

Tuning the Blender Physics Engine via a Genetic Algorithm

A Thesis

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Abstract

Using a physics engine for robotic simulation provides fidelity with the added benefit of lower research costs, minimal space requirements, and even less time as the physical simulation can be run at faster than real-time speeds. However, physics engines have numerous parameters to tune such as friction coefficients, rigid-body constraints, body mass, gravitational acceleration, material elasticity, and collision shapes. Tuning these either programmatically or manually is a daunting task considering the multi-dimensional search space. Simulation fidelity is compromised as some parameters are perfected while others are now maladjusted. This produces a "reality gap" between the simulated environment and the physical environment. However, by using a genetic algorithm to fine tune the physics-engine parameters, the hypothesis is that the physics engine will produce a robot motion model more closely reassembling that of the real-world robot kinematics. Approaching this hypothesis involved three incremental stages. The first stage involved the development of a genetic algorithm that tuned the weights of a neural network where the neural network controlled a paddle in a "Pong"-like game. The second stage involved tuning the parameters of a 3D physics engine using the genetic algorithm developed in stage one and motion data collected on a real robot. Lastly, stage three tested the hypothesis of the thesis in a parameter-tuned, 3D physics-based environment where the motion of a simulated robot was compared to the motion of its real-life counterpart.

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Chapter 1

Introduction

The motivation for thesis was inspired by the creation of a 3D simulator titled BlenderSim. Using Blender¹, a 3D simulator was constructed for a human and robot multi-agent framework known as HRTeam². By using BlenderSim, HRTeam experiments could be conducted in a real-time 3D physics-based virtual environment. The goal of BlenderSim was to provide a robust and high-fidelity simulation such that experimental results produced in simulation would be reproducible in reality.

The physics engine employed by Blender, called Bullet³, proved to be troublesome while developing BlenderSim. The simulated robots would “jitter” erratically, fall through the floor, fly through the air, and/or fall apart even with no applied forces. Many days, turning into weeks, were lost trying to find the correct physics parameters by hand such that the simulation would produce high-fidelity results. In order to progress on the development of the BlenderSim 3D simulation environment, the idea of using the physics engine to model the motion of the robots was abandoned and a constant velocity motion model was used in its place.

¹Blender, released under the GNU General Public License, is a 3D creation suite allowing artists and programmers alike to produce immersive audio/visual works ranging from animation shorts to real-time 3D interactive games. Features include 3D modeling, 3D sculpting, texturing, sound editing, film editing, motion tracking, rigging, rendering, animation, physical simulation, a real-time 3D engine, and extensibility via the integrated Python API [1].

²The purpose of HRTeam is to explore human and robot teamwork interactions [2][3].

³Bullet is the real time physics engine used by Blender. Released under the zlib license, Bullet provides real time continuous collision detection and rigid body dynamics [web].

In the interim, the thesis problem was to tune the Blender physics engine via a genetic algorithm (GA) such that the physics engine would more closely model the motion of a real robot used in HRTeam experiments. This problem was approached in three incremental stages where each subsequent stage built off of the research and development done during the previous stage. Stage one involved the development a GA that tuned the weights of a neural network (NN) where the NN governed the movement of a paddle in a “Pong”-like game titled SimPL. Using the GA developed in stage one, stage two tuned the Blender physics engine as it iteratively compared the motion of a simulated robot to motion data collected on a real robot. Lastly, with the physics engine tuned in stage two, stage three compared the motion of a simulated robot versus a real robot by simulating a previously conducted HRTeam experiment.

1.1 Genetic Algorithms

Inspired by the theory of evolution, GAs attempt to solve problems that involve multidimensional state spaces [4][5]. GAs overcome problems experienced by other algorithms, such as hillclimbing, random search, or simulated annealing, by using a mixture of exploitation and exploration [5]. Running in a loop, a GA generates proposed solutions to a problem, evaluates each proposed solution’s value, and then capitalizes on what it learned to produce further potential solutions. Applications of GAs include numerical function optimization, image processing, combinatorial optimization, and civil engineering [5]. What problems are appropriate for GAs and why GAs work when they do are highly debated topics with no dominant answers [4]. With so many variations and parameters values possible, no two GA implementations are guaranteed to be identical, “...the number of variations that have been suggested is enormous. Probably everybody’s GA is unique!” [4].

The term *genetic algorithm* has both a strict and broad definition [6]. The strict definition of a genetic algorithm is the model formally presented by John Holland in 1975 [4]. More generally, the broad definition is, “any population-based model that uses selection and recombination operators to generate new sample points in a search space”[6]. *Genetic algorithm*, as it is used in this text, should be interpreted with the broad definition. Additional terms used require their own distinctions. *Gene* refers to a single encoded value, representative of a dimension inherent to some multidimensional problem. *Genes* are a collection of

encoded values that represent a state in some multivariate state space. A *Genome* specifies a data structure that contains genes and other types of data such as the genome's fitness. The *population* of a GA is made up of genomes. The terms *genotype* and *phenotype* are interconnected. A genotype is represented by the genes of a genome. By expressing or rather decoding a genotype, a phenotype is constructed. Specifically for SimPL, the genotype was an encoding of the NN's weights and the phenotype was the paddle's movement, as dictated by the NN. For the software developed in stage two (known as BBAutoTune), the genotype was an encoding of the physics engine's parameters and the phenotype was the simulated robot's collision bounds and motion, as modeled by the physics engine.

1.2 SimPL

Instead of diving right into the difficult problem targeted by the thesis, SimPL was an intermediate step to developing a GA capable of tuning a 3D physics engine. The problem for SimPL involved a NN and an on-screen paddle and ball. With the NN controlling the movement of the paddle, the GA developed for SimPL continuously tuned the weights of the NN. With each tuning of the weights, the NN became progressively better at controlling the paddle to hit the ball consistently. This simpler but still related problem provided a tractable context to conduct the needed background research of GAs. With the knowledge gained by solving the problem for SimPL, the thesis project was set up for success.

1.3 BBAutoTune

The core work of the thesis was BBAutoTune. Using the SimPL GA as a base, the goal of BBAutoTune was to tune the Blender physics engine via a GA such that the physics engine would closely model the motion of a real robot used in HRTeam experiments. With a few modifications, the SimPL GA was easily converted to handle the thesis problem. After collecting data on the motion of the real robot, BBAutoTune learned the necessary physics parameters needed to make the physics engine closely model the motion of the real robot. The motion of the real robot learned was its forward motion given a forward command.

1.4 BlenderSim

BlenderSim was a Blender based, 3D simulator developed for HRTeam during the summer of 2013. As a proof of concept of the thesis, BlenderSim (and specifically the physics engine itself) was revisited using the tuned parameters found by BBAutoTune. By rerunning a previously run HRTeam experiment, the motion of the simulated, physics-based robot was compared with the motion of the real robot.

Chapter 2

Genetic Algorithms

2.1 Overview

GAs have been applied to various problem domains since the works of John Holland, Hans-Paul Schwefel, Ingo Rechenberg, Lawrence Fogel, and John Koza [4][7]. There is no guarantee that any two GAs are the same but the central idea is to use a GA to find the globally optimal solution to some multivariate state space. All of the possible states in the state space make up a fitness landscape where one state is more optimal or fitter than another. The goal of the GA is to find the global maximum or minimum point on the fitness landscape. Intuitively, one can think of the fitness landscape as a foggy mountainousness terrain. As the GA progresses, more and more of this landscape is explored as the GA searches for the highest or maybe the lowest point in the terrain depending on the particular problem the GA has been tasked with. A GA may never find this global maxima or minima but may converge to some local optima depending on the GA's implementation and the fitness landscape. Coinciding with the exploration of the fitness landscape is the concept of mutation and crossover. Using both crossover and mutation, the GA can either expand or narrow its search of the fitness landscape.

All GAs have the concept of a population where each member in the population represents a point on the fitness landscape. Initially, a GA's population is usually randomized but could be seeded with some known-to-be *good* solutions by the GA's designer [8]. As the GA runs, new populations are formed from

previous populations where each population instance is known as a generation. When to stop the GA from producing new generations, known as termination, is up to the designer. Some common cases for termination include GA run time or population diversity (how different each population member is from one another) dropping below some threshold [4].

2.2 Genomes

Taking a page from nature, GAs have the concept of genomes (also called chromosomes in some texts). Genomes make up the GA's population at any given time and each represents a possible solution (or possible partial solution) to the problem the GA is attempting to solve or rather find an optimum solution to. Various data structures ranging from strings to classes can be used to construct a genome [4]. However, at the heart of every genome is its genes or vector of variables where each variable corresponds to a dimension in the multidimensional state space the GA is searching.

2.2.1 Genes

The genome as a whole represents a state in some multivariate state space inherent to the problem the GA is attempting to solve. Collectively, the genes of a genome describe a genotype while the structure (hardware and/or software) and behavior they produce is known as the phenotype. A genotype is evaluated by its phenotype's performance [5]. Imagine the genes of a genome being the blueprint of a motorcycle. This blueprint would be the genotype while the motorcycle built by following the blueprint would be the phenotype. If the goal was to produce the fastest motorcycle on earth, each blueprint's score would correlate to its motorcycle's maximum speed. Depending on the encoding the designer has chosen, each gene may be a bit, string, real number, natural number, or some other datum such as a function or s-expression in the case of genetic programming [9]. Furthermore, not all the genes have to be of the same type but collectively could be some mixed tuple of various data types [4].

2.2.1.1 Encoding

How the variables to a problem are encoded into genes is entirely problem dependent and up to the designer.

Typical encoding schemes include:

1. binary—where every gene is a bit or a string of bits;
2. real-coded—where the genes could be real numbers, integers, or character strings;
3. tree—where each gene is a node in a tree that when parsed, forms some kind of expression; and
4. permutation—where the genes are some possible order of a sequence [10].

There is no hard and fast rule governing the encoding of genes. Some have claimed that a binary encoding is best but this notion has been contested [4][11]. For problem domains with variables in \mathbb{R} , precision can be an issue when choosing a binary encoding. Another issue arises during the binary encoding of a finite set of discrete values when the set cardinality is not a power of two [11]. For example, image a variable that has five possible discrete values. To represent the five possible values, a three bit gene would be required. However, the gene configurations 101, 110, and 111 would be redundant or invalid and would need to be handled in the reproduction operators [6].

In [6], Holland's GA model is described as *the conical genetic algorithm*. Binary encoded/coded GAs (BCGA) that use recombination and selection follow Holland's model. A BCGA's search space is $\{0, 1\}^l$. For one-bit genes, each gene represents the act of turning a variable on or off for some multivariate state space. Another interpretation of one-bit genes is that the bit represents the presence or absence of a phenotype trait—an analogy being a phenotype having or not having eyes. However, each gene can be made up of more than bit. In this case, each gene represents the magnitude of some variable or a set of discrete values a variable can be.

Parallel to Holland's work, Hans-Paul Schwefel and Ingo Rechenberg developed the concept of *evolution strategy* (ES) in the 1960's [4]. Originally, ES only used mutation and its population size was one [7]. However, other recombination operators and population sizes were later considered as ES researched progressed [11]. ES employs a real-coded scheme where each population member (genome) contains two vectors of floating point values. The first vector of floats is a point in the search space and the second vector of floats

is a vector of standard deviations for use in the mutation operator [11]. For some population member, let $\vec{\kappa} = \langle \kappa_1, \kappa_2, \dots, \kappa_n \rangle$ be the vector of floats representing a point in the search space and let $\vec{\sigma} = \langle \sigma_1, \sigma_2, \dots, \sigma_n \rangle$ be the corresponding vector of standard deviations. Here, a mutant offspring's $\vec{\kappa}' = \vec{\kappa} + N(0, \vec{\sigma})$ and its $\vec{\sigma}' = \vec{\sigma}$ after mutation where $N(0, \vec{\sigma})$ is a vector of samples from a normal distribution with a mean of zero and a standard deviation $\sigma_i \in \vec{\sigma}$ [7]. This mutant offspring only becomes a population member (by replacing its parent) if it obtains a higher fitness than its parent [7]. One could think of this strategy as being a probing of the fitness landscape, where population members never move from their locations until their random probes discover more optimal locales.

Another paradigm of evolutionary computing, differentiated mainly by its encoding scheme, is genetic programming (GP). GP was developed by John Koza [7]. In 1990, Koza presented the concept in his paper, *Genetic Programming: A Paradigm for Genetically Breeding Populations of Computer Programs to Solve Problems*. Instead of searching for a solution to a problem directly, GP uses evolutionary tactics to search for a best-fit computer program capable of solving the problem at hand on its own. For example, in [9], Koza uses GP to evolve a computer program that dictates the behavior of an autonomous robot where the evolutionary goal was to get the robot to push a box from the center of a room to a wall. The main GP operator is crossover but mutation is used as well [7]. Each population member is a rooted tree, that when parsed, represents a hierarchical computer program. “Internal points of the tree correspond to functions (i.e. operations) and external points correspond to terminals (i.e. input data)” [9].

2.3 Evaluation

Evaluation of each phenotype yields the fitness of the corresponding genotype. Besides the encoding scheme, the fitness function is most critical aspect to get *right* when developing a GA. Fitness functions that are binary, noisy, computationally expensive, erratic, or discontinuous can produce poor results on behalf of a GA [5]. If at all possible, the fitness function should have a gradual gradient and a minimal number of local optima [5].

2.3.1 Criteria

The criteria for evaluation usually lends itself when one envisions what goals a perfect solution would meet. For certain problem domains, the criteria for evaluation may include constraints where a genome is penalized for some constraint violated [5]. Some implementations incorporate constraint adherence within the reproduction operators, so that it is not possible to produce an invalid phenotype.

2.3.2 Fitness Function

Constructing the right fitness function for the problem at hand is paramount when developing a GA. Based on the problem and the way in which the fitness function has been constructed, the GA's task usually boils down to one of either minimizing or maximizing the fitness function [4]. For problems with a unique solution where a genome is either completely correct or completely wrong with no leeway in between, one may want to include subgoals or partial credit for a genome that only provides a partial solution [5]. An analogy would be a professor giving partial credit for an answer on an exam.

Generally, the fitness function should always provide some new knowledge of how well one genome performed in comparison to others, where each fitness value outputted logically and intuitively corresponds to the problem [5]. If, after evaluating an entire population, all genomes have the same fitness value even though they all provide varying proposed solutions, then the GA has gained no new knowledge from which it can capitalize on as it constructs a new generation.

2.4 Operators

The tools of the GA are its operators. Many variants exist but the general operator categories are selection, elitism, crossover, and mutation. Crossover and mutation play off of another another by adding a delicate mix of exploitation versus exploration [5]. Elitism attempts to preserve the best solutions found so far when generating a new population. Mimicking natural selection, the selection operator provides each population member with some opportunity (however small) at passing its genes on to the next generation [5].

2.4.1 Selection

The general concept behind selection is to weight the probability of being selected for reproduction towards fitter genomes. Roulette wheel, rank, and tournament selection are some of the most well-known selection methods. All have been studied in depth, with each method having its own set of parameters. Some researchers have conjectured that by tweaking the parameters of each method, all can be constructed to have similar performance and thus no method is superior over another [5].

