advantage in problems such as robot locomotion. We chose to replace NEAT as the evolutionary method with genetic programming (GP), though, for its simplicity and suggested superiority in certain cases [6]. This change can be seen in Figure 5.1.

Figure 5.1 shows, how our proposed algorithm could be designed with a consideration of modularity. The first block on the left symbolizes the process which tweaks the population in each iteration - in our case GP, in case of HyperNEAT it was the NEAT algorithm. The middle block holds the genotype-phenotype mapping used. Even though we are using hyper-encoding in this paper, some kind of direct encoding could also be used for different tasks. The important part is that only the middle block would need to be changed. The block all the way on the right symbolizes the fitness evaluator. In our case a software simulator is used, but it could also be a module working in the physical world which would evaluate fitness in real time on real robots and feed the data back to the algorithm.

This exchange of NEAT for GP has been done before in [6]. It requires us to reconsider the genotype (CPPN), however. Instead of using a Compositional Pattern Producing *Network*, GP uses functions as genotypes, thus the genotype is called a Compositional Pattern Producing *Function* (CPPF) [6].

The strengths and advantages of indirect encoding for similar tasks have been shown several times [32, 9, 6]. With the use of indirect encoding through hyper-encoding and the genetic programming as the evolutionary method we hope to develop a process that would be able, together with an appropriate robotic simulator, to find some good solutions for the

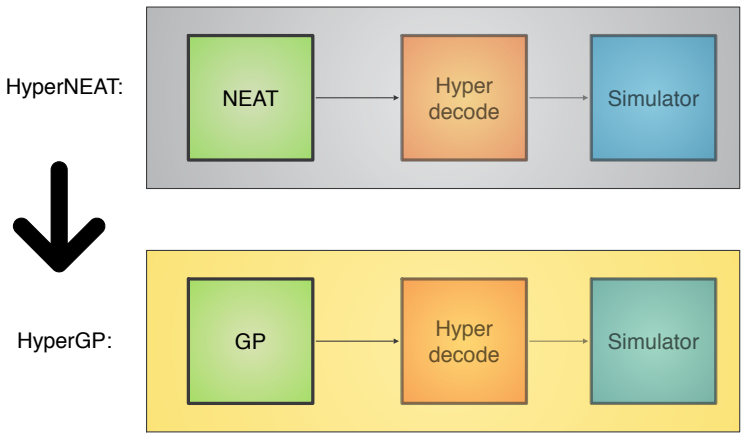



Figure 5.1: HyperGP derived from HyperNEAT

problem. The process is depicted in Figure 5.2.

### 5.1.1 Initial population

The process starts with a randomly generated population of small CPPFs (tree-based functions which generate the weights of the neural network). The random initialization can employ methods such as Full, Grow or Ramped Half-and-Half.

### 5.1.2 Selection

The selection of individuals that are given a chance to reproduce can be performed through Tournament, Roulette or any other selection methods.

### 5.1.3 Mutation

The selected individuals are mutated with a certain small probability in the following matter. A node is chosen in the tree. The subtree originating from that node is removed. A new, randomly generated subtree is placed onto the node instead.

### 5.1.4 Recombination

With a certain probability, two selected individuals can recombine in the following matter. A randomly chosen node is found in the first tree. A randomly chosen node is found in the second tree. The subtrees, originating from those two points are exchanged between the trees. Then, both trees are placed into a new population.

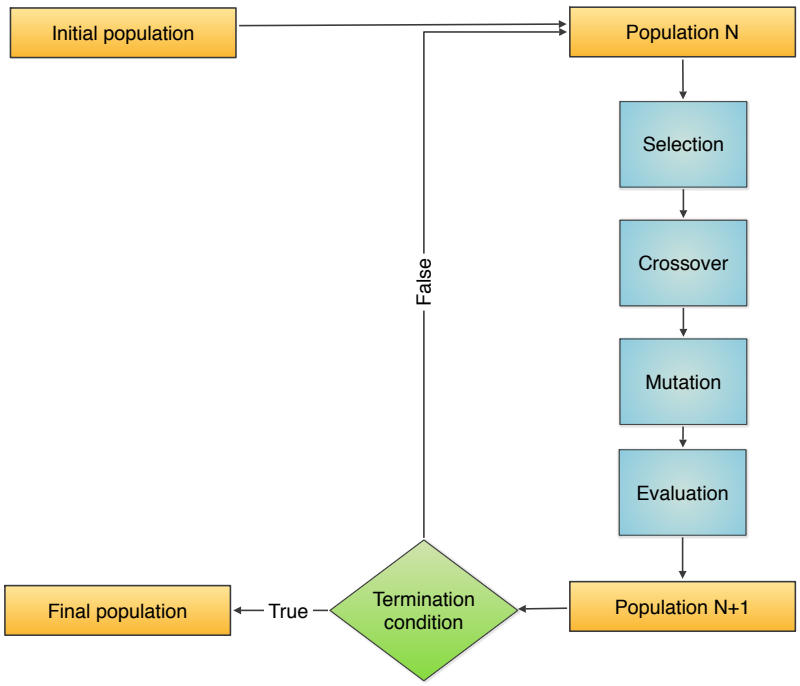



Figure 5.2: GP evolution

### 5.1.5 Evaluation

The fitness evaluation is performed in two phases. The first phase decodes the CPPF into its substrate (a neural network controlling the robot). In the second phase, each individual now possessing both its genotype (CPPF) and phenotype (neural network), is put into the simulator for fitness computation. The fitness value can be defined as the forward traveled distance of the simulated robot, the integrated walked path or any other desired behavior.

### 5.1.6 Termination condition

Since we cannot simulate natural open ended evolution, we need to set a stopping point. The first condition to be satisfied stops the process. One condition is a maximum number of tried generations, another is a goal fitness value, which if any individual in the population possesses, causes the evolution to stop.

## 5.2 Bloat control

A peculiar phenomenon exists in the genetic programming approach. Sometime during the evolution, genetic operators might cause individuals to start developing larger trees with-

out increasing their fitness value. This phenomenon is called *bloat*.

Several hypotheses for the cause of bloat are outlined in [30] and in our paper they are not going to be discussed. The focus here will be on some antidote to bloat. The one which is employed in our approach is proposed in [30] by Silva and is called Dynamic Limits. Two limits are mentioned - depth and size (we only focus on the tree-based representation here). Depth turned out to be a much better tuning parameter [30] which is why we will use it in our process as well (Dynamic Maximum Tree Depth).

The method is rather simple and elegant. Consider the depth of the tree to be our limiting parameter (the Limit). First, the initial population is created with a maximum depth of e.g. 4. Then all individuals acquire their fitness values and the depth of the most fit individual becomes the initial value of the Limit. After that, whenever a new individual is created through a genetic algorithm whose depth is higher than the current Limit, it is allowed into the new population only if its fitness is higher than the fitness of the previously most fit individual. If the processed individual does not pass this test, one of its parents is copied into the new population instead. In the case of its depth being equal to or lower than the Limit, it is always allowed into the new population.

This way, individuals in the population only become larger (deeper) if their fitness is also higher. Experiments [30] have shown that this simple filter can prevent bloat from enlarging the individuals without any increase in fitness.

### 5.2.1 Heavy variant

An extension is also proposed in [30] called heavy variant of a Dynamic Limit. The original Dynamic Limit only increased over time - it never decreased. With the heavy variant, though, the Limit also decreases if the depth of the most fit individual suddenly gets lower. This creates a complication: what happens with the individuals that were under the Limit before, but got above it after the decrease? They become *illegals*.

### 5.2.2 Handling illegals

If a newly created individual has illegal parents, the Limit for that individual becomes the depth of the larger parent. This way, potentially good solutions will not be removed from the population but at the same time they will not have a chance to cause bloat. The minimum value of the limit is the maximum allowed depth during initialization.

### 5.2.3 Very Heavy variant

The very heavy variant is allowed to fall down even below the maximum allowed depth during initialization. With the Dynamic Limits proposed by [30], we hope to be able to prevent bloat from unnecessarily complexifying our individuals without increasing their fitness value.

# Chapter 6

# Implementation

In order to verify the efficiency of the proposed solutions, the whole algorithm needed to be implemented as a computer program. The focus was mainly on:

- maximizing computational speed
- high expandability of the program in the future
- automatic support of multi-core processors
- low memory requirements
- at least some platform independence

These objectives fundamentally affected the choice of the programming language, platform and software design.

## 6.1 Programming environment

### 6.1.1 Programming language

Due to the need of both low level and object-oriented features, C++ was chosen as the programming language that could satisfy all the mentioned goals. There were other candidate languages, but C++ was the best choice for the following reasons.

The other obvious choice would be Java, as the world's most popular application programming language [29]. Although, some sources claim that C++ should be faster than Java by principle (Java runs on a virtual machine) [13]. Certain benchmarks find it difficult to compare languages, since each is better at a different task [8]. Also, Java is much more platform independent than C++. However, we did not choose Java for its lack of user memory control (Java uses runtime garbage collection) in addition to the speed disadvantages.

Another option was Objective-C, a C-based, objective-oriented language in development by Apple, Inc. The platform dependence on the Darwin architecture (poor support on Linux machines) made us not really consider it, even though the choice of the compiler later locked us down for the near future.

### 6.1.2 Compiler

Due to the fact that most of the implementation took place on a MacBook Pro, running OS X 10.8 and Xcode as the development environment, we chose the Clang/LLVM compiler [20] instead of the more common GCC compiler. Some sources claim that Clang/LLVM is faster in compilation, more efficient and produces better binaries of C++ code [17].

Clang/LLVM even uses its own implementation of the C++ standard library (libc++). Unfortunately, tested release versions are only available for the Darwin architecture meaning that compiling at Linux machines would be unreliable at this time (the libc++ library for Linux machines is in the experimental stage at the moment) [21].

Trying to make the code future-proof, we wanted to use the latest C++11 language standard. Clang/LLVM was build to be feature-complete and designed for C++11 from the beginning [20].

### 6.1.3 Platform

Programming on Apple's platform, there were many advantages in using the native compiler with C++. The main one is the support of Grand Central Dispatch (GCD), a multi-thread multi-core management system, available for the C++ language [4].

The advantage of using GCD instead of hard-coding POSIX threads is that only individual blocks of code are submitted to GCD for asynchronous processing. GCD takes care of creating and destroying threads and is able to use all available processor cores. This eliminates the need to know the number of available cores on the target machine. GCD just uses them all without the programmer having to program anything extra [4].

All these features are in development for the Linux platform, as well. However, at the time of this writing, most of them are still in experimental stage and are not recommended to be used for serious work.

The choice of IDE (Integrated Development Environment) was easy. Having worked with Xcode (by Apple, Inc.) [5] for almost two years and knowing that Xcode was built for Objective-C and C++ development, no other IDE was considered. Shell and Python script coding was done in Sublime Text 2 [3] and MATLAB scripts in the MATLAB app [23].

## 6.2 The *cic* framework

In order to successfully test the proposed form of HyperGP algorithm, a solid implementation had to be proposed. Keeping the future modifications in mind, a framework named *cic* was developed. Since we might want to test different algorithms than *GP* or use different encoding than the *hypercube-based*, generic interfaces and types had to be defined in advance.

The best way of to present any *population*-based algorithm is, for our purpose, to look at the **population** as one object and the algorithm as a block **modifying** that object. Also, we needed a way to work with the particular **individuals**, as the items contained by the population.

Starting with the most abstract interfaces, these main three types of objects were defined

- Individual
- Population
- Population Modifier

All the particular types brought in with particular algorithms and processes have to inherit from either of these three types. That is how *cic* was designed. Figure 6.1 shows how two particular algorithms use this sort of design to define all needed types.

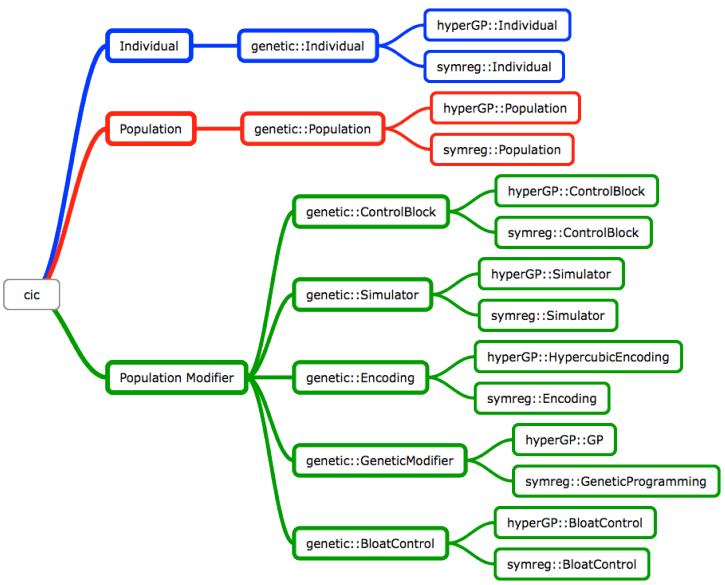



Figure 6.1: *cic* types hierarchy with *symreg* and *hyperGP*

As it was mentioned, the actual implementation of the *cic* framework did not target only one genetic algorithm-based experiment. Since the HyperGP experiment itself was not trivial to program and test, another simpler experiment was used as a proof-of-concept for the framework to help debug it before HyperGP would run in it.

A generic *symbolic regression* experiment was used first. The biggest advantage of this approach was that about a half of the codebase was shared between symbolic regression and HyperGP.

### 6.2.1 Experiment: Symbolic Regression - cic::genetic::symreg

The goal of symbolic regression is finding a *function* that best satisfies certain constraints. Genetic, population-based approach was used here in the following matter (also depicted in Figure 6.2):

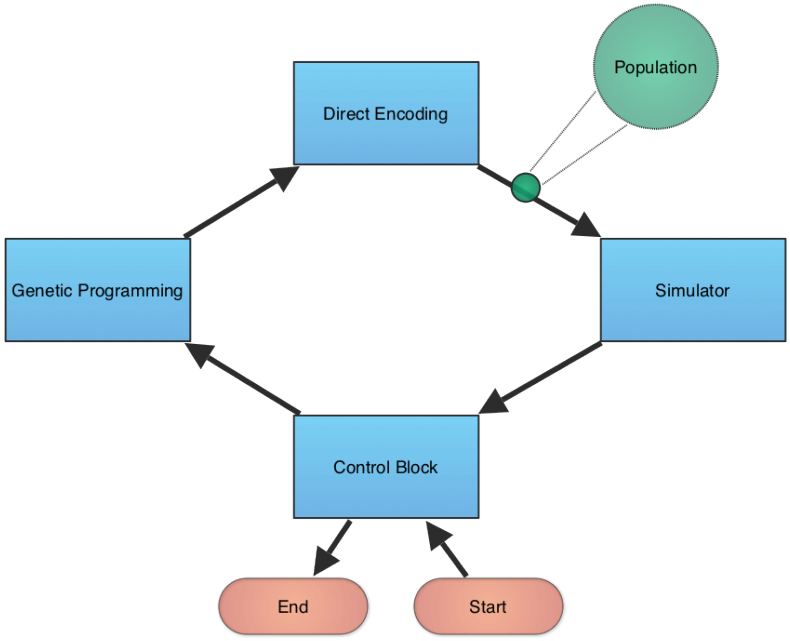



Figure 6.2: *symreg* workings in *cic*

In our case first a function was selected and $n$ equidistant points were chosen in a range $r_{min}$, $r_{max}$. These worked as a reference set of points for the simulator. Each evaluated function was sampled in the same matter and the sum of absolute differences between it and the reference of all points was computed. The negative value of that sum was used as the fitness value (since we used the higher-fitness-is-better approach).

If $x$ is a vector of points computed by a tested function and $r$ is the vector of points generated by our reference function, then fitness of the $i$-th individual $f_i$ was computed as

$$e_i = \sum_{k=1}^{M} |x_k - r_k| \tag{6.1}$$

$$f_i = -e_i \tag{6.2}$$

where $f_i$ is the fitness of the $i$-th individual.

The *symreg* implementation of the symbolic regression experiment was very helpful with debugging of the framework. The framework ran only *symreg* for a couple of weeks during the

development and still works as a benchmark experiment. During that time, support for multithreaded computing was added (with the use of GCD, Section 6.1.3), MATLAB interface was developed (Section 6.4.2) and XML serializer/parser was implemented (Section 6.4.1).

### 6.2.2 Experiment: HyperGP - cic::genetic::hyperGP

The implementation *hyperGP* of the HyperGP algorithm needed a couple of new features in addition to what we developed for *symreg*. The main differences were:

- **Phenotype**: recurrent neural network (RNN) instead of a tree
- **Hypercube Encoding**: way to translate a genotype (function) to a phenotype (RNN)
- **Simulator**: interface between *hyperGP* and *sim*
- **Simulator**: fitness was computed from the translation vector of the robot
- **Bloat Control**: added to the cycle

Figure 6.3 shows the logical setup of HyperGP blocks in *cic*.

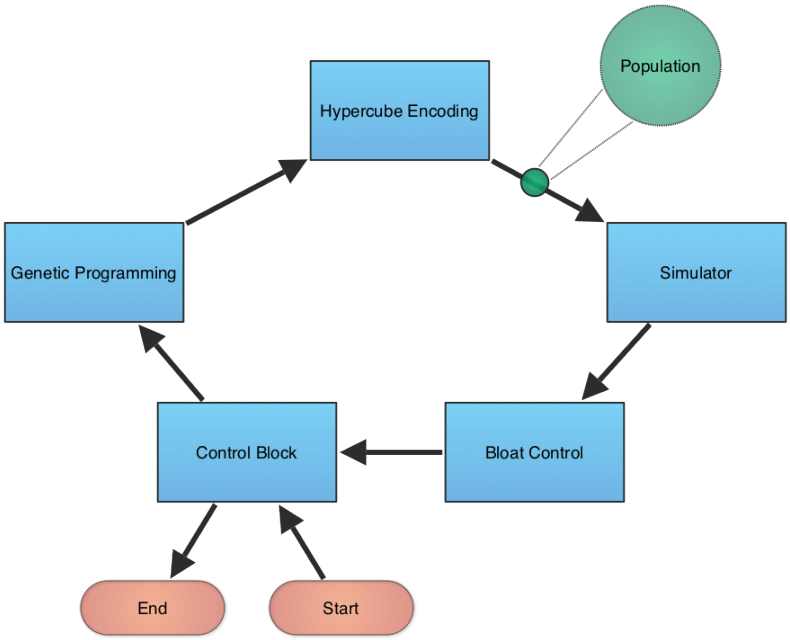



Figure 6.3: HyperGP workings in *cic*

## 6.3 *cic* featured classes

The original goal of the *cic* framework implementation was to use as little 3rd party code as possible. Obviously, the less dependencies that the user has to install in advance, the

better. In the end, several common libraries (Section 6.4) were used for certain purposes, but the actual working of the algorithm does not depend on any of them (the libraries are mainly used as I/O tools).

The implementation of the core pieces is discussed in the rest of this chapter.

### 6.3.1 cic::genetic::Individual

Since all the algorithmic work is achieved by *population modifiers*, in *cic* the Individual class only works as data storage of the particular gene. The genotype, phenotype, fitness value are stored directly in the Individual (Figure 6.4). Optionally, the experiment can use Individual's pointer to its parent - which is taken care of by genetic operators. One more key-value storage is contained in every Individual. Population modifiers can use that storage to assign attributes to the Individual (e.g. Bloat Control needs to mark Individuals illegal in certain cases).