2.4.2 Elitism

Elitism is one of the more simple operators. After the entire population has been evaluated, the top e performers are directly copied into the new population during the reproduction cycle. In addition to being directly copied into the next generation, the e elites could also be crossed and/or mutated. Whether or not the elites are also considered during selection is up to the designer. Deciding on the size of e —in relation to the population size—becomes a delicate balance between premature convergence and the GA losing information about the best solutions found so far thereby forcing it to possibly run longer relearning what it already learned previously [12]. Note that e does not necessarily remain constant but could be varied per generation according to the number (or percentage) of population members that exceed a certain fitness threshold.

2.4.3 Crossover

Crossover employs the notion of exploitation where knowledge gained about points on the fitness landscape is capitalized on to find better points. Exploitation differentiates GAs from random search [5]. Selecting two genomes as parents, the crossover operator produces one or more offspring such that the offspring have some genes from one parent and some genes from parent two. Typical variants of crossover are 1-point crossover, m -point crossover, and uniform crossover where the offspring receives a random number of genes from parent one and a random number of genes from parent two [4]. Note that crossover does not always occur after selection but rather occurs based on some probability known as the crossover probability.

2.4.4 Mutation

Mutation is the exploration component of a GA where mutant offspring may discover previously uncharted points on the fitness landscape [5]. Coupled with a mutation step, the mutation operator disperses current genomes in the population to random points on the fitness landscape like dandelion seeds blowing in the wind; the larger the mutation step, the greater the dispersion. Like most aspects of a GA, there are many mutation operator variants depending on what gene encoding scheme was employed. Central to all variants, however, is some random number generator.

Mutation can occur on a gene-by-gene or on a genome-by-genome basis. With some probability of occurring—known as the mutation probability—a genome’s genes will be mutated (randomly altered) thereby producing a mutant offspring. These mutant offspring allow a GA to escape local optima and also help to keep the population diverse [4]. As the GA progresses, the diversity of the population will ultimately depend on the mutation probability; but by employing some self-adaptation mechanism, the mutation probability can vary over time [4]. Note that, like the mutation probability, the crossover probability could also be self-adapted over time as well.

2.5 Population

2.5.1 Initialization

Typically, at the start of a GA run, the population is randomly generated, but it could be seeded with some high-performing genomes found by an earlier run or by some other mechanism [8][4]. However, if one does seed the initial population, this may lead to premature convergence [4]. Determining the population size, and whether or not the population size remains constant throughout the run of the GA, is a debated topic with no straightforward answers [4].

2.5.2 Reproduction

Once every genome in the population has been evaluated, a GA enters into its reproduction cycle producing a new population known as a generation. There are many approaches to the reproduction cycle, but the most

basic is performing selection, crossover, and then mutation in a loop until the new population size reaches the old population size [5]. This basic approach is known as the generational approach with a generational gap of one between each generation. The generational gap is how much of an old population is replaced by a new population. A generational gap of one indicates that the new generation entirely replaces the old generation or in other words, parents never co-exist with offspring during any given generation [5]. Another approach is the steady-state or incremental approach where the generational gap is greater than one, with only a few offspring being produced and a few population members being terminated during each reproduction cycle [4]. Human beings follow a steady-state approach with some dying and some coexisting with their children, after having reproduced.

2.5.3 Convergence

Population diversity coincides with population convergence. Gene convergence occurs when 95% of the population shares the same gene value while population convergence occurs when every gene in the population has converged [5]. A converged population will be minimally diverse at the gene, genotype, and phenotype level [4].

2.6 Termination

GAs are inherently a stochastic process and will run forever unless constructed otherwise [4]. Deciding when to terminate is entirely up to the designer and their needs. The simplest method of termination is time where the GA is run for some amount of time and then stopped. A more sophisticated method involves terminating a GA after the population has dropped below some threshold of diversity [4]. Additional methods of when to terminate include:

1. the highest or average fitness reaching some predefined metric;
2. the change in fitness from one generation to another falling below some threshold; and
3. the GA reaching some generation number.

Chapter 3

SimPL

3.1 Overview

SimPL is an asymmetric autonomous pong clone with one paddle and one ball. SimPL is comprised of web-based technologies: HTML5, JavaScript, CSS, AJAX, MySQL, and PHP. At the time of this writing, SimPL can be viewed at <http://www.lettier.com/simpl/>. The paddle in SimPL is controlled by a feed-forward neural network. The neural network's weights are tuned via a genetic algorithm.

The focus for SimPL was to learn about and to cultivate a genetic algorithm capable of tuning parameters with respect to a fitness landscape thereby producing an optimum solution to a given parameter space. The genetic algorithm developed for SimPL was used as the basis for the genetic algorithm needed to solve the harder problem of tuning a 3D physics engine.

3.2 Implementation

3.2.1 Arena

The arena for SimPL resides in a browser window. Four transparent walls reside at the top, right, bottom, and left of the screen. The arena contains a ball and paddle with the paddle affixed to the far left of the screen and the ball originating from the far right of the screen. See Figure 3.1.



FIGURE 3.1: The SimPL arena containing the paddle and ball.

3.2.2 Ball

The ball is a physics-based dynamic object. Its starting position and starting velocity magnitude are the same at the start of every round¹. Just before the beginning of a round, a random angle in the range $[135^\circ, 225^\circ]$ is chosen as the ball's starting angle. See Figure 3.2. The ball's position is managed by the physics engine which responds to any collisions against the arena walls and/or the paddle.

If the ball collides with the left wall, the round is over. Otherwise, if the ball collides with the top, right, or bottom wall, the ball is bounced back into the arena via its angle-of-reflection, based on its collision angle-of-incidence. Collisions with the paddle work in the same fashion, where the ball is bounced back via its angle-of-reflection based on its collision angle-of-incidence. See Figure 3.3.

Each collision the ball makes reduces its velocity magnitude. Let m denote the ball's velocity magnitude. The formula used is $m = m - (m * 5\%)$. Once the ball's velocity magnitude drops below 100, the round is over. Note that the ball's velocity magnitude is set to $1000 \frac{\text{pixels}}{\text{second}}$ at the start of every round.

¹A round is defined as the time from when the ball is launched from its starting position to either the time at which the ball collides with the left side of the arena or the time at which the ball's velocity magnitude drops below 100.

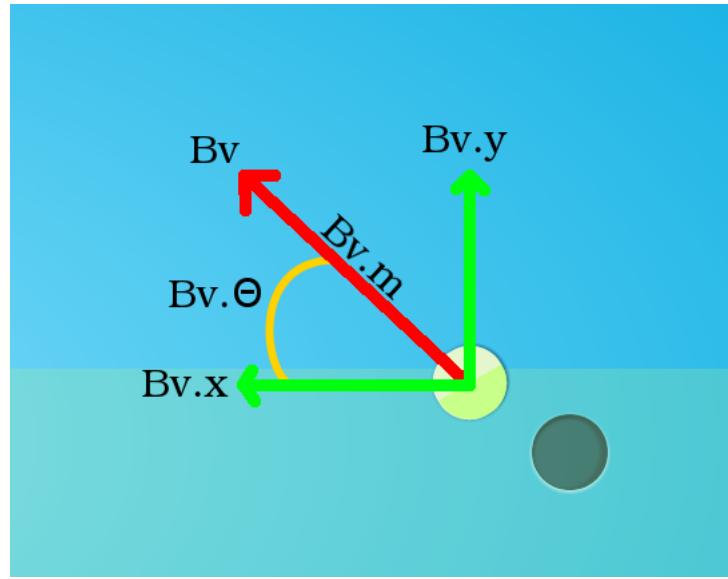


FIGURE 3.2: The ball's dynamic physics properties.

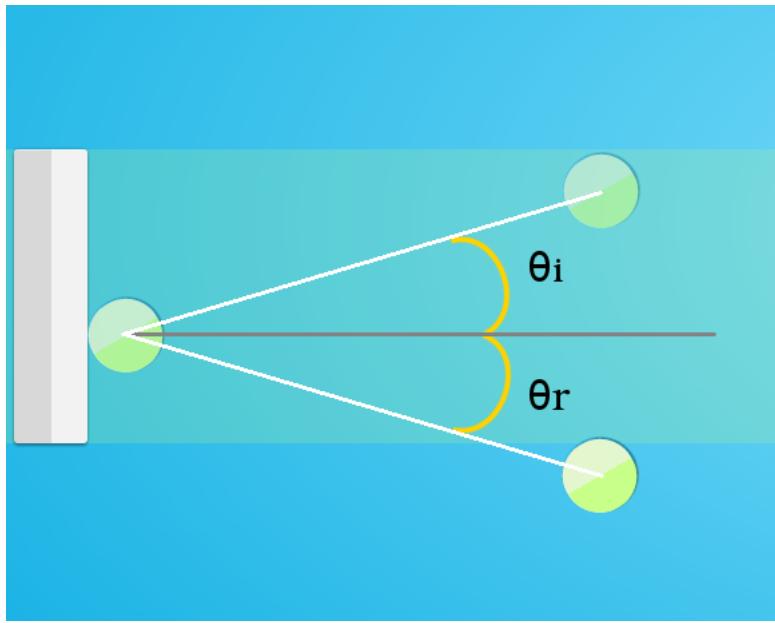


FIGURE 3.3: The ball's collision angle-of-incidence θ_i and its angle-of-reflection θ_r .

3.2.3 Paddle

The paddle is a physics-based dynamic object that has a fixed velocity angle of either 90° or $-90^\circ = 270^\circ$.

See Figure 3.4. Its starting position as well as its starting velocity magnitude are the same at the start of every round.

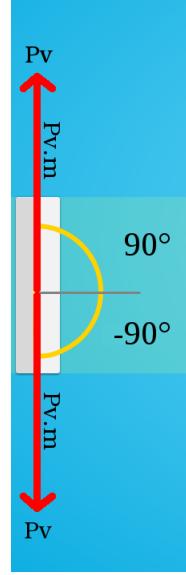


FIGURE 3.4: The paddle's dynamic physics properties.

The paddle's direction and speed are regulated by the output of a neural network. The output of the neural network is in the range $[-1, 1]$. The sign of the output determines the up or down direction of the paddle and the absolute value of the output determines the paddle's speed. A neural network output of 0 results in the paddle not moving from its current position. A neural network output in the range of $(0, 1]$ results in the paddle traveling up by some percentage of $1000 \frac{\text{pixels}}{\text{second}}$. A neural network output in the range of $[-1, 0)$ results in the paddle traveling down by some percentage of $1000 \frac{\text{pixels}}{\text{second}}$. For example, say the neural network output is -0.68 and let m denote the paddle's velocity magnitude. The paddle's velocity angle would be set to 270° (since the sign of the neural network output was negative) and its velocity magnitude would be set to $m = |-0.68| * 1000 \frac{\text{pixels}}{\text{second}}$. Here, the paddle can always travel as fast or faster than the ball, given that the ball's velocity magnitude at the start of a round is $1000 \frac{\text{pixels}}{\text{second}}$, the ball's velocity magnitude

decreases during a round, and the paddle’s velocity magnitude is always some percentage of $1000 \frac{\text{pixels}}{\text{second}}$ throughout the duration of a round depending on the NN output. It is never the case that the paddle does not have the possibility to reach the ball in time during the duration of any round. The paddle can always reach the ball given the neural network output is correct. Thus, at any time t during any round R_i , the paddle’s velocity magnitude is $0 \leq m \leq 1000 \frac{\text{pixels}}{\text{second}}$ since $m = |[-1, 1]| * 1000 \frac{\text{pixels}}{\text{second}}$ where $|[-1, 1]|$ is the absolute value of the neural network’s output range. Furthermore, at any time t during any round R_i , the paddle’s velocity angle (direction) is either 90° or 270° depending on the sign of the neural network output.

Collisions can occur for the paddle between the top wall, the bottom wall, and the ball. Collision with either the top or bottom wall results in the paddle’s top or bottom being placed just before the wall. Collision with the ball results in no change of movement for the paddle—the paddle merely continues moving as it was before the collision occurred with the ball.

3.2.4 Physics Engine

Handles to all dynamic and static objects are passed to the physics engine before the first round. Once every draw loop of the SimPL game, the physics engine tests for collisions between dynamic objects and other dynamic objects and between dynamic objects and static objects. Those dynamic objects that are found to be colliding with either another dynamic object and/or static object are flagged as such and their collisions are handled as described above. For those dynamic objects that are not colliding, their positions are updated based on their velocity.

3.2.5 Neural Network

The neural network is a feed-forward neural network that contains one input layer consisting of six input nodes, one hidden layer consisting of 5 hidden nodes, and one output layer consisting of one output node [13]. Each threshold input to the hidden nodes and the output node is included among the weights of the network and thus are optimized or tuned via the genetic algorithm. In total, there are 41 weights $((6 + 1) * 5 + (5 + 1) * 1 = 41)$ contained in the network. See Figure 3.5. Thus, there are 41 genes per genome in the genetic algorithm’s population. All output from the hidden nodes and the output node are

run through a sigmoid, hyperbolic-tangent-activation function ($\tanh(x) = \frac{e^{2x}-1}{e^{2x}+1}$) resulting in an output range of $[-1, 1]$.

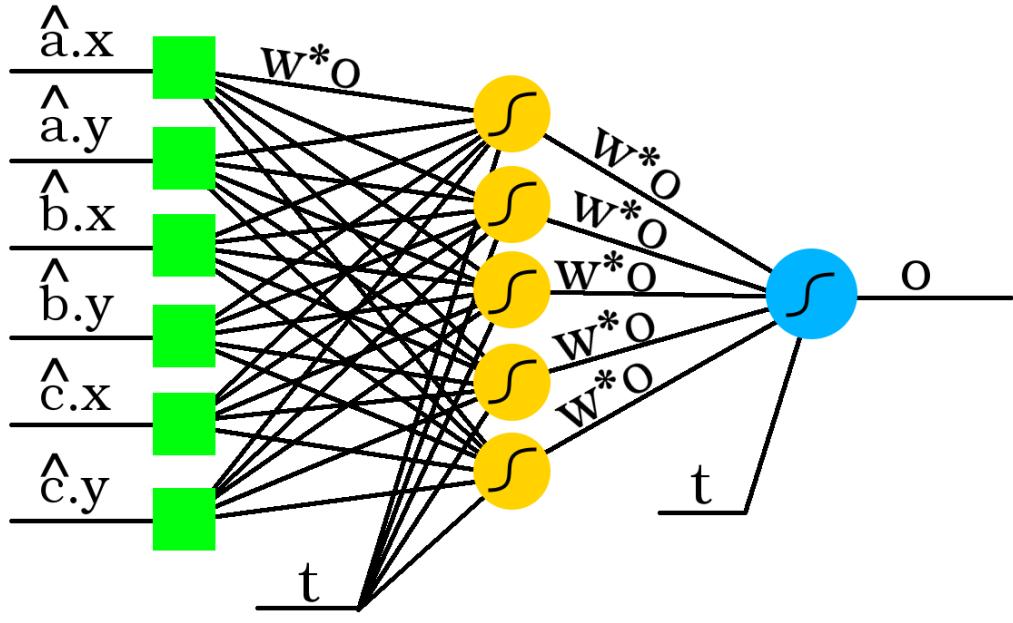


FIGURE 3.5: The neural network as constructed in SimPL.

Input to the neural network is normalized as three unit vectors: from the ball's center to the paddle's center, the ball's velocity, and from the window's origin to the paddle's center. See Figure 3.6. These three unit vectors are broken down into their components resulting in six inputs to the neural network. See Figure 3.7.