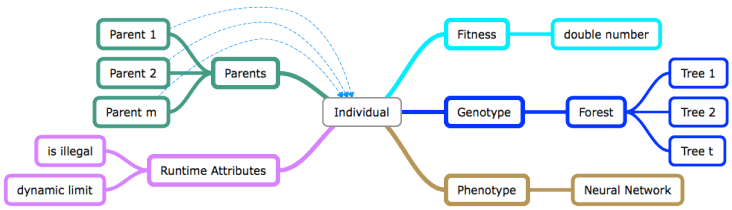



Figure 6.4: cic::Individual

### 6.3.2 cic::genetic::Population

The Population class is a container of Individuals. Support of iterators has been added for easier enumeration of Individuals. An integer marking the Population's iteration number works as its identifier (Figure 6.5). Individuals are stored by making a copy of their shared pointer. This way, when the last owner deletes the pointer, the Individual gets deleted from memory automatically. A copy of the Population is exported to a XML file during and at the end of each experiment and can be again loaded as the starting point for a new experiment.

### 6.3.3 cic::tree::Tree

The genotype in the HyperGP experiment was a multidimensional (hypercubic) function. Functions can be easily digitally represented in the form of a binary tree. In order to increase the speed of the tree result computation, decision was made to save more information into the tree nodes at the cost of memory consumption. A proprietary implementation was needed and one was proposed and implemented.

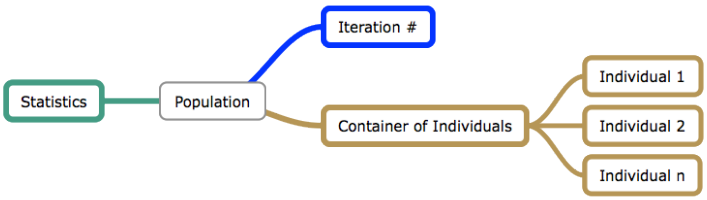



Figure 6.5: cic::Population

#### 6.3.3.1 Node

The tree is an expression tree. Node can be either a function (blue) or a terminal (red) as shown in Figure 6.6. Functions can have one or two arguments which are represented by child nodes. Terminals only hold information about the variable or the constant they carry. An example of such an organization can be seen in Figure 6.6. The resulting expression of that tree is

$$f(x, y) = (x + 0.57)sin(cos(y)) \tag{6.3}$$

With this pattern, each node represents the subtree underneath it. The information about the subtree node count and depth are accessible right away, obliterating the need to compute it again every time such information is requested. Especially in cases of very deep trees, such computations could add very expensive milliseconds to the computation time, since both the depth and node count computation has an exponential complexity.

When subtrees are exchanged between two trees, only a minor update of *registering* the subtree into its new tree propagates that information to the root node. These actions have linear complexity, thus once setup, our tree implementation should be independent of the absolute tree depth - and computational requirements should scale linearly with this parameter.

#### 6.3.3.2 Tree

Understanding the above mentioned design pattern of *informed* nodes, the tree object only works as a public interface and a wrapper for the root node. Hiding the inside workings, user of the *cic::tree::Tree* class is only presented with sensible information getters (total tree depth, total tree node count, etc.).

Figure 6.7 shows what extra information is saved in the *Tree* class.

### 6.3.4 Tree Generator

Another crucial problem to tackle was the way of creating the initial individuals. Individuals were represented by an expression tree (genotype), thus redirecting the problem of

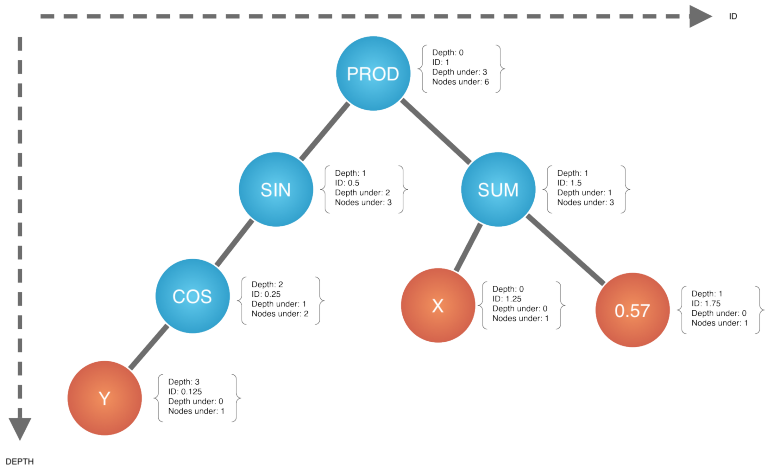



Figure 6.6: Example nodes connected into a tree

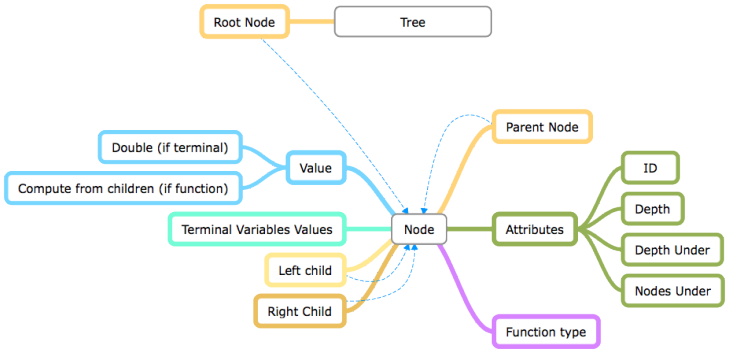



Figure 6.7: Tree types hierarchy

individual generation to tree generation. The random tree generation is important in several parts of the experiment:

- initial trees of the initial population
- subtree generation for the mutation operator
- creation of new individuals after some get removed from the population (e.g. bloat control)

There are several known and used methods, which are fairly simple, such as Grow, Full and Ramped Half-and-Half [16]. In addition, another one, called *PTC1* [22] was implemented to be able to control the generated trees' parameters more precisely.

For the scope of the following methods, $A$ is the set of all available nodes, $T$ the set of all available terminal nodes and $F$ the set of all the function nodes. The maximum depth is denoted $d_{max}$.

#### 6.3.4.1 Grow

Grow is one of the most efficient and used tree generation methods. The only thing Grow guarantees about the generated tree set is that all the trees will have a depth between 0 and $d_{max}$.

Implemented as a recursive algorithm, Grow chooses to use a *terminal* node when reaching the maximum depth $d_{max}$ and a *terminal* or *function* node otherwise. Below is the pseudo-code of Grow.

```
1: function GROW(d_max)
2:     Node n ← 0
3:     if d_max > 1 then
4:         n ← randomNode(A)
5:     else
6:         n ← randomNode(T)
7:     end if
8:     for all children(n) do
9:         child ← Grow(d_max − 1)
10:    end for
11:    return n
12: end function
```

#### 6.3.4.2 Full

As opposed to Grow, Full can guarantee the precise depth of all generated trees - and that is the maximum possible depth $d_{max}$. Full achieves that by choosing a *terminal* node when reaching the maximum depth $d_{max}$ and a *function* node otherwise.

Below is the pseudo-code for Full. Note the only difference to Grow in line 4, where Full chooses from the set of just the *function* nodes ($F$), but Grow takes any type of node ($A$).

```
1: function GROW(d_max)
2:     Node n ← 0
3:     if d_max > 1 then
4:         n ← randomNode(F)
5:     else
6:         n ← randomNode(T)
7:     end if
8:     for all children(n) do
9:         child ← Grow(d_max − 1)
```

```
    end for
    return n
end function
```

#### 6.3.4.3 Ramped Half-and-Half

Grow is great for creating a population diverse in depth, whereas Full guarantees that all trees will be as full as possible. However, neither of these methods works perfectly for all applications, which is why a combination of these two, called *Ramped Half-and-Half* has been the most preferable. It uses Grow and Full as described above in the following matter: half of the population is created with Grow; the other half is created by applying Full with a small maximum depth (0, 1, 2 or any other) gradually ramping up to $d_{max}$. Equal number (if possible) of the half population devoted to Full gets created with different maximum depths applied to Full.

This particular method enables the population to be diverse both in depth and in used nodes. Ramped Half-and-Half's ratio of effectiveness to simplicity makes it a great candidate for our application.

#### 6.3.4.4 PTC1

Trying to expand the theoretical boundaries of our tree generator, one more generation method was implemented. Described in [22], PTC1 (*Probabilistic Tree-Creation*) provides much more control over the generated tree set. Being able to guarantee the average tree size, maximum depth and even the occurrence probability of each node provides us with much more power.

The gist of PTC1 is that it is a modified version of the Grow generation method, mentioned above. The input data to PTC1 is

- expected (average) tree size $E_{tree}$
- arity $b_f$ for each function node $f \in F$
- probability $q_f$ for each function node $f \in F$
- probability $q_t$ for each terminal node $t \in T$
- maximum depth $d_{max}$

The algorithm first computes $p$, the probability of choosing a *function* node. This probability is constant for the whole run, so it needs to be computed only once before the start of the generation.

$$p = \frac{1 - \frac{1}{E_{tree}}}{\sum_{f \in F} q_f b_n} \tag{6.4}$$

Once $p$ is computed, the tree generation runs as follows

```
1: Tree ← PTC1(0)
2: function PTC1(d)
3:     if d == d_max then
4:         return terminal from T (by q_t probabilities)
5:     else
6:         if chose f from A with probability p then
7:             choose f ∈ F (by q_f probabilities)
8:             for all arguments of f do argument ← PTC1(d + 1)
9:             end for
10:            return f
11:        else
12:            return terminal from T (by q_t probabilities)
13:        end if
14:    end if
15: end function
```

### 6.3.5 cic::nn::Network

In the HyperGP algorithm, the phenotype of each individual is a *neural network*. This neural network is the manifestation of the genotype (function), since the synaptic weights between neurons are computed by the genotype's function. The problem faced with a regular neural network is the lack of memory-like behavior. In the HyperGP simulator, a concept of time needs to be present in the genotype. To solve this issue, a *recurrent* neural network was used. Recurrent types can simulate discrete time systems through synapses not only going from input to hidden (1) layer and hidden to output (2), but also hidden to hidden (3), output to output (4) and even output to hidden (5). And all synapses not going in the forward direction (types 3, 4, 5) need to be evaluated with one time step delay (Figure 6.8).

In other words, the network will hold internal values from the past and take them into account when computing the future outputs. This is exactly what is needed to avoid bringing time as an extra input into the network. In our particular implementation, every neuron saves into memory its output value and the current time. When the network outputs are being computed and this information is queried, the neuron looks into its memory first and then if it does not find the value for the current time, just computes it and saves it again. This way, we - once again - sacrifice a piece of memory for faster evaluation.

The spatial setup of the network needs to conform to the robot spatial architecture (as explained in Section 3.3). An example of such a network can be seen in Figure 6.9. On the other hand, neural networks are generally approached from a layer-focused point of view (Figure 6.10). The layer approach also makes clearer why some synapses transfer signal immediately (forward going) and some need to be one time step delayed (all other).

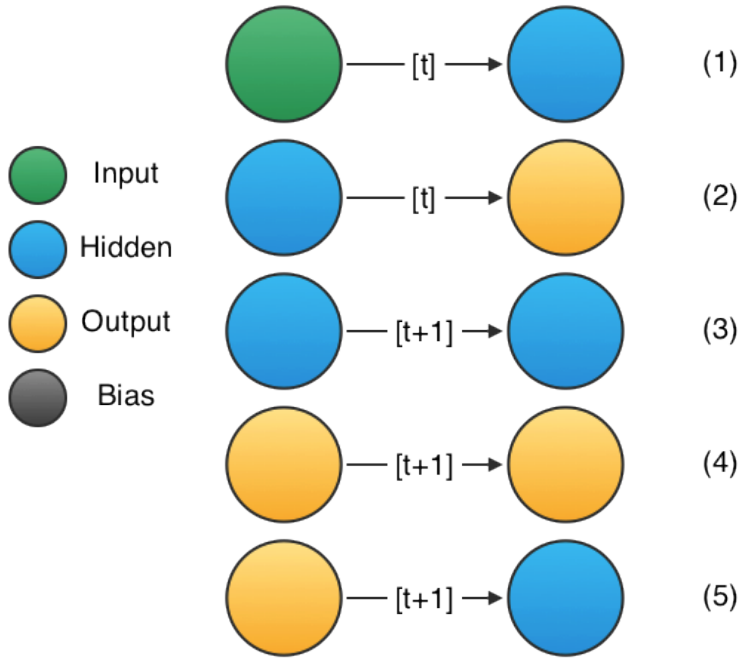



Figure 6.8: Neural network - synapsis delay by type

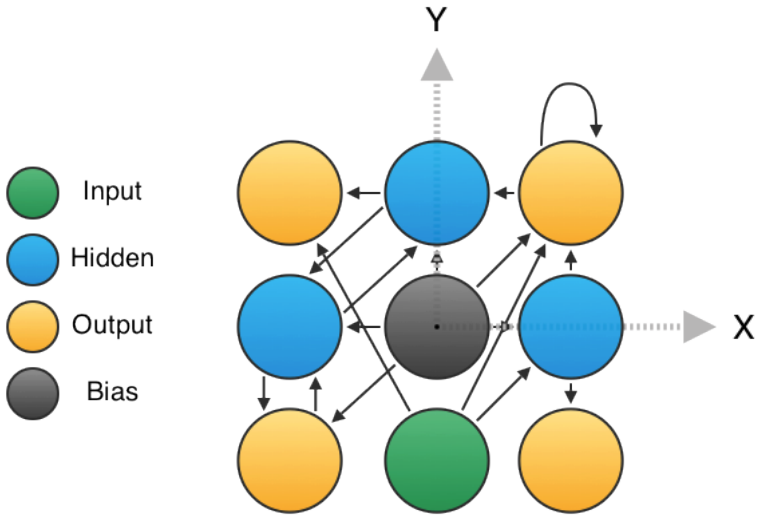



Figure 6.9: Recurrent neural network example - spacial view

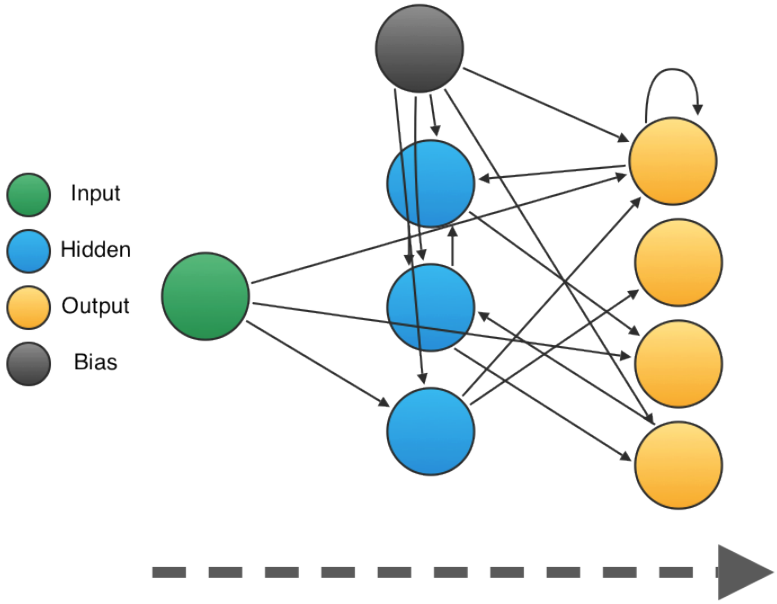



Figure 6.10: Recurrent neural network example - layer view

## 6.4 Tools and libraries

There was no need to re-implement certain tools for our needs, such as the robotic simulator and a simple plotting tool. Several common libraries and tools were used for those purposes.

### 6.4.1 libxml2

Any computations that take place in the *cic* program are immediately lost with the termination of the program. That is the reason why a decent way of saving results, individuals and settings to a permanent storage was needed. One of the most popular choices was XML (Extensible Markup Language) [33, 25]. The great advantage of saving data to XML, instead of a binary file, for example, is that it is human readable. This way, even after the XML has been exported from the program to the hard drive, we can read and modify the file by hand. These modifications do not corrupt the file content, meaning it can be again loaded into the program and used as a starting point for further experiments.

In the search for a simple XML C++ parser library the winner ended up being *libxml2*, because it is very simple, robust and already present on every Mac (thus eliminating the need to install extra software) [35].

### 6.4.2 MATLAB

Average and maximum fitness, tree depth, size etc. are all the properties developed during the runtime of the experiment and all this data is most helpful when seen in a plot of

some sort. The MATLAB libraries, distributed with every copy of the MATLAB app seemed appropriate for several reasons. For one, once the data is out of the experiment and in a MATLAB file, further analysis can take place independently on the actual experiment. For another, MATLAB libraries provide a simple way of opening and using a MATLAB instance on the background, invoked and controller from C++ code.

The MATLAB integration in *cic* is very crude at its current state. All data is only copied into a MATLAB instance, saved to a **.mat** file and optionally plotted right away for the experimenter to see. Some simple inter-experiment data analysis is done by extra MALTAB scripts that are distributed with the *cic* codebase.

### 6.4.3 Sim

The intention from the start was to use the robotic simulator developed by D. Fiser and V. Vonasek at FEE, CTU in Prague for the SYMBRION/REPLICATOR projects [31]. The main advantages over the other Robot 3D simulator are [2]

- lightweight
- can perform faster-than-real-time simulations
- supports running of several instances in several threads

The simulator setup consists of subclassing the Sim class and setting up the simulation world parameters, creating the arena and creating the actual robot. Then another object is assigned as the controller of the robot and the simulator queries the controller for updates of the desired rotations of the robot legs regularly. In the case of HyperGP, a Neural Controller was created to take care of translating the outputs of the neural network (substrate - mentioned in Section 3.3) into desired rotation angles of the robot joints.

### 6.4.4 Other tools

Other software tools were crucial during the implementation phase. One was the package manager for Mac called *homebrew* [12]. Homebrew was very useful during installation of libraries and tools. Also, other than C++, Python was also used for automation of file sorting (each experiment output 6 files and we ran hundreds of experiments).

# Chapter 7

# Testing

Rigorous experiments are crucial to every algorithm development. In order to either confirm or dismiss the efficiency of the HyperGP algorithm, we needed to prepare tests which would cover as much parameter space as possible and inform us about HyperGP's strengths and weaknesses.

Fortunately, as part of the *cic* framework, a powerful experiment I/O and result recording was implemented. This way, after each test run was over, the framework exported the data in the *xml* format (settings, population with all individuals) and the statistics in the *mat* format. This way, we wrote scripts to account for any number of repeating experiments and statistically process the data in a matter of seconds.

This chapter first describes the setup of the experiments, the types of robots used and all the different tested parameters. Then it proceeds to the experimental data recorded during our testing phase.

Rendered videos of selected developed robots are present on the disclosed disk as well as on the website of this project [11].

## 7.1 Experimental setup

### 7.1.1 Tested robot topologies

For the proof-of-concept testing, we created three types of robots. The goal was to test several robot types, the way they are assembled, whether extra legs affect fitness and so on. The types are

- Robot $R0$, 5 x 5 cubes, $x$-axis movement, Figure 4.2
- Type $R1$, 7 x 7 cubes, $y$-axis movement, Figure 7.1
- Type $R2$, 7 x 5 cubes, $y$-axis movement, Figure 7.2

### 7.1.2 Fitness

The search for the perfect fitness function for each robot was not trivial. We tried exponential functions dependent on the distance traveled, mentioned in [9] and very sophisticated measures like this. However, the added complexity did not bring any improvements, so we used a very simple equation instead.