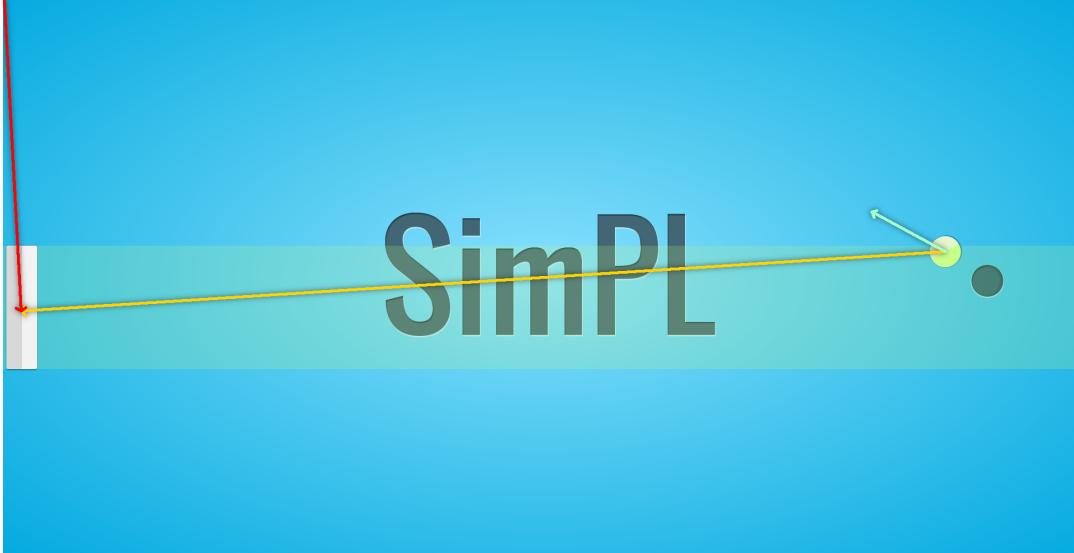


FIGURE 3.6: The three input vectors to the neural network. Note that these vectors are normalized thereby turning them into unit vectors.

3.2.6 Genetic Algorithm

Instead of using back-propagation to train the weights of the neural network, a genetic algorithm is used to optimize or tune the weights of the neural network [13]. The genetic algorithm consists of a population of genomes with each having a fitness property and an array of genes. For SimPL, the genes represent a solution of weights to be used in the neural network. Each genome is evaluated by a fitness function. As the genomes evolve over generations to produce fitter genomes, the neural network becomes increasingly accurate at outputting what the paddle should do (move up, stay still, or move down) based on the state of the ball and the paddle.

The genetic algorithm contains four operators that work to produce fitter generations during the creation of a new population. The operators include: the elitism operator, the selection operator, the crossover operator, and the mutation operator. Initially, the genetic algorithm creates a random population of genomes. These initial genomes have zero fitness and a fixed number of genes. Each gene in every genome is given a random value sampled from a uniform distribution coinciding with some valid range. The genes are the input parameters to the mechanism the genetic algorithm is working to optimize. In the case of

```
Paddle:  
    id: paddle  
    magnitude: 134.7752765851305  
    PI: 3.141592653589793  
    angle: 1.5707963267948966  
  
Ball:  
    id: ball  
    magnitude: 205.891132094649  
    PI: 3.141592653589793  
    angle: 2.5307274153917776  
  
NN Input: 0.989 0.146 -0.819 0.574 0.082 0.997  
  
NN Output:  
    0: -0.13477527658513053  
  
Current Genome: 1  
  
NN:  
    number_of_inputs: 6  
    number_of_outputs: 1  
    number_of_hidden_layers: 1  
    neurons_per_hidden_layer: 5  
    bias: -1  
  
NN Weights:  
    0: -1  
    1: 0.9813534922958044  
    2: -1  
    3: 1  
    4: 0.19044709740921306  
    5: 0.45017305545771064  
    6: 0.8754844796792515  
    7: -0.21012540145260464  
    8: 0.6151249941406718  
    9: 1  
    10: -1  
    11: -0.6453344198759198  
    12: 0.17499051310257202  
    13: 0.31071486210448007  
    14: 0.9123286228335877
```

FIGURE 3.7: The normalized input to the neural network.

SimPL, the mechanism is the neural network. Each gene has a valid range of $[-1, 1]$.

Once every genome in the population has been evaluated by the fitness function, the genetic algorithm constructs a new population from the previous generation. First, the elitism operator selects the n fittest genomes from the old generation. These elite genomes are allowed to survive intact (however their fitnesses are reset to zero) and are placed into the new generation. Second, the genetic algorithm enters into a loop creating new genomes via the crossover operator and the mutation operator until an entirely new generation has been created. This new generation goes on to be evaluated as their predecessors were and the cycle repeats until some termination criteria is met. See Figure 3.8.

```

BEGIN
    Generate a random population  $P$ 
    While not terminate do
        Evaluate population  $P$ 
        Create empty population  $P'$ 
        Sort  $P$  in order of fitness
        Select  $n$  fittest from  $P$  and add them to  $P'$ 
        While size of  $P' \leq$  population size do
            If perform crossover and mutation together then
                Select two genomes from  $P$ 
                Generate two offspring via crossover with probability  $C$ 
                Mutate the two offspring generated from crossover with probability  $M$ 
                Add the generated offspring to  $P'$ 
            Else
                Select two genomes from  $P$ 
                Generate two offspring via crossover with probability  $C$ 
                Add the offspring to  $P'$ 
                Select one genome from  $P$ 
                Mutate the selected genome with probability  $M$ 
                Add the mutated offspring to  $P'$ 
            End if
        End while
         $P = P'$ 
    End while
END

```

FIGURE 3.8: The basic genetic algorithm.

The selection operator uses roulette selection where the probability of some genome being selected is proportional to their fitness. Roulette selection and roulette selection with rank fitness was experimented with as outlined later [14]. The crossover operator takes two selected genomes to produce offspring where

the offspring have some combination of their parents' genes. SimPL uses one-point crossover throughout each experiment. To select the crossover point per crossover operation, the crossover operator samples a random integer from a uniform distribution ($crossoverPoint = X \sim U(0, n - 1)$ letting n denote the number of genes per genome). The mutation operator takes a selected genome and mutates its genes using various means. If the mutation scope is at the gene level, the mutation operator traverses through the genome's gene array where for each gene, the mutation operator samples a random integer from a uniform distribution ($X \sim U(0, 1)$) and if this random integer X is less than or equal to the mutation probability, the mutation operator mutates the gene value either via uniform mutation ($geneValue_i = X \sim U(0, 1) * \varepsilon$) or Gaussian mutation ($geneValue_i = X \sim N(\mu, \sigma^2)$). If the mutation scope is at the genome level, the mutation operator samples a random integer from a uniform distribution ($X \sim U(0, 1)$) and if this random integer X is less than or equal to the mutation probability, the mutation operator mutates all of the genome's gene values one after the other via either uniform mutation ($geneValue_i = X \sim U(0, 1) * \varepsilon$) or Gaussian mutation ($geneValue_i = X \sim N(\mu, \sigma^2)$). These means of mutation were experimented with as outlined later. Crossover and mutation can be carried out together (applying them both to one set of selected parents) or can be done separately with one operator not interfering the other operator's offspring. This was experimented with as outlined later.

Crossover and mutation are not guaranteed to always occur. Rather, crossover and mutation occur based on some probability. If the crossover and mutation probabilities are both set to 1.0, then they always occur. Before the genetic algorithm is initialized, the crossover and mutation probabilities are set [15]. These initial crossover and mutation probability values can be arbitrary or can be based on some a-priori knowledge of the fitness landscape. The probabilities can change over time or can remain static throughout the run of the genetic algorithm. Different static settings and self-adaptation of the probabilities were experimented with as outlined later.

The fitness function evaluates each genome in the current population based on some fitness criteria. The fitness criteria coincides with finding the optimum solution to the parameter space of the mechanism the genetic algorithm is producing fitter and fitter solutions to. For SimPL, the parameter space is the weights of the neural network. Each genome represents a solution or point in the weights space. An optimal solution

in the weights space will make the neural network always give a correct output as to what movement the paddle must make based on the ball's and the paddle's current states. This will result in the paddle always following the ball or in other words, the paddle will never let the ball leave the left side of the screen. Thus the fitness criteria for SimPL could include how much or how well the paddle follows the ball and/or how many times the paddle hits the ball. Different fitness criteria were experimented with, as outlined later.

3.2.7 Database Manager

A database manager interfaces with a remote MySQL server either asynchronously or synchronously. Experiment data is recorded in the MySQL database as each experiment is carried out. Additionally, each generation produced by the genetic algorithm is logged to the database. Upon visiting the SimPL site, the last generation produced can be loaded into the genetic algorithm, thereby allowing the simulation to pick up where it left off last.

3.3 Platform

The browser window size has a significant influence over the fitnesses of the genomes being evaluated. While the arena fits to whatever size the browser window is, the size of the paddle and the ball do not directly change in proportion to the window size. Thus, a small browser window gives the paddle less screen real estate to cover in comparison to a large browser window. For example, imagine a browser window size with a height as large as the paddle's height. Here the paddle can never move—it always follows the ball and always hits the ball. Thus, the resulting fitnesses observed would be erroneously high. Therefore, all experiments were run using the same browser window size.

Experiments were run on a Lenovo Z580 Ideapad laptop running 64-bit Fedora 18 and was equipped with an Intel Core i5 CPU running at 2.5 GHz and 7.7 GiBs of memory. Google Chrome version number 30.0.1599.114 was used on the laptop. Screen resolution was 1366×768 . Browser window size (both reported and actual) was 1366 pixels wide by 681 pixels tall. Paddle size reported (by the browser) was 50 pixels wide by 200 pixels tall and the actual size was the same. Ball size reported (by the browser) was 50 pixels wide by 50 pixels tall and the actual size was the same. The paddle had $681 - 200 = 481$ pixels of available

screen-space to traverse.

3.4 Experimental Designs

Each SimPL experimental design (with the exception of experiments six and seven described below) was constructed in such a way as to focus on a set of one or more facets to the genetic algorithm. See Table 3.1. With each progressive experiment, the facets not focused on were kept the same from the previous experiment. The goal was to create a genetic algorithm that would eventually—with efficiency—produce the optimal set of neural-network weights needed in order to generate a paddle that performs as well as the performance-standard paddle constructed in experiment six. Ultimately, the performance of any paddle in SimPL is how long it keeps the ball-in-play before the termination of any round.

Experiments one and two revolved around the fitness function, the selection operator, and the static crossover and static mutation properties of the genetic algorithm. Experiments three, four, and five revolved around the self-adaptation of the crossover and mutation probabilities and whether allowing the mutation operator to disrupt the offspring, produced by the crossover operator, degraded the performance of the genetic algorithm. Experiment six revolved around constructing a paddle as an optimal-performance standard by which any other paddle could be measured by. Finally, experiment seven revolved around constructing a randomly behaving paddle thereby producing a performance lower bound.

For each experiment, the genetic algorithm was run for 100 generations. For each generation, the population’s average fitness was recorded. Once every 10th generation, the current population’s top performing genome was saved. After the run of the genetic algorithm was over, the saved top-performers were run in a tournament. This tournament consisted of running each top-performer for five rounds where for each top performer, the time in seconds they kept the ball-in-play per round was recorded. Once an every-10th-generation-top-performer was done with their five rounds, the average of their ball-in-play time per round was calculated and recorded.

GA Parameters × Experiment	<i>One</i>	<i>Two</i>	<i>Three</i>	<i>Four</i>	<i>Five</i>	<i>Six & Seven</i>
Population Size	10	10	10	10	10	10
Fitness Function Type	Partial/Full	Full	Full	Full	Full	Full
Number of Elite Offspring	2	2	2	2	2	10
Roulette Selection - Actual Fitness	True	False	False	False	False	N/A
Roulette Selection - Rank Fitness	False	True	True	True	True	N/A
Sequential Crossover & Mutation	True	True	False	False	True	N/A
Self-adaptation	False	False	True	False	False	N/A
Crossover Type	One-point	One-point	One-point	One-point	One-point	N/A
Crossover Probability	0.7	0.8	0.5	0.7816	0.7816	N/A
Mutation Type	Uniform	Gaussian	Gaussian	Gaussian	Gaussian	N/A
Mutation Scope	Gene	Gene	Genome	Genome	Gene	N/A
Mutation Probability	0.1	$(\frac{1}{n}) = (\frac{1}{41}) \approx 0.0244$	0.5	0.2184	0.2184	N/A
Mutation Step	$X \sim U(0,1) * 0.3$	$X \sim N(\mu, \sigma^2)$	$X \sim N(\mu, \sigma^2)$	$X \sim N(\mu, \sigma^2)$	$X \sim (\mu, \sigma^2)$	N/A
Mutation Step μ	N/A	Gene Value	Gene Value	Gene Value	Gene Value	N/A
Mutation Step σ	N/A	0.5	$M_{Prob.}$	$M_{Prob.}$	$M_{Prob.}$	N/A

TABLE 3.1: The genetic algorithm parameters used per experiment. The highlighted cells indicate the experimental variables per experiment. Experiment six and seven are included in the table for completeness but no evolution ever took place.

3.4.1 Experiment one: use of a full and partial credit granting fitness function.

Experiment one centered around the use of a fitness function that would give full and partial credit based on the behavior of the neural network and thus the paddle. The genetic algorithm parameters used are listed in Table 3.2.

Population Size	10
Number of Elite Offspring	2
Roulette Selection using Actual Fitness	True
Roulette Selection using Rank Fitness	False
Crossover Probability	0.7
Crossover Type	One Point Crossover
Mutation Probability	0.1
Mutation Scope	Gene Level
Mutation Step	$X \sim U[-1, 1] * \text{Max-Perturbation}$
Max-Perturbation	0.3
Sequential Crossover and Mutation	True
Fitness Function	Partial/Full
Fitness Credit for Hitting the Ball	1.0
Fitness Credit for Following the Ball	0.1
Fitness Credit for Matching the Ball's Center Y-coordinate	0.1
Fitness Credit for not Following the Ball	-0.1

TABLE 3.2: The genetic algorithm parameters for experiment one.

During each generation of the genetic algorithm, each genome from the population was allowed to run one round until the round terminated either due to the ball leaving the left side of the screen or the ball's velocity magnitude dropping below 100. Note that during the round, the paddle's movement (in relation to the ball's movement) was tracked via an array (see below) as well as how many times the paddle hit the ball during the round. Once the round terminated, the genome was evaluated by the fitness function. During evaluation, if the genome's phenotype (the paddle's observable characteristics) followed the ball (from one draw loop to next) it would be given a positive partial fitness credit of 0.1 every time it followed the ball. If the phenotype managed to collide with the ball, the genome was given a full fitness credit of 1 every time it hit the ball. However, if the phenotype moved away from the ball (from one draw loop to the next), it was given a negative partial fitness credit of -0.1 every time it moved away from the ball. Lastly, if the phenotype didn't move at all (while the ball moved from one draw loop to the next) it was given 0 fitness every time it did not move. At the end of the fitness function, all of these partial and full fitness credits were summed giving the currently-being-evaluated genome its total fitness. If the total summed fitness was

less than zero, the total summed fitness was set to zero. That is, no genome's fitness—after having been evaluated by the fitness function at the end of its round—was ever negative.