Each robot has a preferred axis of movement, so we used the distance traveled along that axis as the base value of our fitness value. In addition, we also wanted to encourage the robots to get their bodies up in the air, rather than crawl on the ground. And we were mainly interested in the *locomotion* part of the simulation. Inspired by [7], we used the same tweak where instead of measuring the traveled distance from the center of the arena $\vec{x} = \vec{0}$, we wait 2 seconds and mark the robot's position as the starting point. Robots tend to behave differently in the first 2 seconds of the simulation (get-up procedures) and this enabled us to filter them out efficiently. Our delayed-start position is marked $\vec{s} = (s_x, s_y, s_z)$. At the end of the simulation, we marked robot's position $\vec{t} = (t_x, t_y, t_z)$. The position of a robot is defined as the position of its center cube. If $r$ is the evaluated robot, $p$ the preferred axis of movement of the robot and $f(r)$ the fitness function, the following form was used

$$f(r) = |t_p - s_p| + (t_z - s_z) \tag{7.1}$$

So the sum of the distance traveled in robot's preferred direction and the difference in elevation was recorded as fitness. Though very simple, it proved to be sufficient for our task. It makes sense, because we used *tournament selection* in the genetic programming block. Tournament selection only takes into account which fitness is higher or lower. If we used some fitness-proportional selection method, such as *Roulette selection*, our fitness function would need to be more sophisticated in order to produce good results.

## 7.2 Experimental results

Each experiment was run 10 times and the results presented here are the mean values of all the experiments. We will be looking at several traits of the experiments. Namely at the number of trees in a genotype, the effect of sample time on performance, whether robots perform better with four or six legs and last but not least, which robot topology performed best.

### 7.2.1 Genotype size: 1 vs. 4 trees

The reason of generalizing the genotype from a tree to a forest is explained in Section 7.3.1. Here we look at how it affected the fitness and depth of the resulting individuals.

The comparison of robots $R1$ and $R2$ with their 1-tree versions versus their 4-tree versions in Figure 7.4 shows the following. The extra number of trees did not have a positive effect on the maximum fitness (Figure 7.4a). What more, in both robots, their 4-tree versions were in fact inferior to their 1-tree versions. Also, their depth (sum of all genotype's trees

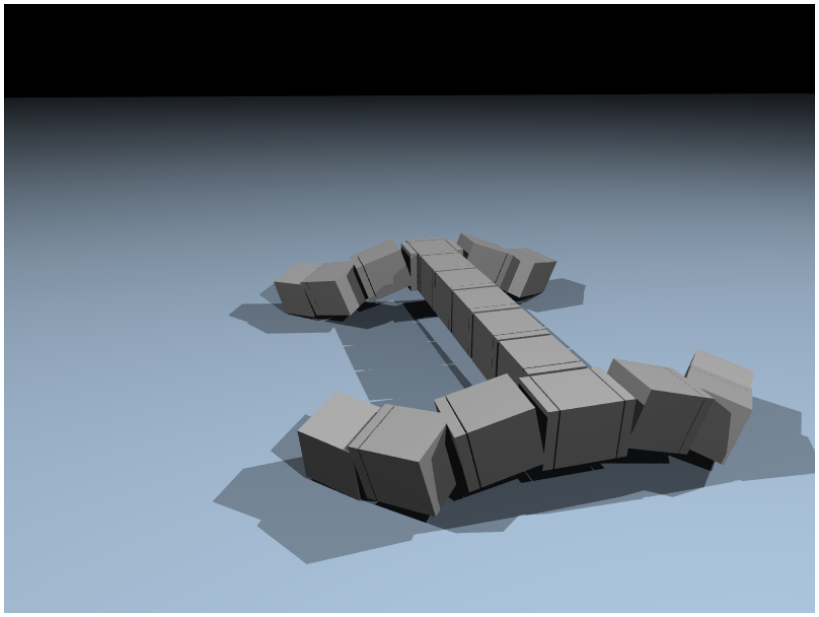


Figure 7.1: Robot $R1$

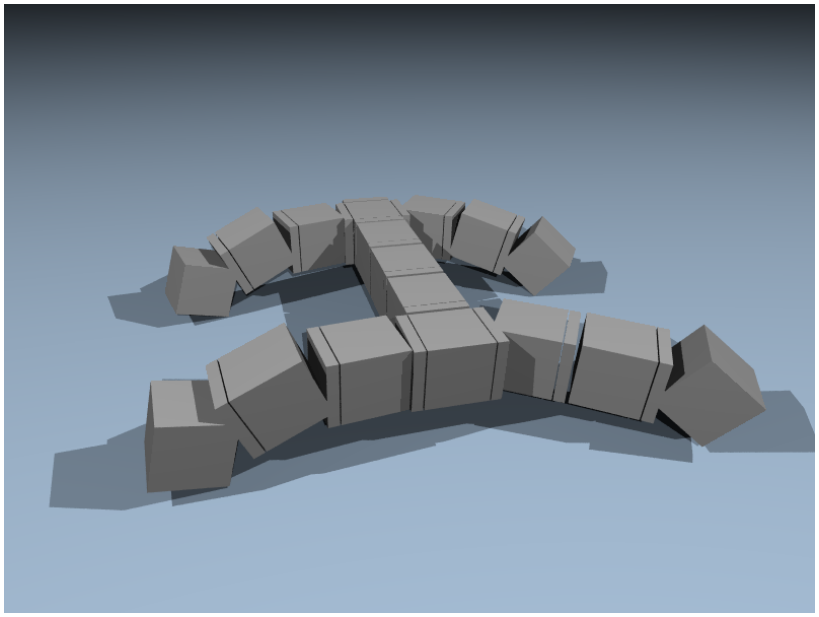


Figure 7.2: Robot $R2$

depths) is much greater, thus having a larger memory footprint (Figure 7.4b). Judging by our experimental results, we would not recommend using more than one tree in the genotype.

On the other hand, we can claim that more trees do not help the fitness only based on our

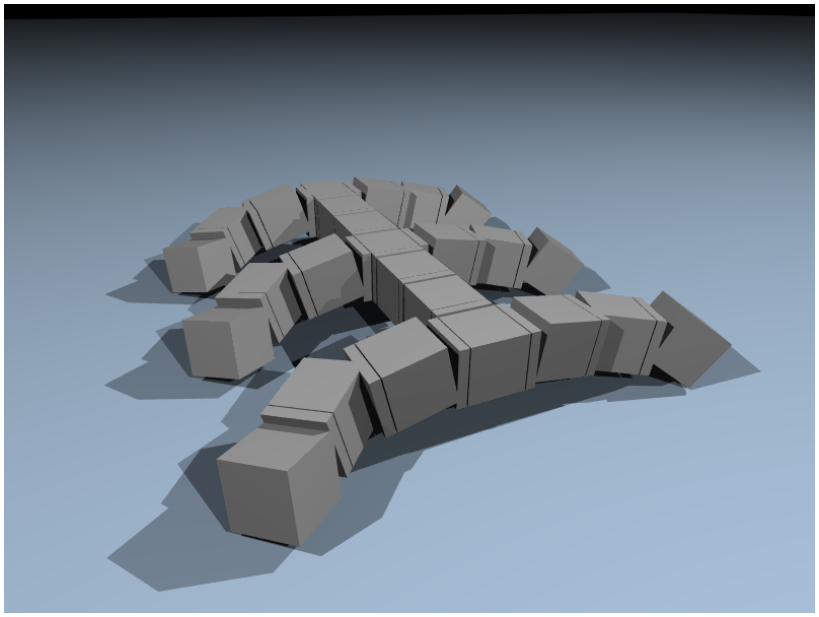
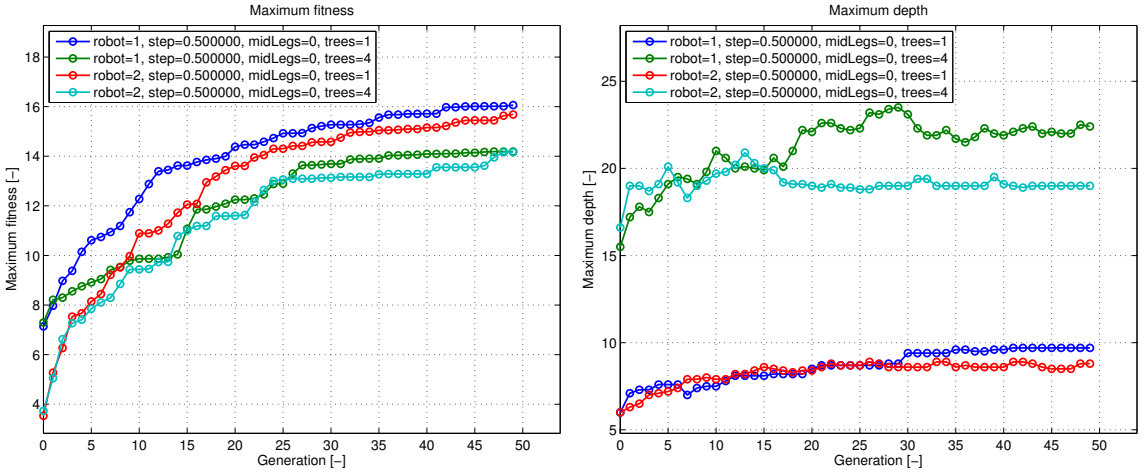


Figure 7.3: Robot $R1$ with 6 legs

presented experimental results. Our tests did not exceed 50 generations with populations of 50 individuals. This is a small subset of the usual experimental data available, which covers population behavior up to 300 generations. We will perform much longer-running experiments in the future, but the current time constraints prevented us from having them processed by this writing. Our claims are thus backed up only in the up-to 50 generations range.




(a) Maximum fitness (b) Maximum depth

Figure 7.4: Comparing genotypes with 1, respectively 4 trees

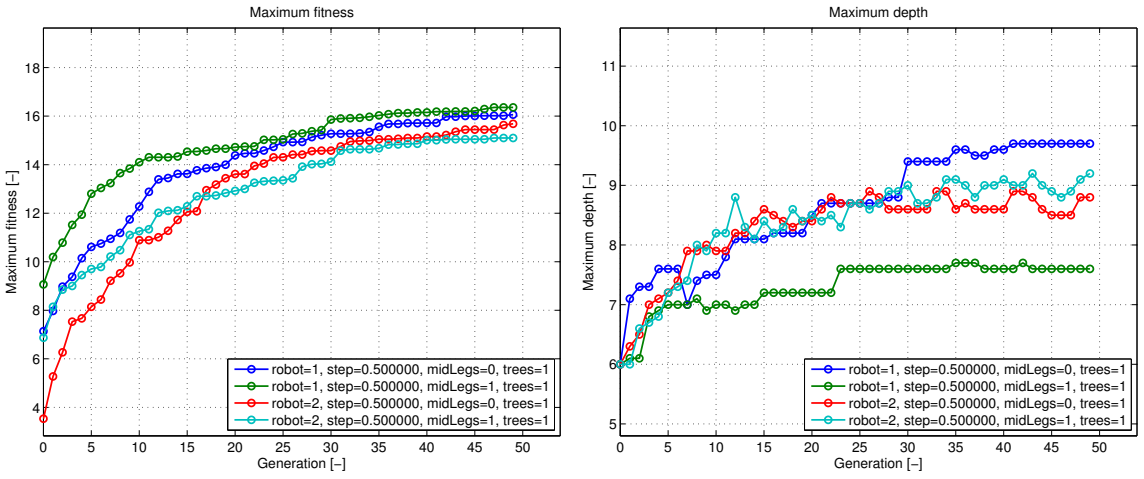
### 7.2.2 Number of legs: 4 vs. 6

Another probed parameter of the robots was the number of used legs. The robots $R1$ and $R2$ had their torso long enough that they could receive an extra pair of legs in the middle. An example is the robot $R1$ depicted with only 4 legs in Figure 7.1, but with the extra pair, having a total of 6 legs in Figure 7.3.

The gist was that the extra pair of legs might work as an assistant pair for the front and rear pairs. The 6-legged robots could theoretically develop a more complex motion pattern and solve the locomotion problem more efficiently.

The results can be seen in Figure 7.5 ($midLegs = 0$ marks robots with 4 legs, $midLegs = 1$ marks robots with 6 legs). It seems that up to the 15th generation, both the $R1$ and $R2$ developed better with the extra pair of legs (Figure 7.4a). However, by the 20th generation, the 4-leg versions caught up to them and from then on, the fitness was very similar. Thus the extra pair of legs really did help the robot, especially in the beginning phase of roughly developed individuals.

When looking at the maximum depth parameter in Figure 7.4b, we see that the robot $R1$ was forced to develop significantly larger trees in the 4-leg version. This fact corresponds with the fitness, meaning that the lower the fitness, the larger trees are explored by genetic programming (with the help of bloat control, forcing the trees to grow gradually rather than randomly). Robot $R2$ had very similar results for both 4 and 6-leg versions. This might be caused by $R2$'s torso being only 5 cubes long as opposed to $R1$ that has 7 cubes across. The leg pairs are much closer in $R1$, enabling more frequent collisions between them - stripping the robot of its advantage. This would explain the similarity between the fitness of the two versions.




(a) Maximum fitness (b) Maximum depth

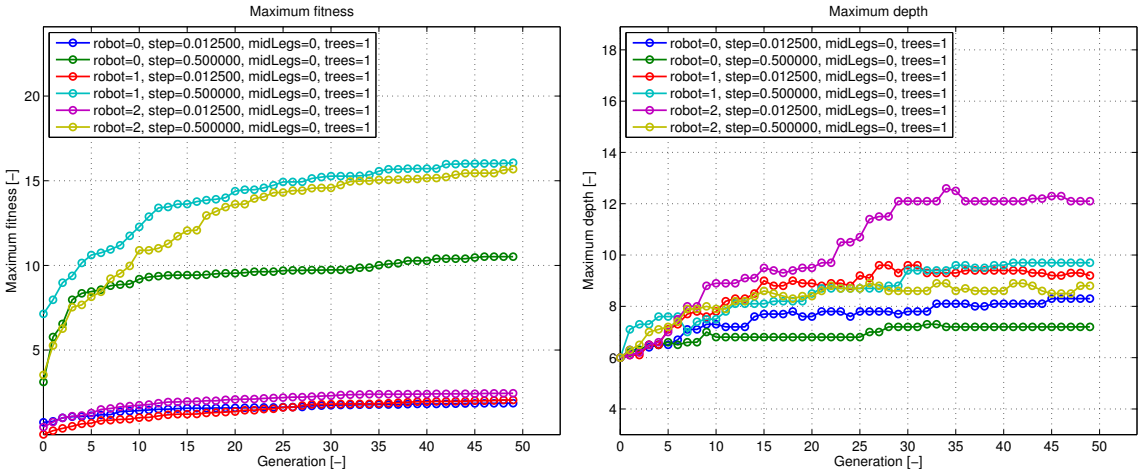
Figure 7.5: Comparing robots with 4, respectively 6 legs

### 7.2.3 Simulation sampling frequency

One underestimated issue came with the choice of the simulation sampling frequency (thus the length of one time step). The sample time was the time quantum of the simulator. In other words, how often the robot got chance to recalculate its outputs and send that change to the simulator. The neural networks, being discreet time-based, were very sensitive to this parameter since the output of the network at time $t$ depended on the state of the network at time $t-1$. The problems are closely described in Section 7.3.2. We will only look at the results at the moment.

The fitnesses and depths of the experimented robots are depicted in Figure 7.6. We compared two sample times: one being $0.5s$ (2 Hz) and the other $0.0125s$ (80 Hz). Here we really stumbled on something serious - robots with the *higher* refresh frequency performed drastically worse than those only being able to refresh their outputs twice per second (Figure 7.6a). The causes and implications of this are discussed later in length.

As can be seen in Figure 7.6b, the lousy fitness also caused the genetic programming to search for solutions in larger space - increasing the depth of the genotype. Here we can clearly see that genetic programming was trying to solve the problem the right way - looking into more complex space after it searched the simpler one. Unfortunately, not enough generations were given to the experiment yet. And even if it were, no guarantees are given that a decent solution would be found. This problem will be a subject of our future research.




(a) Maximum fitness

(b) Maximum depth

Figure 7.6: Comparing robots ran on sample time 0.5s, respectively 0.0125s

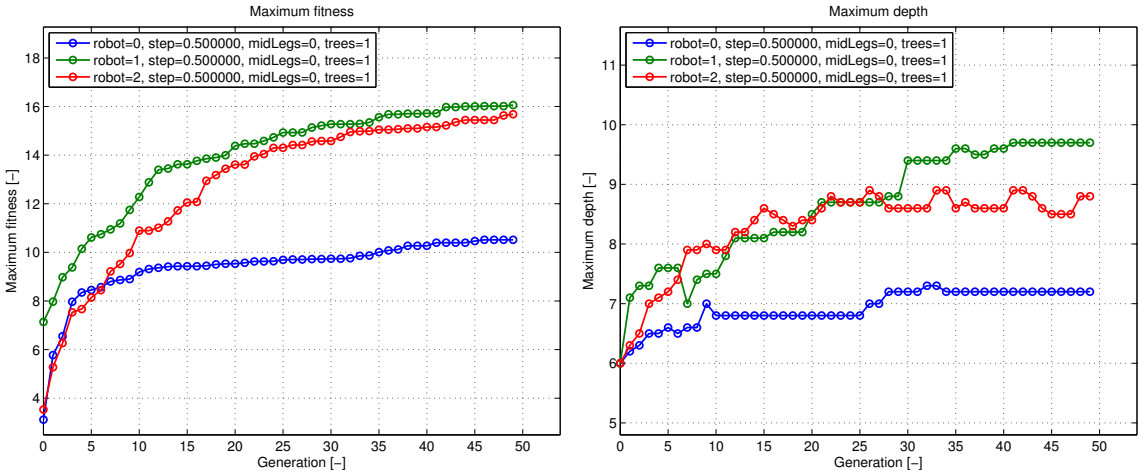
### 7.2.4 Robot topologies

The last comparison made with our experimental results is the one of the robot topology. We wanted to find out which of the predefined robots would perform the best. They each have a slightly different size and joint rotation axes.

We are using a right-handed Cartesian coordinate system, with the $y$ axis pointing into the screen. The legs of each robot are be represented by their joints' rotation axes. All the robots have a torso along the $y$ axis, legs pointing in the $x$ axis.

- $R0$ - torso: 5 cubes, leg: 2 cubes ($y$, $y$)
- $R1$ - torso: 7 cubes, leg: 3 cubes ($y$, $z$, $y$)
- $R2$ - torso: 5 cubes, leg: 3 cubes ($z$, $y$, $y$)

The robots all performed decently well, with $R0$ being obviously the worst one. It only had legs consisting of two cubes and moved in the direction of the $x$ axis (Figure 7.7a). However, it also kept the lowest maximum depth of all robots (Figure 7.7b), making it very efficient with the performance / depth ratio. The performance of $R1$ and $R2$ was again very similar, with $R1$ being the slight winner. It also required the largest trees for its genotype.




(a) Maximum fitness (b) Maximum depth

Figure 7.7: Comparing robot topologies: $R0$, $R1$ and $R2$

## 7.3 Issues encountered during testing

The version of HyperGP algorithm described so far has been implemented with the description of HyperNEAT in [32, 9] and Genetic Programming. No further knowledge about the shortcomings in implementing a Hyper-* algorithm was known at the time. However, after the main part of the HyperGP algorithm in the *cic* framework was done, a couple of issues surfaced and needed to be taken care of. The problems are described in the following section.