To facilitate tracking the paddle's movements in relation to the ball's movements (during the round), the absolute difference in heights between the paddle's center and the ball's center were recorded every draw loop into an array. Once the genome was ready to be evaluated, this array of differences was analyzed linearly in pairs, that is, $A[i]$ was compared with $A[i + 1]$. If $A[i] > A[i + 1]$, this indicated that the paddle's center was moving closer to the ball's center and thus the genome was awarded a positive partial credit fitness. If $A[i] < A[i + 1]$, this indicated that the paddle's center was moving away from the ball's center and thus the genome was awarded a negative partial credit fitness. If $A[i] = A[i + 1]$, this indicated that the paddle's center was neither moving toward nor away from the ball's center and thus the genome was awarded 0 fitness. A special case for $A[i] = A[i + 1]$ was that if $A[i] = 0$ and thus $A[i + 1] = 0$ as well, the paddle was awarded a positive partial fitness as the paddle's center was dead center with the ball's center and therefore the paddle was directly in the path of the ball which is ultimately the goal—that is, the paddle should always match its center with the ball's center thereby always preventing the ball from leaving the arena.

The hypothesis for using a full and partial fitness credit schema was that every new generation produced would have genomes that at least performed somewhat better than their predecessors at the optimal behaviors. Those optimal behaviors are following the ball and hitting the ball. Originally, only hitting the ball was going to be the fitness criteria. However, early generations may never hit the ball and thus would have zero fitness. Genomes that at least followed the ball could have been erroneously discarded due to having zero fitness. By giving partial credit for at least following the ball, it was hypothesized that it would seed early generations with promising genomes or rather promising solutions to the parameter space. Picture a classroom of students taking a test. Upon evaluation, it is either all or nothing credit per question and no student finds the solution to any problem. In other words, every student received a zero. This would give the teacher no information as to the quality of the students at least in terms of comparing them to one another. However, if partial credit is given for getting part of the solution correct, then this would give at least some information as to who performed well among the students. In other words, it was hypothesized

that by using a finer-grained fitness function, there would be some information gained as to the fitness of one genome compared to another (aiding elitism and the selection process), versus no information gained using only a coarsely-grained fitness function, resulting in every genome having a fitness of zero after being evaluated.

3.4.2 Experiment two: use of a simplified fitness function, use of rank fitness in selection, higher crossover probability, mutation probability based on the number of genes per genome, and a Gaussian distribution sample mutation step.

Experiment two had a simplified fitness function, used a genome's rank fitness during selection, increased the crossover probability, based the mutation probability on the number of genes per genome, and used Gaussian distribution sampling as the mutation step. The genetic algorithm parameters used are listed in Table 3.3.

Population Size	10
Number of Elite Offspring	2
Roulette Selection using Actual Fitness	False
Roulette Selection using Rank Fitness	True
Crossover Probability	0.8
Crossover Type	One Point Crossover
Mutation Probability	$\frac{1}{n \text{ genes}} = \frac{1}{41} = 0.024390244$
Mutation Scope	Gene Level
Mutation Step	$X \sim N(\mu, \sigma^2)$
Mutation Step μ	Gene Value
Mutation Step σ	0.5
Max Perturbation	N/A
Sequential Crossover and Mutation	True
Fitness Function	Full
Fitness Credit for Staying in the Path of the Ball	1.0
Fitness Credit for not Staying in the Path of the Ball	0.0

TABLE 3.3: The genetic algorithm parameters for experiment two.

Going from awarding full and partial credit fitness based on two behaviors to only awarding a fitness credit of 1 if the paddle was in the path of the ball per every draw loop, the fitness function was simplified. Here the paddle doesn't necessarily have to be dead center to the ball but rather the paddle's top must be at or above the ball's top while, at the same time, the paddle's bottom has to be at or below the ball's bottom. See Figure 3.9. The reasoning behind this was that if the paddle were to always be in the path of the ball, then it would always hit the ball and thus the paddle would never let the ball leave the arena; or in other words, the paddle would exhibit the optimum desired behavior. Therefore, this fitness function correctly

evaluates the paddle's behavior in relation to the ball's movement throughout any round.

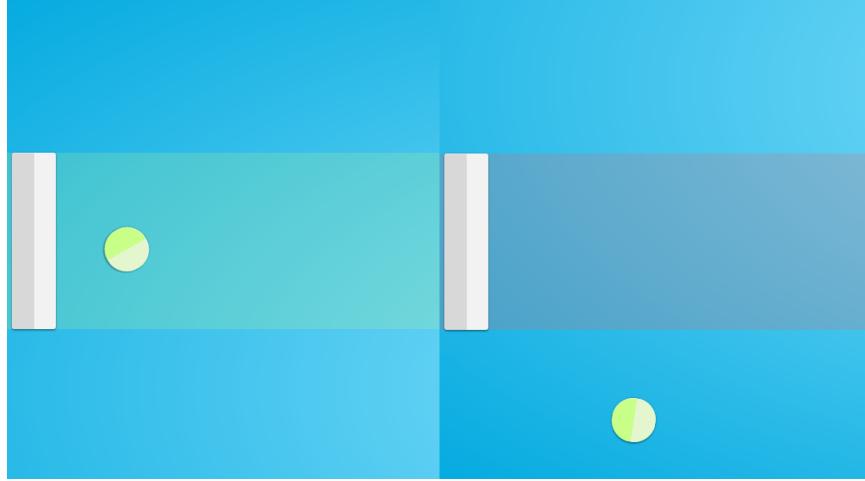


FIGURE 3.9: The simplified fitness function shown graphically, where the paddle on the left is gaining fitness (as indicated by the green-hued bar) while the paddle on the right is gaining no fitness (as indicated by the purple-hued bar).

Instead of using the actual fitness of any particular genome in the population to determine its probability of being selected during the roulette wheel selection process, a genome's rank fitness was used to determine its probability of being selected [14]. It was observed during early runs of the genetic algorithm that after evaluation, the population had wide gaps of fitness. The genomes with zero or relatively low fitness had absolutely little to no chance of being selected for crossover and mutation while the genomes with a relatively high fitness had a high chance of being selected for crossover and mutation. These early top performers were continuously selected, crossed, and mutated generation after generation. Population diversity dwindled thereby causing the population to converge too early (due to an ever narrowing search of the fitness landscape) resulting in poor performance on behalf of the genetic algorithm. Thus it was hypothesized that by using rank fitness instead of actual fitness to determine a genome's probability of being selected, population diversity would remain sufficient generation after generation, thereby avoiding early convergence.

Rank fitness is a genome's fitness according to their index in the population after the population is sorted in increasing order of fitness [16]. After sorting the population, genome one is given a fitness of one, genome two is given a fitness of two, and so on and so forth, until genome n is given a fitness of n or rather

the population size. See Figure 3.10. Now all genomes have a better chance of being selected to undergo crossover and/or mutation thereby keeping the population diversity high and thus keeping the search scope of the fitness landscape large resulting in better performance of the genetic algorithm.

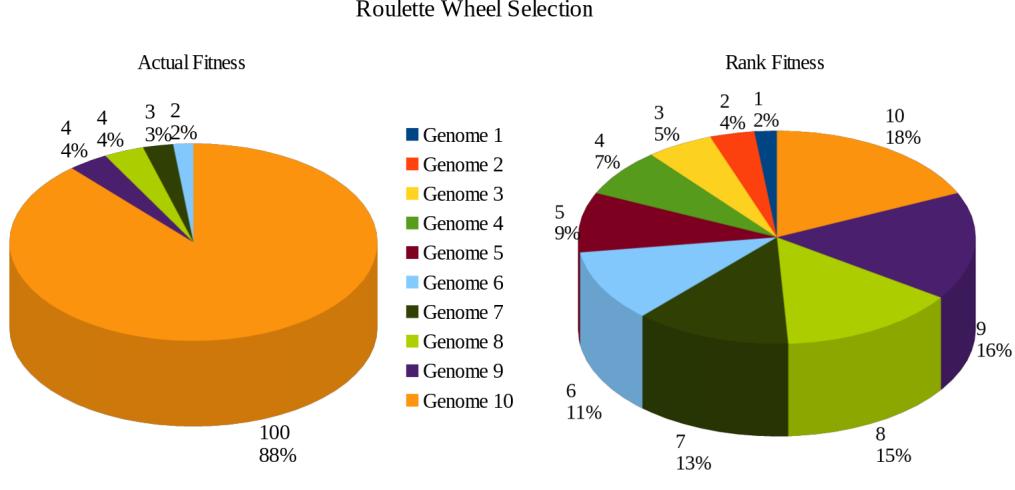


FIGURE 3.10: The roulette selection using actual fitness versus rank fitness for a population of 10 genomes. On the left, the integers are the genomes’ actual fitness and the percentages are their probabilities of being selected. On the right, the integers are the genomes’ rank fitness and the percentages are the genomes’ probabilities of being selected. Observe that Genome 10 no longer dominates the wheel when using its rank fitness (10) versus using its actual fitness (100).

Crossover probability was increased from 0.7 to 0.8. This would result in more observed crossovers being generated as new populations were created. Since crossover produces an offspring solution somewhere between its parents in the fitness landscape, it was hypothesized that by increasing the crossover probability, the local search capability of the genetic algorithm would also increase.

Based on empirical studies performed by others, setting the mutation probability to $\frac{1}{n}$ —where n is the number of genes per genome—is a sufficiently random enough search to allow the genetic algorithm to escape local maxima in the fitness landscape [17]. The reasoning behind $\frac{1}{n}$ is that per mutation on a gene-by-gene basis, only one gene is mutated on average. In addition to changing the mutation probability, the mutation step was changed from adding and/or subtracting a percentage of a maximum perturbation parameter value to and/or from the gene value to sampling a value from a Gaussian distribution where the distribution $N(\mu, \sigma^2)$ is defined by the mean μ being the gene’s current value before mutation and the standard deviation σ being one fourth the valid range of the gene/parameter ($\frac{1-(-1)}{4} = 0.5$). Here the

standard deviation σ is one fourth the range, and thus most of the sampled values will be within two standard deviations of the mean μ . Any sampled gene value that was outside the valid range of $[-1, 1]$ was clipped to the valid range. Note that by going with this new mutation step schema, the maximum perturbation parameter to the genetic algorithm could be removed thereby lowering the number of parameters that need to be evaluated.

3.4.3 Experiment three: self-adaptation of crossover and mutation probabilities with the crossover and mutation operators working in parallel.

Experiment three involved self-adaptation of the crossover and mutation probabilities. The genetic algorithm parameters used are listed in Table 3.4.

Population Size	10
Number of Elite Offspring	2
Roulette Selection using Actual Fitness	False
Roulette Selection using Rank Fitness	True
Self-adaptation	True
Initial Crossover Probability	0.5
Minimum Crossover Probability	0.001
Crossover Type	One Point Crossover
Initial Mutation Probability	0.5
Minimum Mutation Probability	0.001
Mutation Scope	Genome Level
Mutation Step	$X \sim N(\mu, \sigma^2)$
Mutation Step μ	Gene Value
Mutation Step σ	Mutation Probability
Sequential Crossover and Mutation	False
Fitness Function	Full
Fitness Credit for Staying in the Path of the Ball	1.0
Fitness Credit for not Staying in the Path of the Ball	0.0

TABLE 3.4: The genetic algorithm parameters for experiment three.

As outlined in [15], the crossover and mutation probabilities self-adapt based on the crossover and mutation operators' ability to produce fitter genomes from one generation to the next. To facilitate the self-adaptation, the crossover and mutation operators' viability to produce fitter and fitter offspring needed to be tracked from one generation to another. As the operators were being evaluated on their own accord, they were not allowed to interfere with each others' offspring and thus they were not used together on the same selection parents but rather were used separately, each with their own selection of parents. With each new generation produced, elite offspring were marked accordingly as well as offspring produced by crossover

and offspring produced by mutation. For those offspring that were created by crossover, their parents' weighted-mean fitness was annotated along with their offspring. In other words, the weighted-mean fitness was recorded in the offspring's data structure later being used to calculate the crossover operator's progress. This weighted-mean fitness was calculated based on the crossover point which determines what percentage of genes came from parent one and what percentage of genes came from parent two. For example, let there be 41 genes per genome and let the crossover point be gene 10. Thus, offspring one received 10 genes from parent one and received 31 genes from parent two while offspring two received 10 genes from parent two and received 31 genes from parent one. Therefore, offspring one's weighted-mean parent fitness would be calculated as $\overline{PF} = (PF_1 * \frac{10}{41}) + (PF_2 * \frac{(41-10)}{41})$ where \overline{PF} is the weighted-mean parent fitness while offspring two's weighted-mean parent fitness would be calculated as $\overline{PF} = (PF_2 * \frac{10}{41}) + (PF_1 * \frac{(41-10)}{41})$. For those offspring created via mutation, their parent fitness was whatever the fitness was of the pre-mutated genome.

With the genomes marked as to how they were created and their parent fitness annotated, now when it came time to produce a new population, each operators' ability to produce fitter offspring could be tracked and calculated. Once a population was evaluated, all genomes created by crossover were used to calculate the average crossover progress and all genomes created by mutation were used to calculate the average mutation progress. If the crossover progress average was greater than the mutation progress average, then the crossover probability would be adjusted up and the mutation probability would be adjusted down. Alternatively, if the crossover progress average was less than the mutation progress average, then the crossover probability would be adjusted down and the mutation probability would be adjusted up. If the crossover progress average equaled the mutation progress average, then neither were adjusted. Adjustment of the crossover and mutation probabilities was handled by the adjustment parameter. Let the adjustment parameter be denoted as θ . Here θ was self-adjusted as well, as outlined in [15]. Once the probabilities were adjusted, they were clamped to the range [0.001, 1.0]. With a minimum probability of 0.001, there would always be some crossover and/or mutation, albeit not much. See Figure 3.11. Note that, to insure a level playing field, both the crossover and mutation probabilities were set to an initial value of 0.5 before the start of the genetic algorithm.

```

BEGIN
    Population P has been evaluated
    cCount = mCount = 0
    CPsum = MPsum = 0
    CP̄ = MP̄ = 0
    For j = 1 to population size do
        If P[j] created by crossover then
            CPsum = CPsum + (P[j].fitness - P[j].parentFitness)
            cCount = cCount + 1
        Else if P[j] created by mutation then
            MPsum = MPsum + (P[j].fitness - P[j].parentFitness)
            mCount = mCount + 1
        End if
    End for
    CP̄ = CPsum / cCount
    MP̄ = MPsum / mCount
    If P.bestFitness > P.worstFitness then
        Adjustment θ = 0.01 * P.bestFitness - P.meanFitness
    Else if P.bestFitness = P.meanFitness then
        Adjustment θ = 0.01
    End if
    If CP̄ > MP̄ then
        Crossover Probability C = C + θ
        Mutation Probability M = M - θ
    Else if CP̄ < MP̄ then
        Crossover Probability C = C - θ
        Mutation Probability M = M + θ
    End if
    Clamp C to range [0.001, 1.0]
    Clamp M to range [0.001, 1.0]
END

```

FIGURE 3.11: The self-adaptation algorithm.

Unlike previous experiments, the mutation probability was not set on a gene-by-gene basis but rather on a whole genome-by-genome basis. Every time through the population creation loop, a random float value was sampled from a uniform distribution between 0.0 and 1.0. If this random float value was less than or equal to the mutation probability, every gene in the selected genome was mutated using the Gaussian distribution mutation step method outlined earlier. However, the standard deviation was set to the mutation probability instead of it being statically set to 0.5 as before. The reason being that a high mutation probability would give way to a larger mutation step (since the standard deviation would be relatively large) allowing for larger random leaps around the fitness landscape, while a low mutation probability would give way to a smaller mutation step (since the standard deviation would be relatively small) allowing for a more finely tuned search as the population converges to the optimum in the fitness landscape.