### 7.3.1 Genotype: forest instead of a tree

The issue of insufficient complexity space for the genotype seemed to be a problem. In theory, one function (genotype in our case), with the neuron coordinates as inputs (together

with certain constants) could only hardly encode the whole complexity of a neural network to produce sensible outputs. Other sources also used more than one function to generate neural network synaptic weights [6] with HyperGP. In addition, the original CPPN neural network, proposed in the original HyperNEAT [32], has multiple outputs where each is used for different type of synaptic weights. However, our CPPF (function) only has one output, forcing the function to encode the weight of all the different synapses into one structure. CPPN might theoretically dedicate parts of the network to certain synapses which it shows in the dedicated output. CPPF does not possess that option. This fact led us to try to generalize the genotype to not take only a single tree, but use a forest (a vector of trees) instead and simulate the expanded storage and computational ability of a neural network in multiple trees.

Modifications of the genetic operators (mutation, crossover) were necessary in order to make them work efficiently with this change. The simplest way seemed to use the forest only as a wrapper and container for the trees, but applying a genetic operator would only mean to apply the operator to all the contained trees. Thus, ordered collection of trees was needed as the storage for the trees. When mutation was applied to the forest, it was just applied to the first tree. A new instance of the operator would be applied to the second tree and so on. With crossover, the first trees in both the forests were crossed-over, then the second ones and so on. This way, the trees in the forest worked together to create the neural network (phenotype), but were in fact independent of each other during genetic modifications.

### 7.3.2 Neural network outputs

#### 7.3.2.1 High-frequency oscillations

After initial tests were undertaken, desired results were far from being reached. It seemed that certain individuals were receiving a high fitness value in the simulator, but were not really high-quality under our terms. Some of these individuals, when observed in the visual mode of the simulator, achieved relocation of their bodies not by walking, strictly speaking, but rather by *shaking* their joints. These robots usually did not elevate their body from the ground, but just quickly moved the joints up and down. These high-frequency oscillations dominated the first, undeveloped populations in their early stage. Unfortunately, their success meant the gradual removal of all other solutions from the population set. However, the progress of these individuals seldom ended after the 10th generation, meaning that even if simulation was run for 100 generations, no more improvements were discovered - thus ruining the experiment.

This particular issue was difficult to find. The fast movements could be observed in the visual simulations, but reasoning went in a way that the high-frequency oscillations were just a feature of low-fitness individuals and that these solutions would disappear from the population naturally. After spending some time on improving the HyperGP implementation, improvements did not come, which forced us to add some other means of introspection into the *cic* framework.

The MATLAB integration came in useful once again. It enabled us to send the output data of the neural network right into the MATLAB instance to get it plotted out. After seeing a couple of plots, such as the one in Figure 7.8, we recognized the issue.

Clearly we needed a way to slow down these radical changes in every consecutive step of the neural output. Decision was made to contact Jeff Clune, the co-author of [9, 36, 18]. He advised us to look into [36, 18], when encountered the exact same problem, providing us with a hint that this might have been solved before. Eventually, solution recorded in [18] was implemented. In this case, a down-sampling was used by averaging consecutive $n$ steps. Meaning if the neural outputs were computed with a frequency of 100 Hz and we used 4 averaging steps, the corrected output would have a frequency of 25 Hz. That enabled us to get from original outputs shown in Figure 7.8 to somehow corrected ones in Figure 7.9 or even more in Figure 7.10.

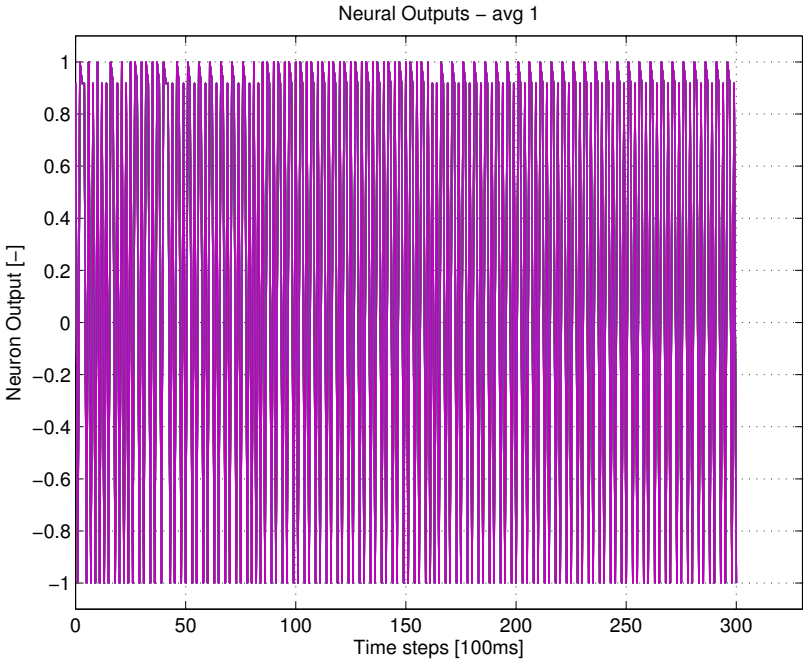



Figure 7.8: Neural network outputs: High frequency oscillations - original (no averaging)

However, even with this tweak, we could not achieve significant increase in fitness. One possibility is that due to the longer time requirement for longer experiments (days), we did not run the experiment for long enough time to see the difference. Additional experiments will be performed and presented if any notable improvements come. The plan is to also implement the punishment of high-frequency oscillating individuals by decreasing their fitness. Unfortunately, we did not have time to implement that in the original version.

One more possible solution of this problem would be to change the type of neurons. Right now, with the classic ANN, signal inputs are added and applied to an activation function (hyperbolic tangent in our case). Meaning that output values can change drastically in every

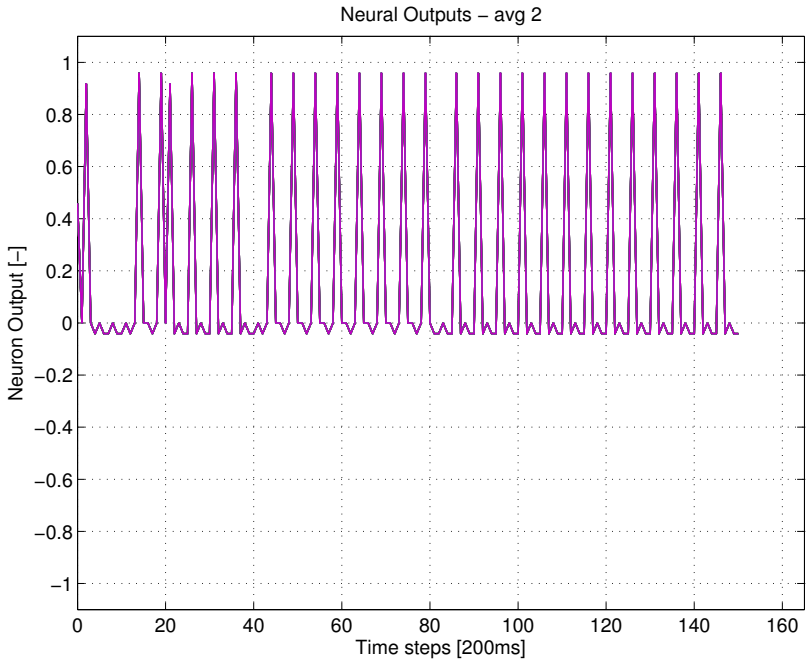



Figure 7.9: Neural network outputs: High frequency oscillations - averaging 2 consecutive samples

time step. However, for simulating real-life objects, such as robot legs, an *integrating neuron* could be more efficient. Real-life objects cannot move infinitely fast, they only apply force and gradually change their position. With an integrating neuron, the activation function would not provide an absolute value of the neuron for the current time step, but would rather provide a change in the current value. Thus the absolute output value of a neuron at time $t$ would be the sum of the absolute value at time $t-1$ and the relative value at time $t$.

$I$ represents the set of input synapses.

$$rel[t] = \tanh \sum_{i \in I} signal(i) \tag{7.2}$$

$$abs[t] = abs[t-1] + rel[t] \tag{7.3}$$

This tweak would forbid the neurons from outputting unreal updated positions for real-life objects. This, as well, is a subject of future research.

#### 7.3.2.2 Neuron output saturation

Another issue that can be seen in Figure 7.8 is the output saturation. Since the activation function of the hidden and output neurons is *hyperbolic tangent* (Figure 7.11), meaning that even very large inputs are transferred into outputs between -1 and 1. However, the farther the inputs are from 0, the less difference on the input gets transferred to the output.

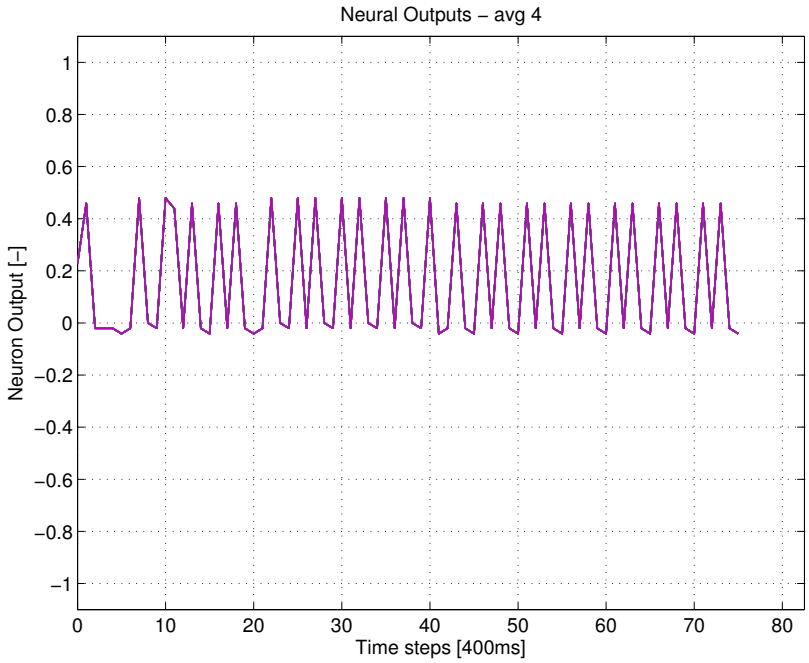



Figure 7.10: Neural network outputs: High frequency oscillations - averaging 4 consecutive samples

Figure 7.8 shows how when the values get very close to +1 and -1, respectively, showing huge inputs to the neurons. The neural network is best functional when it operates in the lower and middle range of the output (taken on a 0 to 1 basis). Our future efforts should focus on enforcing lower input signals. One way to do that is to reduce the number of input connections of each neuron, because during our testing, there were neural networks with 30 - 40 inputs, however better would be networks with neurons having less than 10 input connections. This will be a subject of future research.

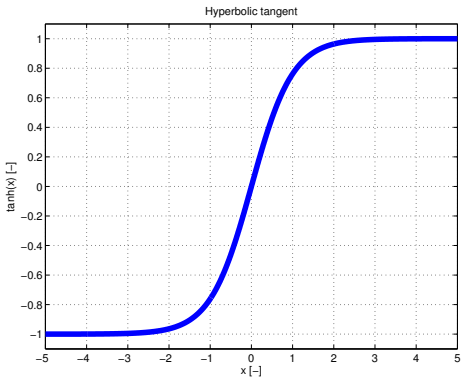



Figure 7.11: Hyperbolic tangent

# Chapter 8

# Conclusion

In an attempt to push robot locomotion methods further, a research has been performed to find a suitable approach to solving the problem. One method, called HyperNEAT seemed to possess most of the desired properties (symmetry exploitation, indirect encoding, etc.) which made us consider it. A modification, called HyperGP was used in our work instead. The hyper-encoding of HyperNEAT was preserved, but NEAT got replaced by genetic programming. This change greatly simplified the implementation and had previously yielded even better results than HyperNEAT [6].

The considerable insight supplied by our intense work on HyperGP provided us with a great deal of motivation to continue research in this direction. Due to time constraints, only a subset of all possible HyperGP configurations were run in the experiments. However that did not prevent HyperGP from successfully developing neural networks for robot locomotion control, even given the limited size of the population and number of generations.

We remain confident that with extra effort put into solving the mentioned shortcomings, we could bring great improvements of the HyperGP performance. Since both indirect encoding and genetic programming are inspired by biology, we believe there is some merit in putting more time into improving these methods for computer applications. This work was the first attempt to use HyperGP with robot locomotion and it partially succeeded. Thus the effort should not end here, rather on the contrary.

As a side effect of implementing the digital environment for the experiments, an algorithm-testing framework called *cic* was developed[1]. Written in modern C++ and using the best-of-breed compiler and language libraries, it is able to take a full advantage of the hardware it runs on. Running on any number of processor cores and having full control over the memory with C++, *cic* has a huge potential to perform much faster than alternative frameworks, which are based on high-level garbage-collecting languages, such as Java. Already showing how two types of experiments could easily run in the framework, additional improvements

[1]The source code to the *cic* framework, together with the *hyperGP* and *symreg* experiments is available at [10] and released under the Lesser GPL licence [1].

to *cic*'s codebase are in the pipeline.

In addition, *cic* has been offered to the scientific community as an open-source project, enabling anyone to use it for their experiments. The goal of making *cic* widely useful has been kept in our minds from the beginning, influencing the block-like design of the inside workings. Any alternative algorithm can be tested in the same environment by merely plugging in new blocks. We have a vision of what *cic* could become if guided correctly and we see many experimenters wanting to test their algorithms without the need to write thousands of lines of code. The MATLAB integration, xml serialization and more is built-in for anyone to use. We believe researchers should spend more time on improving their ideas and less on battling programming bugs.

Overall, this work discovered the strengths and weaknesses of HyperGP when applied to the robot locomotion problem. Many improvements have been suggested and will be tested in the future. Experiments have shown that HyperGP is suitable for developing robot locomotion solutions. In the future, the *cic* framework should enable us to improve the HyperGP algorithm and overcome the issues we encountered so far. Moving HyperGP forward should help us explore the true capabilities of computer optimization and find its new, truly useful applications.

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# Appendix A

# Important terms and abbreviations

**Genotype** genetic material of a robot, can always be decoded into one or more phenotypes

**Phenotype** expression (manifestation) of genotype in particular environment

**ANN** artificial neural network (or just neural network), mathematical model inspired by biological neural networks

**NEAT** Neuro-Evolution of Augmented Topologies, an algorithm for evolving neural networks

**HyperNEAT** NEAT algorithm employing hypercube encoding

**GP** genetic programming, a genetic algorithm using tree-like structures as the genotype

**HyperGP** GP employing hypercube encoding, first named in [6]

**EANT2** Evolutionary Acquisition of Neural Topologies, Version 2

**CPPN, CPPF** Compositional Pattern Producing Network / Function, the genotype of HyperNEAT / HyperGP

**GCD** Grand Central Dispatch - multithread control system for C++ developed by Apple, Inc.

**Clang/LLVM** C/C++/Objective-C compiler developed by Apple, Inc.

**PTC1** Probabilistic Tree-Creation, version 1, a tree-generation method with extra control over parameters of generated trees

# Appendix B

# Experimental setup

The detailed setup of experiments mentioned in Chapter 7. Each key has its desired state saved in an xml file with appendix _ *settings.xml*. Experiments used this file to set the desired state for the run. The *settings* file had several major categories, namely *GP* for genetic programming, *Simulator* for simulation-specific settings, *Control* for more implementation-specific data, *BloatControl* for setting up the Bloat Control block and *Neural* for global variables used in neural networks.

Table B.1: Experiment parameters

| **Parameter key** | **Used value(s)** | **Description** |
|---|---|---|
| *GP* | | |
| defaultFitness | 1.0 | The default fitness value of individuals before they are evaluated. |
| generatedPopulationSize | 50 | The number of individuals in each generation. |
| expectedGeneratedTreeSize | 30 | Tree generation parameter mentioned in Section 6.3.4.4. |
| maximumGeneratedTreeDepth | 6 | Tree generation parameter, maximum allowed depth of generated trees. |
| minimumGeneratedTreeDepth | 2 | Tree generation parameter, minimum allowed depth of generated trees. |
| terminalVariableCount | 4 | Number of tree variables in terminals. HyperGP used $[x_1, y_1, x_2, y_2]$. |
| functionCount | 5 | Number of tree functions in nodes. HyperGP used $[x + y, x * y, atan(x), sin(x), e^{-x^2}]$. |

| | | |
|---|---|---|
| functionProbabilities | all = 1.0 | Relative occurencies of functions in trees (for PTC1), Section 6.3.4.4. |
| functionProbabilities | all = 1.0 | Relative occurencies of functions in trees (for PTC1), Section 6.3.4.4. |
| terminalConstsCount | 2 | Number of extra terminals - constant numbers for tree generation. HyperGP used $[1.0, -1.0]$. |
| tournament_size | 5 | Number of individuals in Tournament selection used in GP. |
| selection_type | 0, 1 | GP selection type. 0: Tournament, 1: Roulette. |
| tournamentSelection | 1 | If two individuals have the same fitness, select the smaller one (use lexicographic parsimony pressure). |
| numberOfTreesInForestGenotype | 1, 4 | Described in detail in Section 7.3.1. |
| preventDuplicates | 1 | Generated trees are guaranteed to be unique. |
| *Simulator* | | |
| sample_from | 0.0 | Simulation start time. |
| sample_step | 0.5s, 0.0125s | The simulator time quantum. Marks re-calculation frequency of new outputs. Discussed in Section 7.2.3. |
| sample_to | 15.0 | Simulation stop time. |
| delayed_start | 2.0 | Mark the robot position with a delay, mentioned in Section 7.1.2. |
| robot_type | 0, 1, 2 | Robot type, as described in Section 7.1.1. |
| extraTimeStepDivider | 1, 20 | For cases with low refresh frequency, simulation still had to run faster to generate sensible results. This parameter marked how much faster simulation should be computed than the frequency of output recalculations. |

| | | |
|---|---|---|
| generatePovrayFiles | 0, 1 | Would be turned on if we wanted to generate files to render video from the simulation. |
| *Control* | | |
| maximumIterations | 50 | The maximum number of generations / iterations. |
| minimumFitness | 50 | The minimum fitness reached to stop the experiment prematurely. Never used with HyperGP. |
| populationXmlLoadFrom | $path of population xml$ | Input population into the experiment if we did not want a new population generated but continue with a developed one. |
| useMatlabPlot | 0, 1 | Turned on if we wanted to generate plots with statistics from the experiment. |
| isAutonomousExperiment | 0, 1 | Turned on to never show the simulator visually (which pauses the experiment). |
| *BloatControl* | | |
| useBloatControl | 1 | Whether bloat control should be used with the experiment. Discussed in Section 5.2. |
| bloatControlVariant | 0, 1, 2 | Version of Dynamics Limit bloat control. 0: simple, 1: heavy, 2: very heavy. |
| *Neural* | | |
| synopsisThreshold | 0.2 | Minimum synapsis absolute value to be present in the substrate (otherwise not added). |
| useMiddleLegs | 0, 1 | Whether robot should use its 4 or 6-leg variant. |
| sampleAverageCount | 1, 4 | Consecutive sample averaging - explained in Section 7.3.2.1. |

# Appendix C

# Attached CD content

The printed version of this work is accompanied by a CD.

**README.md** File describing the CD content.

**cic_2013may20.zip** Snapshot of the *cic* source code.

**dvorsky_bt.pdf** The text of the bachelor thesis.

**videos/** Folder containing several rendered videos of robots from the testing phase.