3.4.4 Experiment four: static crossover and mutation probabilities with the crossover and mutation operators working separately.

Experiment four had an identical setup to experiment three, with the exception that the crossover and mutation probabilities were statically set throughout the experiment to the crossover and mutation probabilities arrived at after the 100th generation of the genetic algorithm in experiment three. The genetic algorithm parameters used are listed in Table 3.5.

Population Size	10
Number of Elite Offspring	2
Roulette Selection using Actual Fitness	False
Roulette Selection using Rank Fitness	True
Self-adaptation	False
Crossover Probability	0.7816
Crossover Type	One Point Crossover
Mutation Probability	0.2184
Mutation Scope	Genome Level
Mutation Step	$X \sim N(\mu, \sigma^2)$
Mutation Step μ	Gene Value
Mutation Step σ	Mutation Probability
Sequential Crossover and Mutation	False
Fitness Function	Full
Fitness Credit for Staying in the Path of the Ball	1.0
Fitness Credit for not Staying in the Path of the Ball	0.0

TABLE 3.5: The genetic algorithm parameters for experiment four.

Experiment four, as well as experiment five, were devised as comparisons to experiment three. The

hypothesis was that self-adaptation, along with non-interfering operators, would have the fastest average fitness growth rate among the three.

3.4.5 Experiment five: static crossover and mutation probabilities with the crossover and mutation operators working together.

Experiment five had an identical setup as experiment four, with the exception that the crossover and mutation operators were used together instead of separately. By using the operators together, the mutation operator could disrupt the offspring created by the crossover operator. The genetic algorithm parameters used are listed in Table 3.6.

Population Size	10
Number of Elite Offspring	2
Roulette Selection using Actual Fitness	False
Roulette Selection using Rank Fitness	True
Self-adaptation	False
Crossover Probability	0.7816
Crossover Type	One Point Crossover
Mutation Probability	0.2184
Mutation Scope	Gene Level
Mutation Step	$X \sim N(\mu, \sigma^2)$
Mutation Step μ	Gene Value
Mutation Step σ	Mutation Probability
Sequential Crossover and Mutation	True
Fitness Function	Full
Fitness Credit for Staying in the Path of the Ball	1.0
Fitness Credit for not Staying in the Path of the Ball	0.0

TABLE 3.6: The genetic algorithm parameters for experiment five.

3.4.6 Experiment Six: fitness and ball-in-play upper bound.

The goal of experiment six was to obtain the average fitness over 100 generations, the fitness of every 10th generation top performer, and the average ball-in-play time of five rounds per every 10th generation top performer **where the paddle always performed the correct movement** no matter the state of the paddle and the ball at any time during any round. In other words, the goal of experiment six was to obtain an average fitness upper bound and an average ball-in-play time of five rounds upper bound utilizing the same fitness function as was used in experiment two, three, four, and five.

To accomplish the goal of experiment six, the neural-network output was ignored and instead, the paddle's center height (y-coordinate) was always set to the ball's center y-coordinate once every draw loop.

With this modification, the paddle was always dead center with the ball, was always in the path of the ball, and thus always kept the ball from leaving the left side of the arena. That is, it always hit the ball back into the arena. At no point was the paddle ever not in the path of the ball and thus the paddle always obtained the maximum fitness possible as well as the maximum ball-in-play time possible for any particular round. The only way any round ever terminated was by the ball's velocity magnitude falling below the 100 threshold.

3.4.7 Experiment seven: random paddles and an approximate lower bound.

The goal of experiment seven was to obtain the average fitness over 100 generations, the fitness of every 10th generation top performer, and the average ball-in-play time of five rounds per every 10th generation top performer **where the paddle always performed a random movement**. By obtaining these metrics for randomly moving paddles, it could be demonstrated that the genetic algorithm either did or did not ultimately produce paddles that performed better than the randomly moving paddles.

To accomplish the goal of experiment seven, the neural-network output was ignored and instead, the paddle's movement was always randomly generated once per draw loop. To generate the random movement, a random float was sampled from a uniform distribution $X \sim U(-1, 1)$. If X was in the range $[-1, 0]$, the paddle's velocity angle was set to 270° and the paddle's velocity magnitude was set to $m = |X| * 1000 \frac{\text{pixels}}{\text{second}}$. If X was in the range $(0, 1]$, the paddle's velocity angle was set to 90° and the paddle's velocity magnitude was set to $m = |X| * 1000 \frac{\text{pixels}}{\text{second}}$. Otherwise, if X was zero, the paddle did not move from its current position.

3.5 Experimental Results

The results of each experiment are presented below (Subsections 3.5.1 through 3.5.7), followed by a comparison of all results (Subsection 3.5.8).

For each experiment (one through seven), there are three plots shown. The first plot shows the average fitness over 100 generations. The second plot shows the fitness of the top performer for every 10th generation (over 100 generations). The third plot shows the ball-in-play time, averaged over 5 games, for the top performers whose fitness is illustrated in the second plots.

3.5.1 Experiment one: use of a full and partial credit granting fitness function.

Experiment one (Figures 3.12-3.14) showed that the player learned to keep the ball in play longer after generation 49, improving from 3.00584 seconds per round on average to 28.30964 seconds. This is despite the fact that the average fitness doesn't begin to show significant improvement until generation 80. The improvement in average ball-in-play time drops in generation 79, but then improves and exceeds the previous maximum (generation 69) after generation 89.

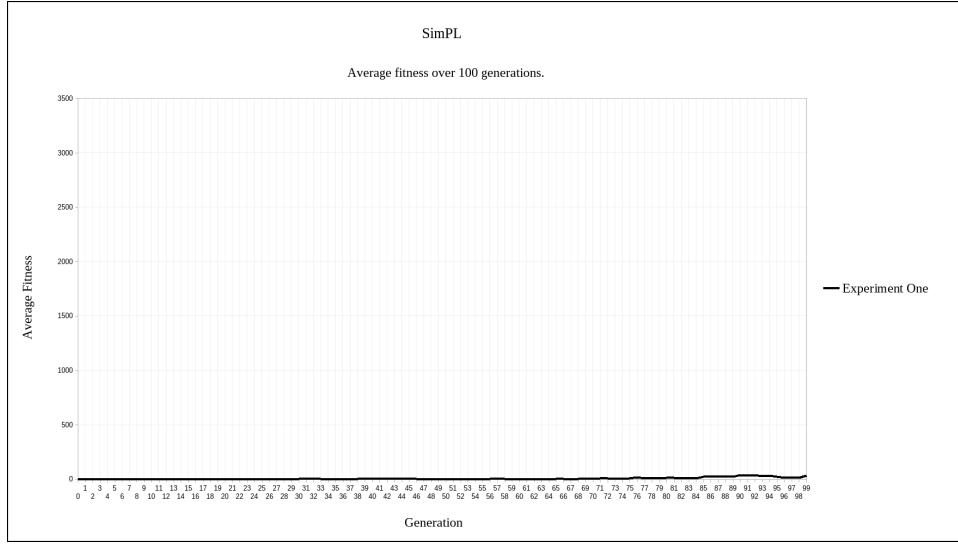


FIGURE 3.12: The average fitness over 100 generations for experiment one.

3.5.2 Experiment two: use of a simplified fitness function, use of rank fitness in selection, higher crossover probability, mutation probability based on the number of genes per genome, and a Gaussian distribution sample mutation step.

Experiment two (Figures 3.15-3.17) shows marked improvement in average fitness to generation 20, and then a more gradual improvement for the remaining 80 generations. The average ball-in-play times improve dramatically from 10.1 seconds to 37.8 seconds within the first 20 generations, but levels off and does not show marked improvement for the remainder of the experiment.

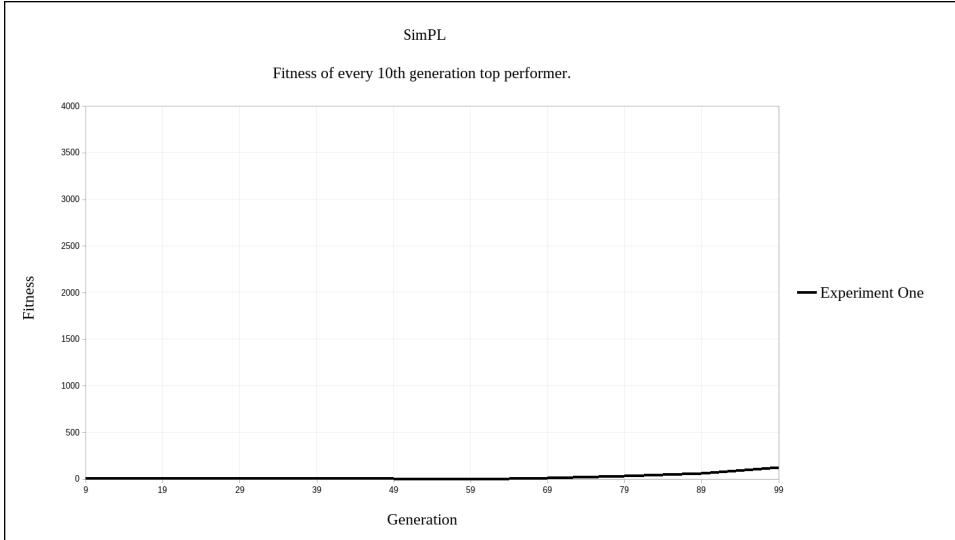


FIGURE 3.13: The fitness of every 10th generation top performer for experiment one.

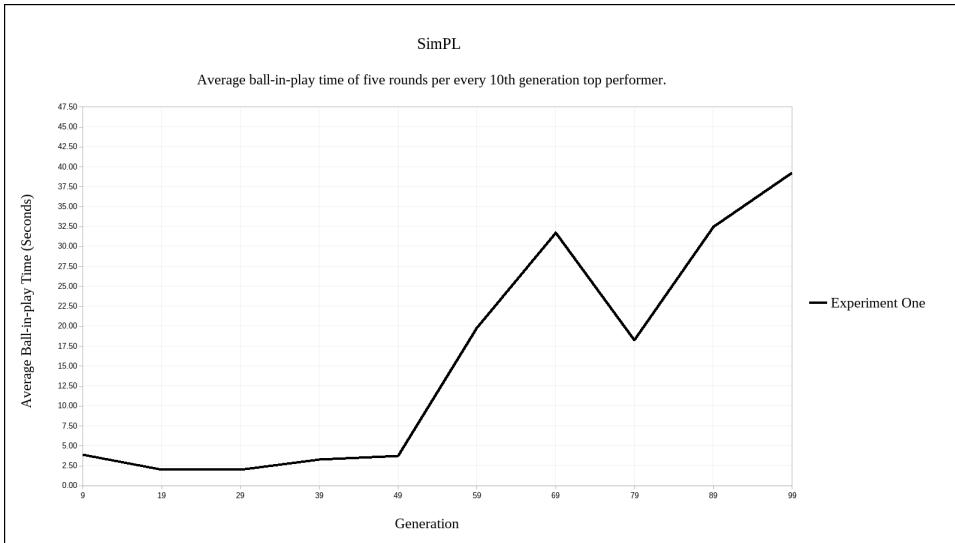


FIGURE 3.14: The average ball-in-play time (in seconds) of five rounds per every 10th generation top performer for experiment one.

3.5.3 Experiment three: self-adaptation of crossover and mutation probabilities with the crossover and mutation operators working in parallel.

Experiment three (Figures 3.18-3.21) shows initial improvement in average fitness for the first 12 generations, but then oscillates and does not show measurable improvement for the rest of the experiment. This result is reflected in the average ball-in-play time metric, which starts at 35.7314 seconds and oscillates but does not

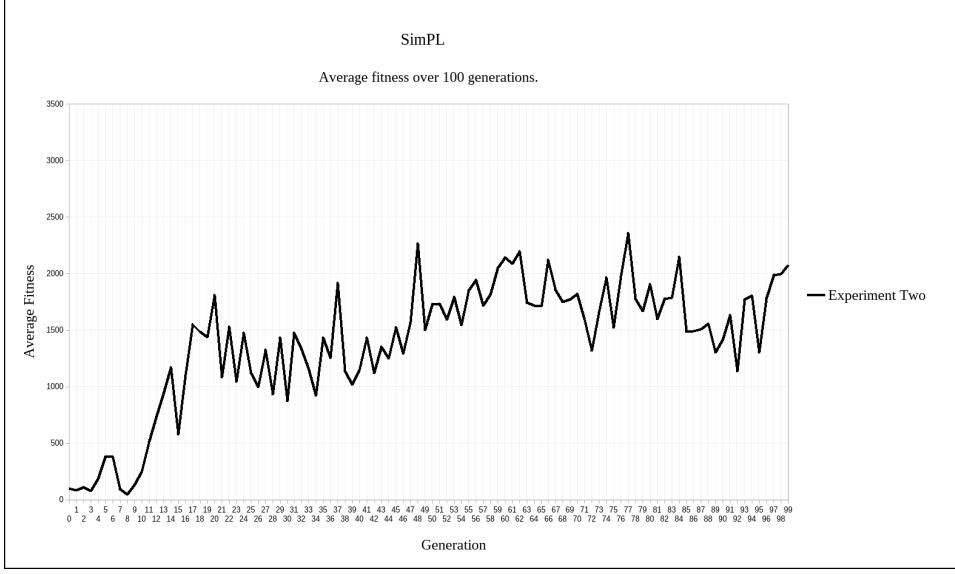


FIGURE 3.15: The average fitness over 100 generations for experiment two.

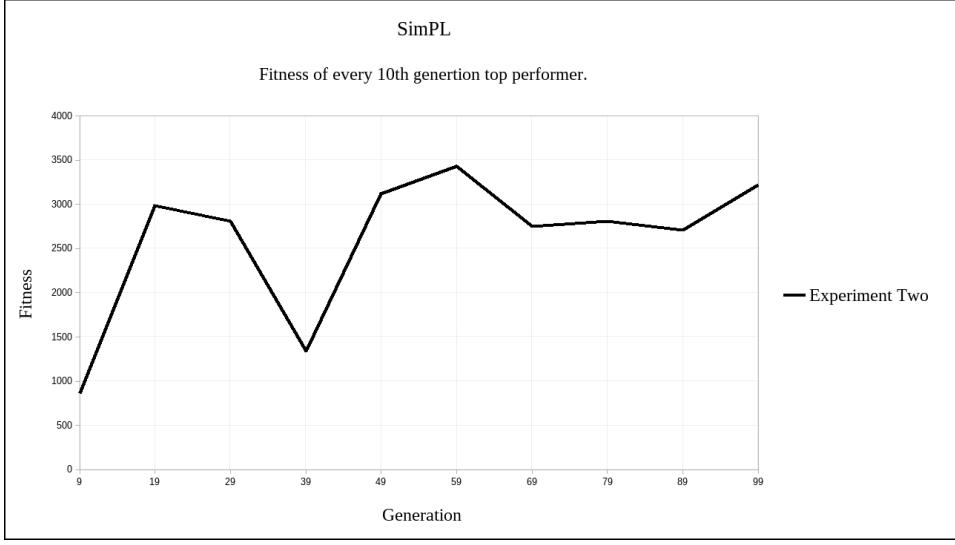


FIGURE 3.16: The fitness of every 10th generation top performer for experiment two.

trend significantly. Figure 3.19 illustrates the self-adaptation of the crossover and mutation probabilities, as chosen by the algorithm at run-time. Although the proportions change, they do not appear to correlate with the fitness or average ball-in-play time results.

The crossover and mutation probabilities were both initially set to 0.5 before the start of the ex-

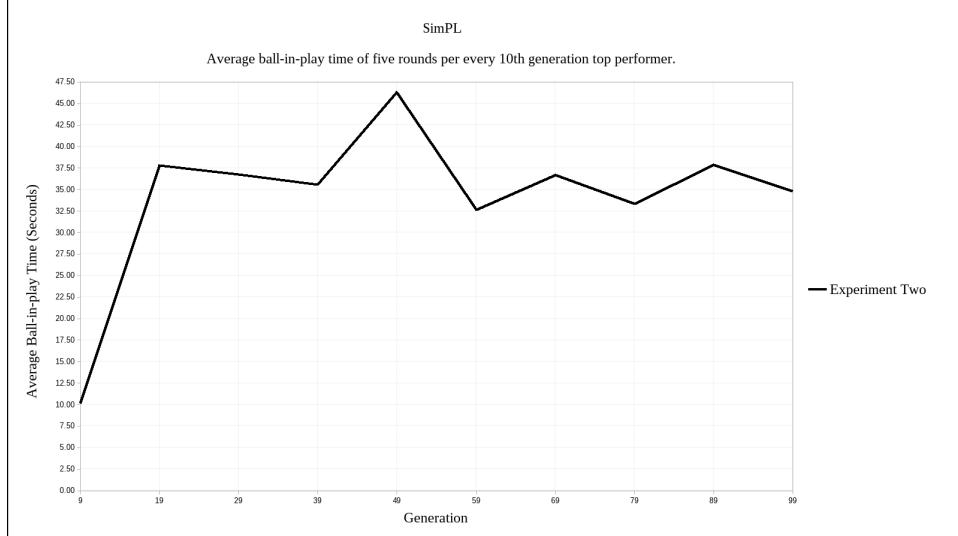


FIGURE 3.17: The average ball-in-play time (in seconds) of five rounds per every 10th generation top performer for experiment two.

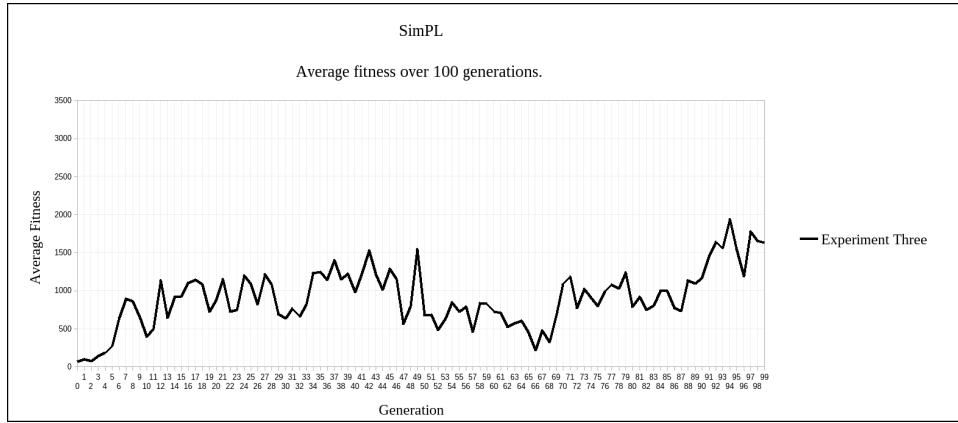


FIGURE 3.18: The average fitness over 100 generations for experiment three.

periment. After the experiment was over, the genetic algorithm self-adapted the crossover probability to 0.7816 and self-adapted the mutation probability to 0.2184. Notice in Figure 3.19 that the mutation probability overtook the crossover probability at first, but the two probabilities eventually diverged with mutation becoming less probable and crossover becoming more probable as the genetic algorithm produced fitter generations. This outcome is almost the exact opposite of the outcome shown in [15].

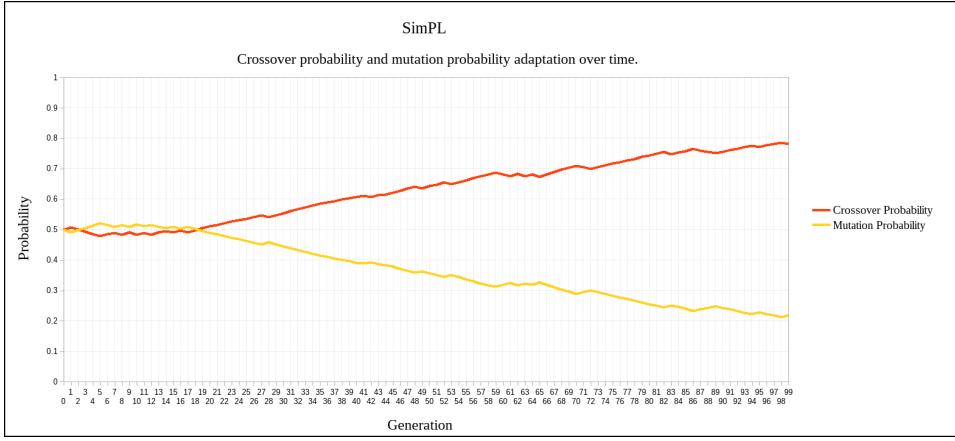


FIGURE 3.19: The self-adaptation of the crossover and mutation probabilities for experiment three.

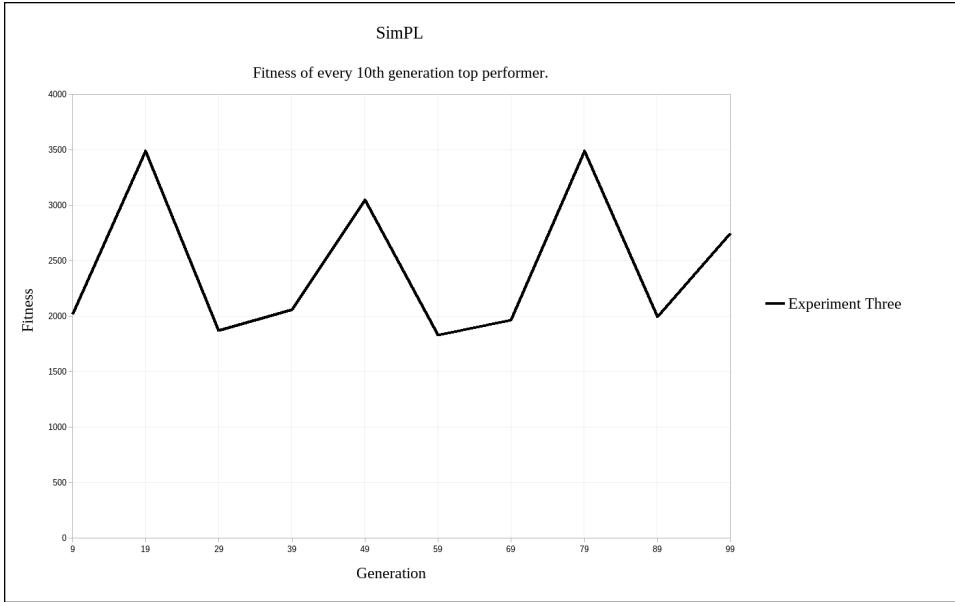


FIGURE 3.20: The fitness of every 10th generation top performer for experiment three.

3.5.4 Experiment four: static crossover and mutation probabilities with the crossover and mutation operators working in parallel.

Experiment four (Figures 3.22-3.24) produces similar results, with initial improvement in average fitness for the first 10 generations, but oscillation thereafter. However, the mean of the average ball-in-play times was 37.28646 seconds, over the mean 35.33994 seconds shown for the player learned in Experiment three and the mean 34.18604 seconds in Experiment two.

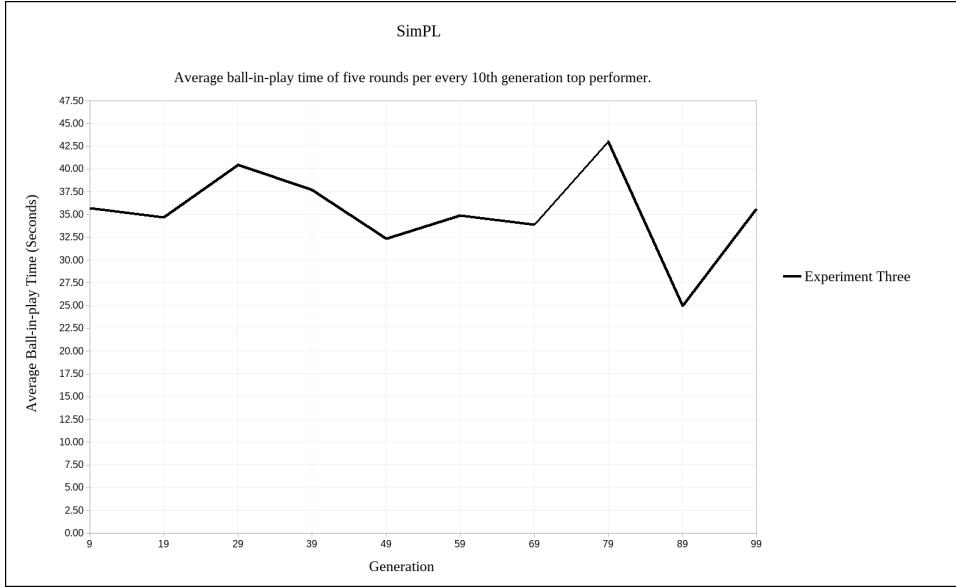


FIGURE 3.21: The average ball-in-play time (in seconds) of five rounds per every 10th generation top performer for experiment three.

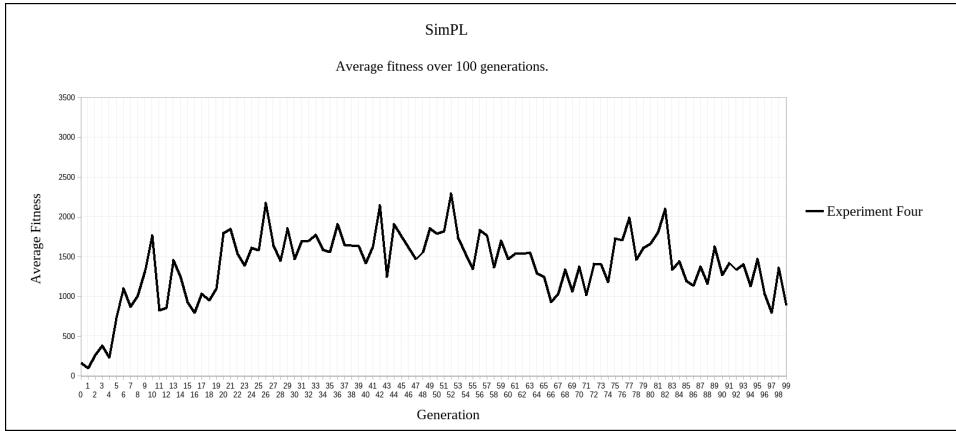


FIGURE 3.22: The average fitness over 100 generations for experiment four.

3.5.5 Experiment five: static crossover and mutation probabilities with the crossover and mutation operators working in sequence.

Experiment five (Figures 3.25-3.27) shows more gradual improvement in average fitness over the first 31 generations. Overall, the mean of the average ball-in-play times was 37.91126 seconds—higher than that of Experiment four.

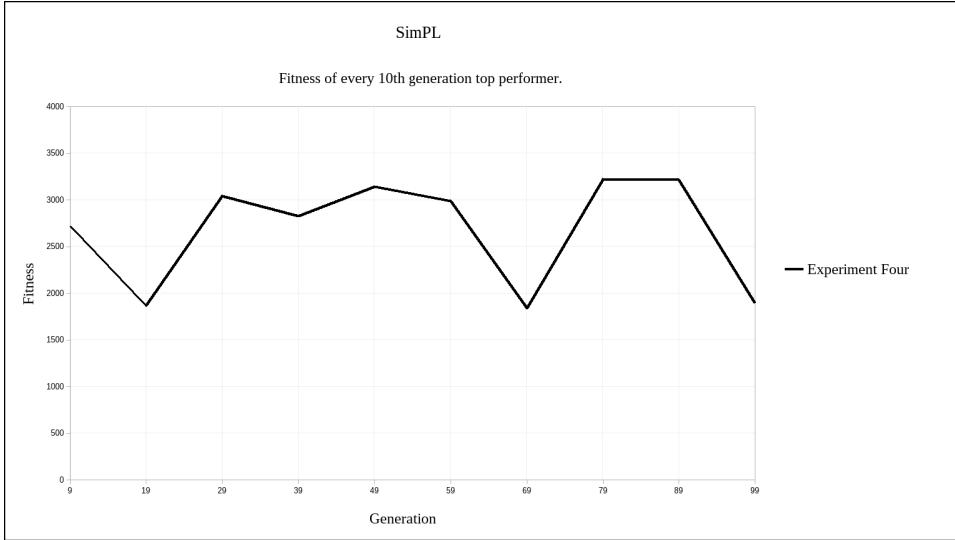


FIGURE 3.23: The fitness of every 10th generation top performer for experiment four.

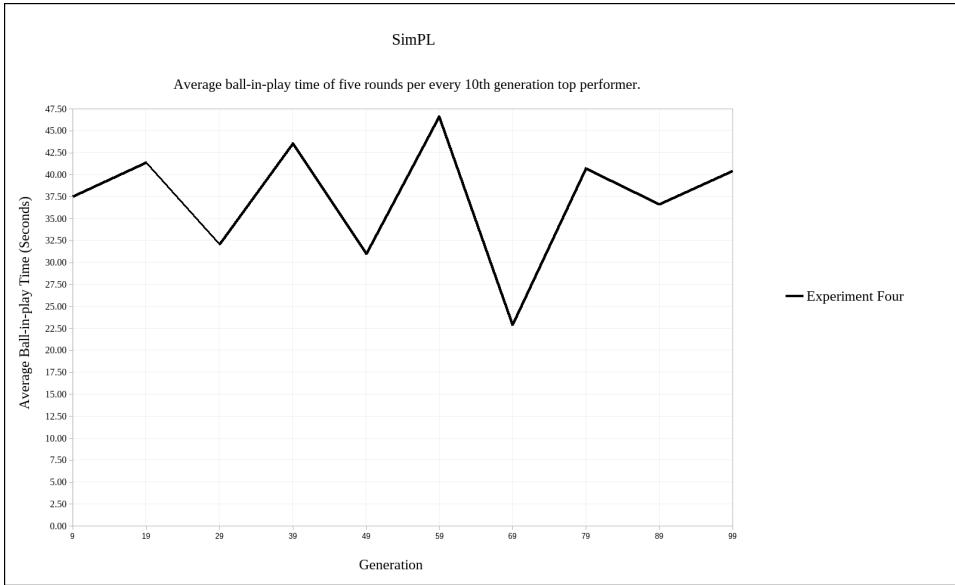


FIGURE 3.24: The average ball-in-play time (in seconds) of five rounds per every 10th generation top performer for experiment four.

3.5.6 Experiment six: fitness and ball-in-play upper bound.

Experiment six (Figures 3.28-3.30) illustrates the *perfect* results possible for a player who always behaves correctly. These metrics demonstrate optimal values, which can be considered targets for the evolution experiments. The mean of the average ball-in-play times was 40.01528 seconds, which means that Experiment

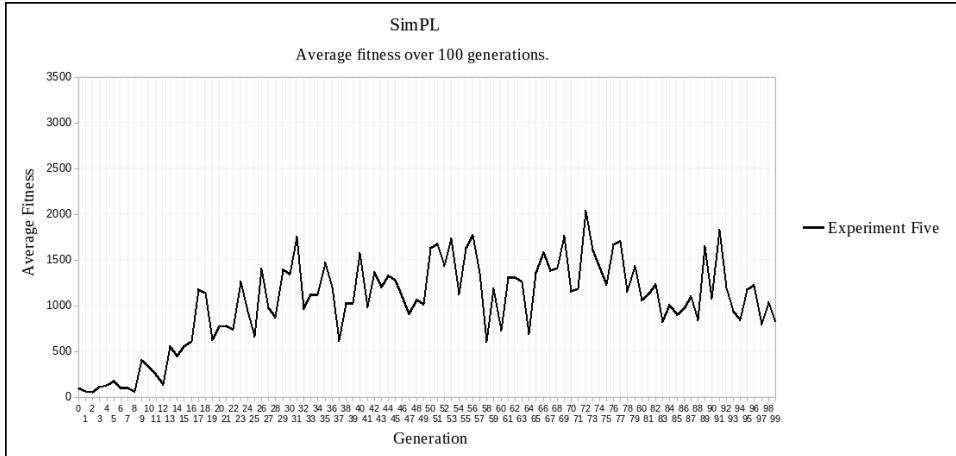


FIGURE 3.25: The average fitness over 100 generations for experiment five.

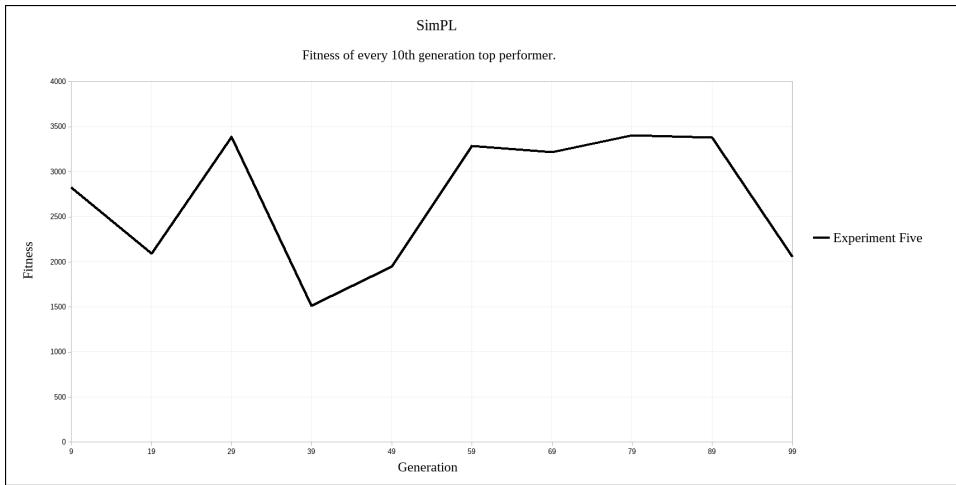


FIGURE 3.26: The fitness of every 10th generation top performer for experiment five.

five (above) comes closest to optimal performance.

3.5.7 Experiment seven: random paddles and an approximate lower bound.

Experiment seven (Figures 3.31-3.33) illustrates the results of a player who behaves randomly. This provides an example of worst case metrics. The mean of the average average ball-in-play times was 5.2656 seconds, which is comparable to the first-generation games of the evolved players.

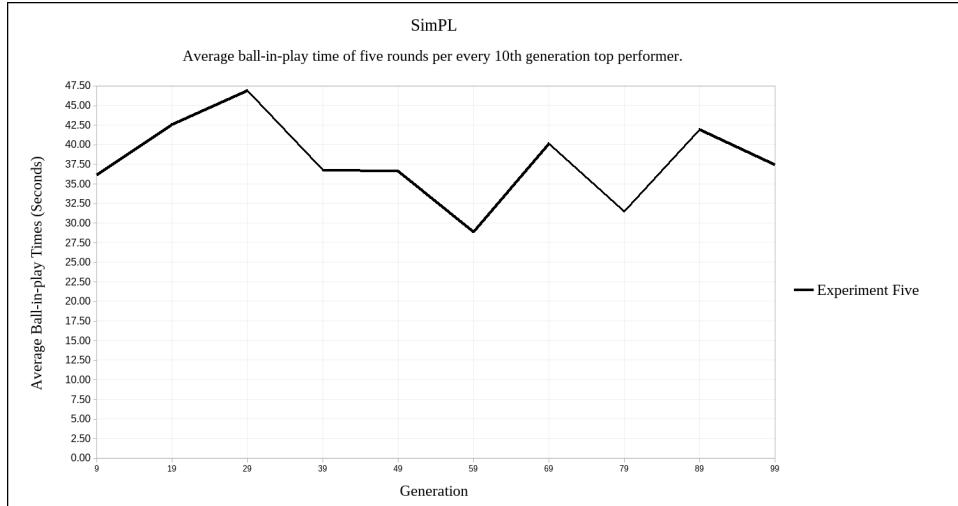


FIGURE 3.27: The average ball-in-play time (in seconds) of five rounds per every 10th generation top performer for experiment five.

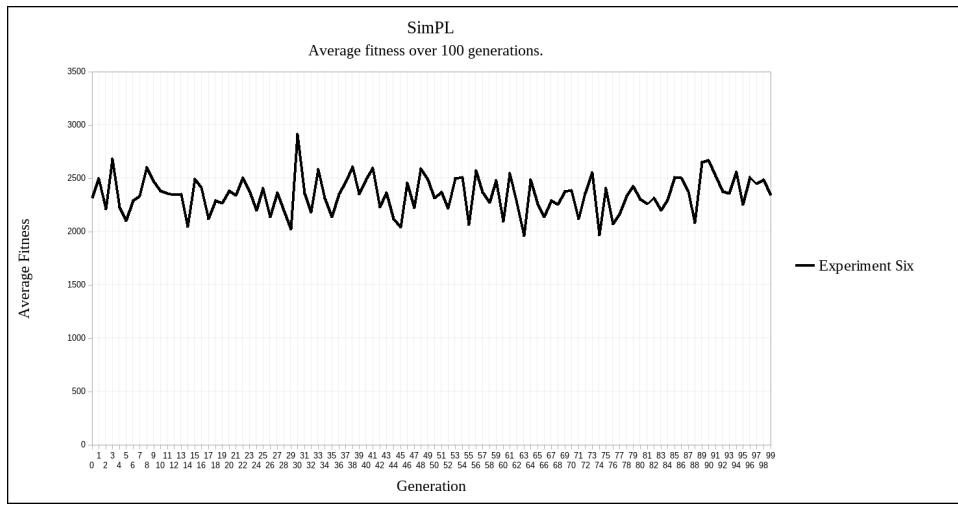


FIGURE 3.28: The average fitness over 100 generations for experiment six.

3.5.8 Comparative Results

This section illustrates comparative results by plotting all curves on the same axes (Figures 3.34 through 3.36). Figure 3.34 shows the average fitness over 100 generations for experiments one through seven. Figure 3.35 shows the fitness of every 10th generation top performer for experiments one through seven. Lastly, Figure 3.36 shows the average ball-in-play time (in seconds) of five rounds per every 10th generation top performer for experiments one through seven.

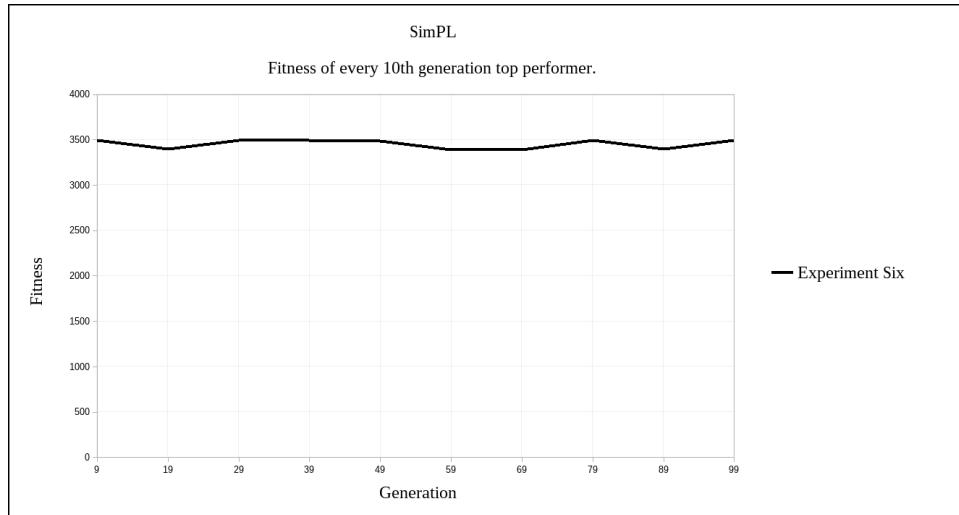


FIGURE 3.29: The fitness of every 10th generation top performer for experiment six.

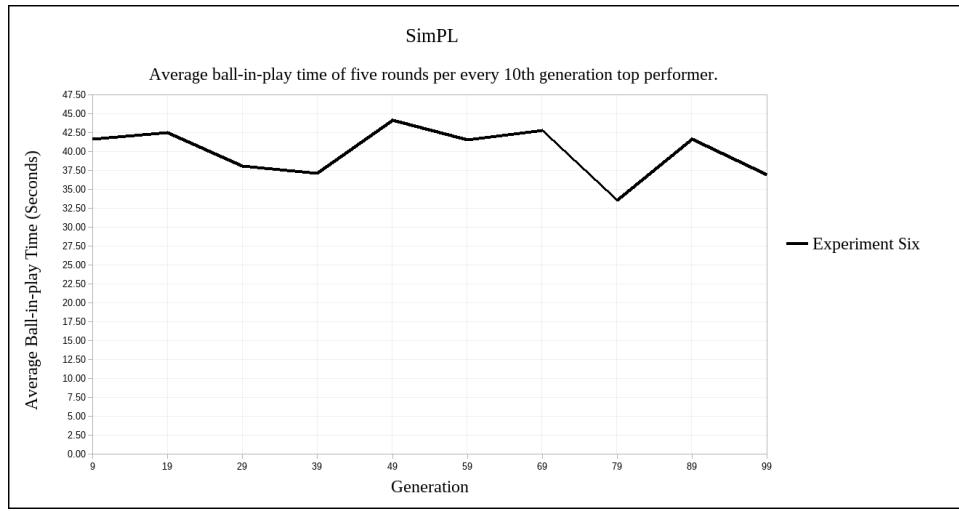


FIGURE 3.30: The average ball-in-play time (in seconds) of five rounds per every 10th generation top performer for experiment six.

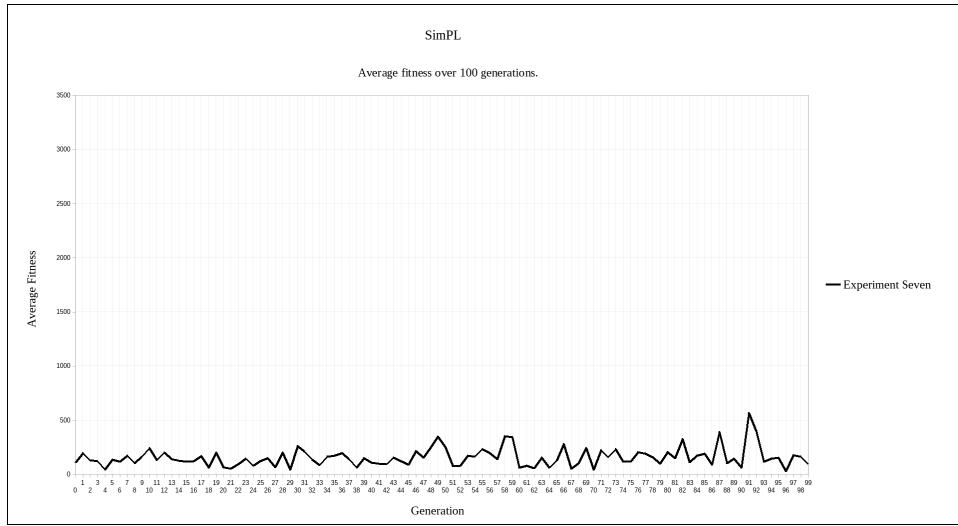


FIGURE 3.31: The average fitness over 100 generations for experiment seven.

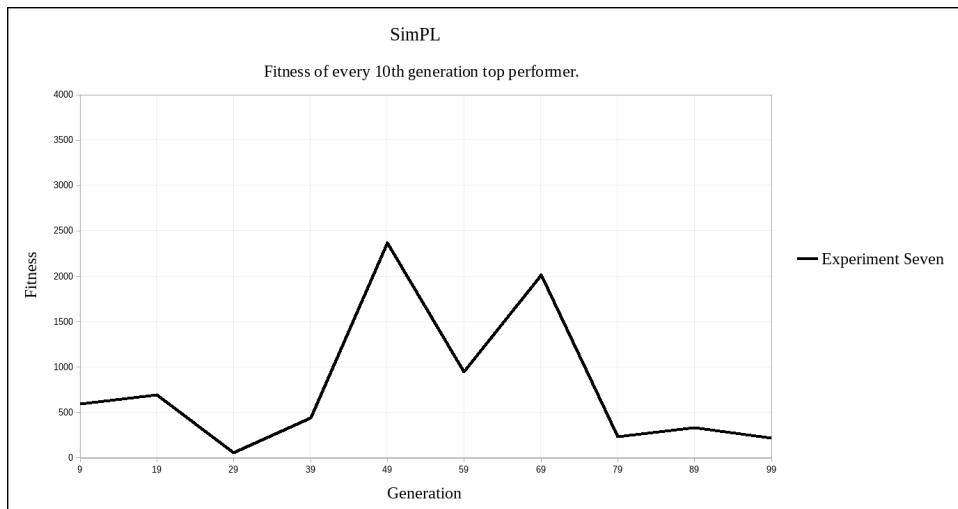


FIGURE 3.32: The fitness of every 10th generation top performer for experiment seven.

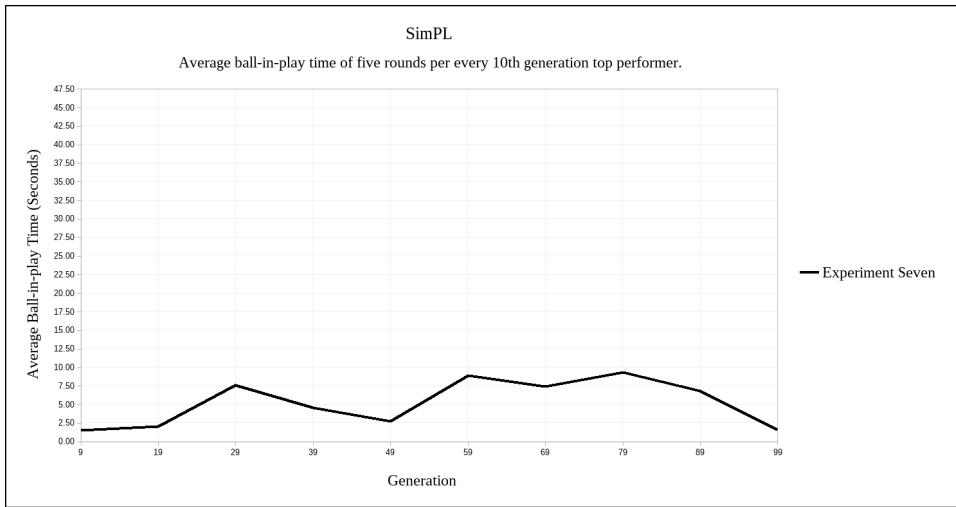


FIGURE 3.33: The average ball-in-play time (in seconds) of five rounds per every 10th generation top performer for experiment seven.

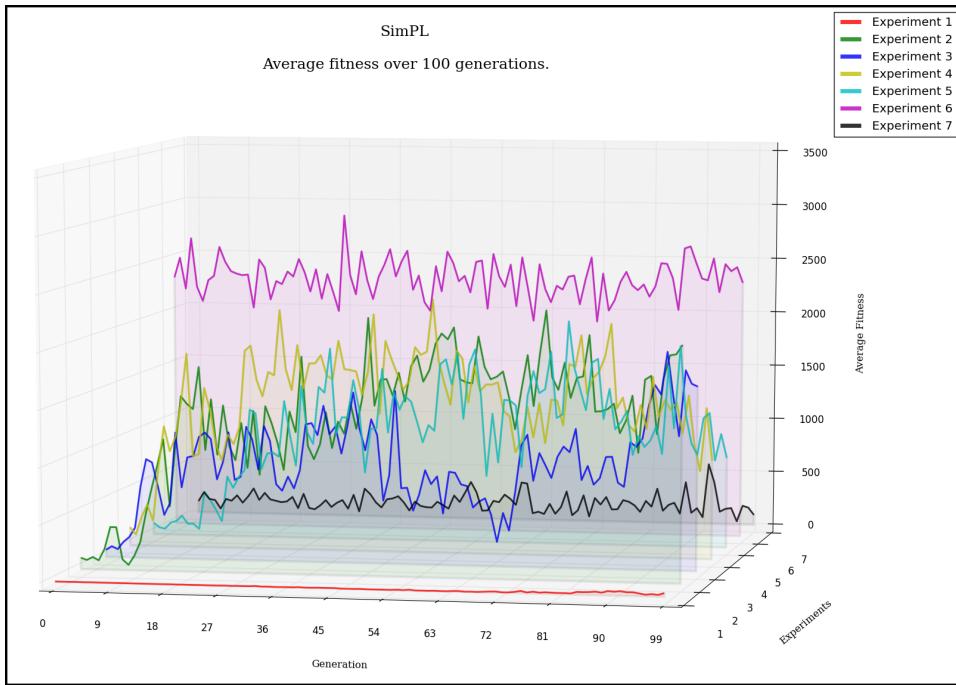


FIGURE 3.34: The average fitness over 100 generations for experiments one through seven.

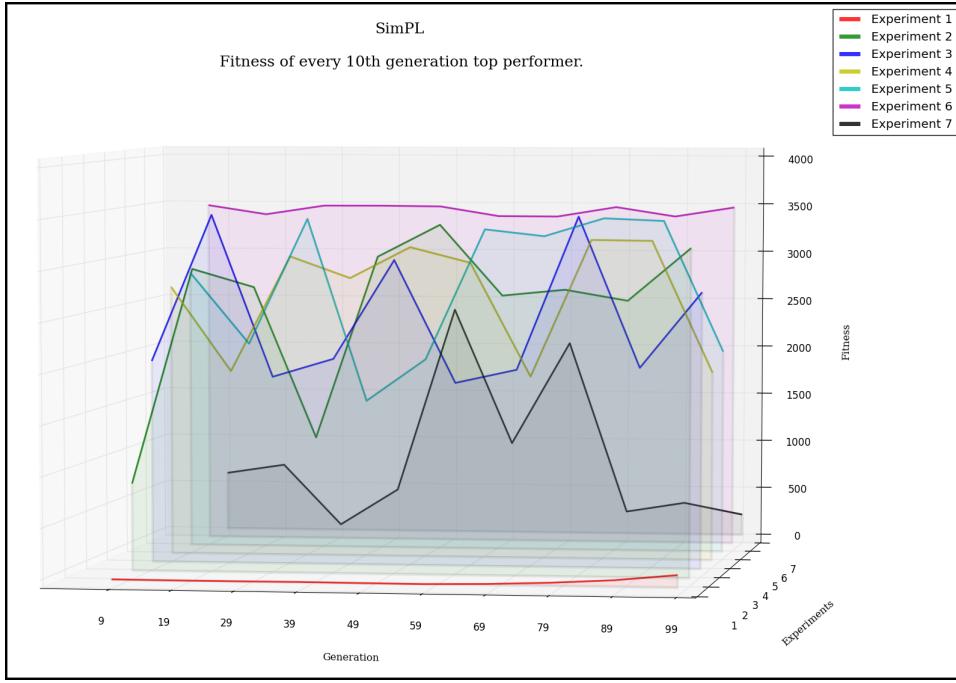


FIGURE 3.35: The fitness of every 10th generation top performer for experiments one through seven.

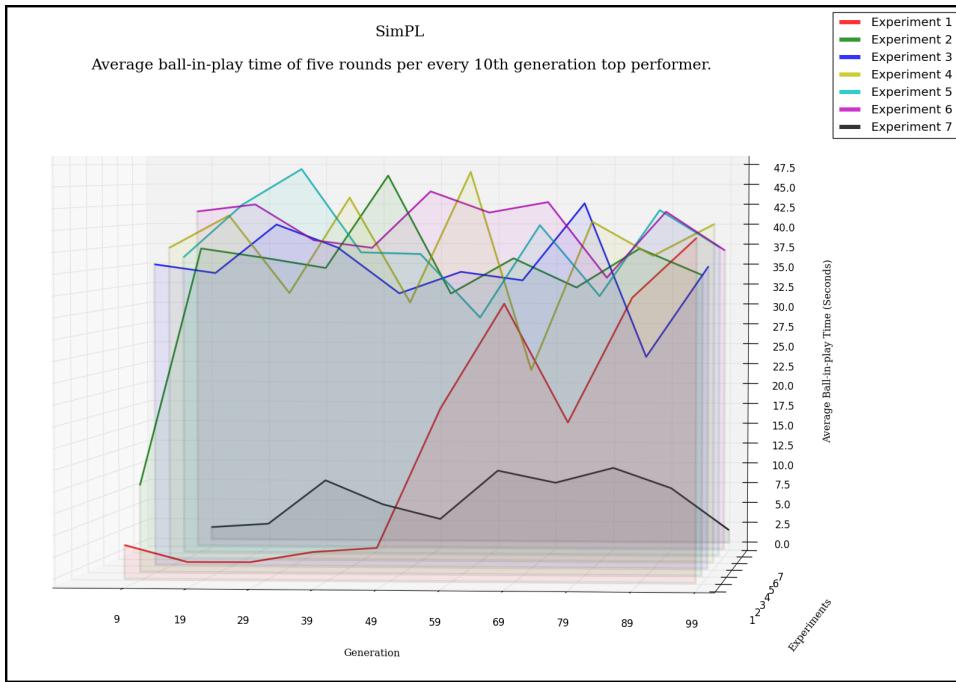


FIGURE 3.36: The average ball-in-play time (in seconds) of five rounds per every 10th generation top performer for experiments one through seven.

Chapter 4

BBAutoTune

4.1 Overview

The purpose of BBAutoTune is to find the correct combination of physics parameters such that the motion of a simulated robot is indistinguishable from its real-world counterpart. Components of BBAutoTune include a genetic algorithm, database manager, a graphical user interface (GUI) panel, and an external progress monitor which tracks various metrics of the running genetic algorithm.

4.2 Implementation

BBAutoTune's implementation builds off a 3D content creation platform known as Blender. Blender's various features allow one to author static or real-time interactive 3D content. Figure 4.1 shows Blender's GUI. Most of the components to BBAutoTune run inside of Blender itself with the exception of the external GA monitor. Blender's API uses the Python programming language and thus BBAutoTune was written entirely in Python.

4.2.1 Surveyor SRV-1 Blackfin 3D Model

The robot used during experimentation was a 3D model of the Surveyor SRV-1 Blackfin. This model is dimensionally and aesthetically based on the real robot. The extents of the model are $17.64cm \times 14.53cm \times 14.33cm$ including the Braille hat that rests above the body of the robot [3]. The base and the wheels are the only physics based objects on the model with the wheels being connected to the base via a rigid body hinge joint. See Figure 4.2. The robot's base was centered at the world origin and the robot was faced down

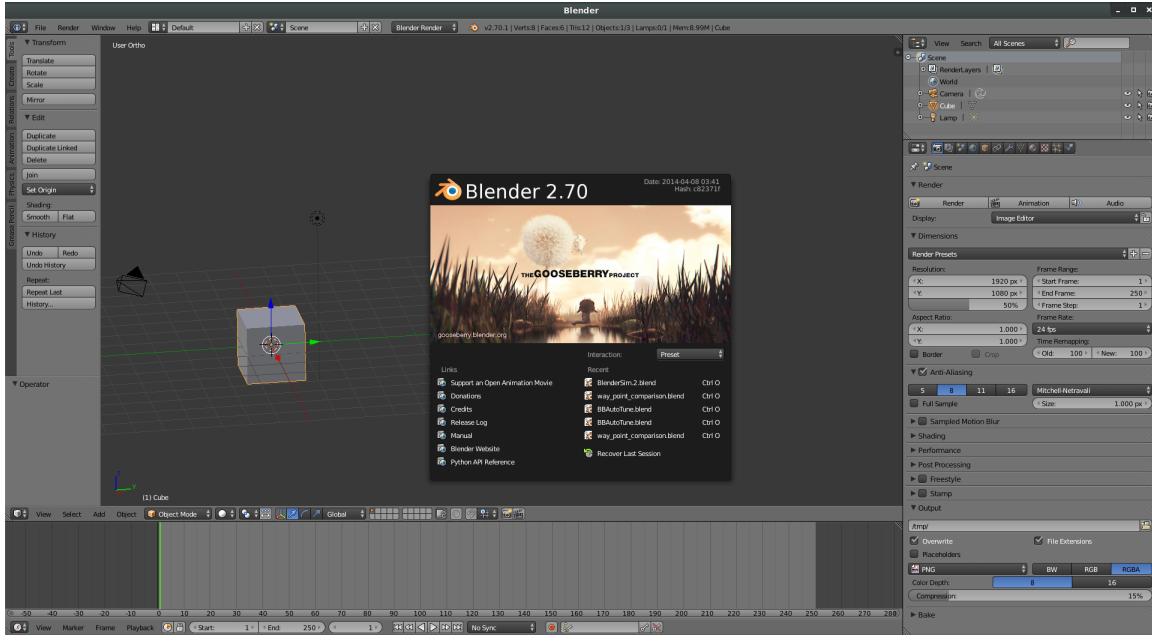


FIGURE 4.1: The Blender interface.

the global positive x-axis. All wheel geometry origins had a global z-axis position of 0.0 and were placed 1.37cm above the floor.

4.2.2 GUI

Blender's GUI can be extended via its Python API. BBAutoTune adds a custom panel to Blender that allows the user to specify certain parameters pertaining to the GA and the overall tuning loop. Once the user specifies their preferred parameters, they press start to begin the tuning process. After pressing start, BBAutoTune will continue to run until the GA has reached the maximum number of generations specified. See Figure 4.3.

4.2.3 Physics Engine API

To provide the capability of authoring 3D interactive content, Blender uses a real-time physics engine known as Bullet. Blender exposes the Bullet physics engine API via its own Python API. Most, if not all, of the parameters to Bullet can be modified via the physics engine API during or before running the Blender game engine. Ignoring duplicate ways to set the same parameter and duplicate parameters per dimension, there

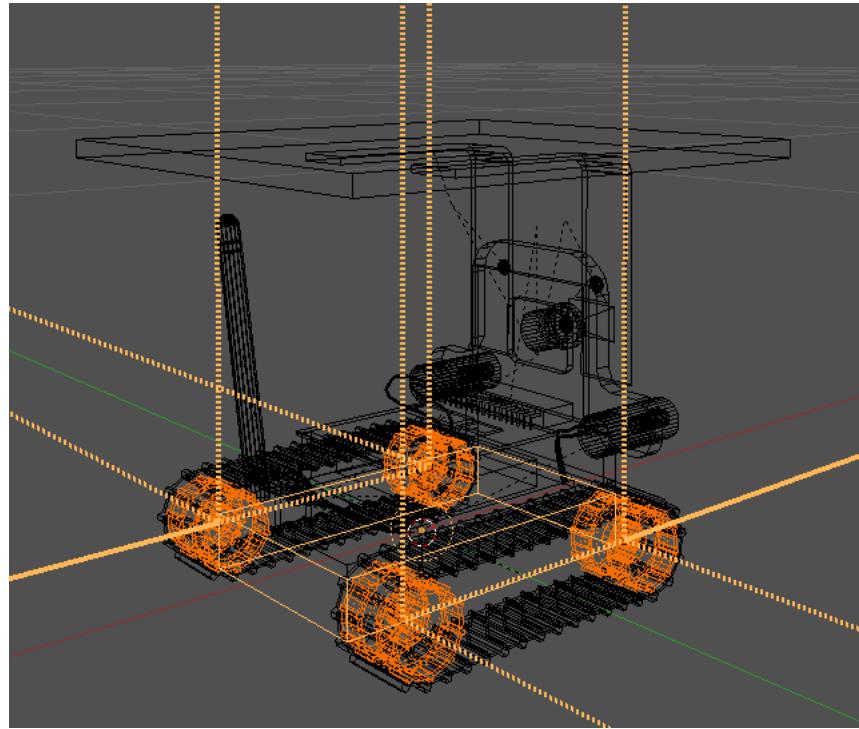


FIGURE 4.2: The 3D model of the Surveyor SRV-1 Blackfin with the wheels connected to the base via rigid body hinge joints.

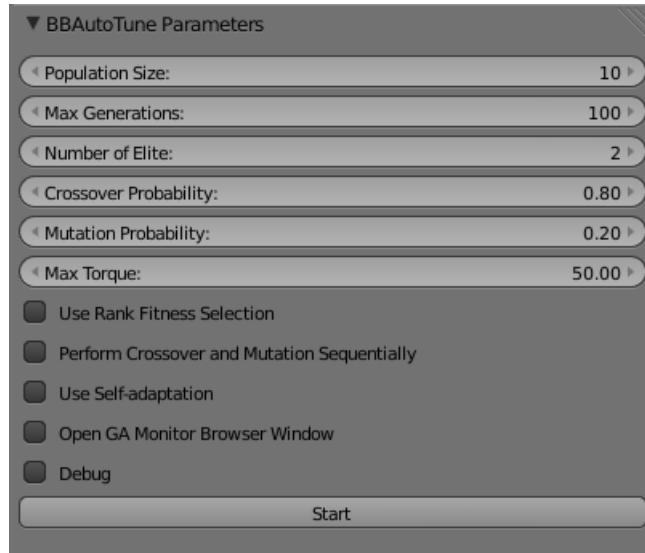


FIGURE 4.3: The BBAutoTune GUI panel added to Blender.

are 42 different physics engine parameters that can be set via the API.

4.2.3.1 Parameter Set

Blender's physics parameters can be set via its GUI or API. The API provides multiple avenues to set the same parameter depending on whether or not an API call is made from within Blender's built-in game engine or not. Each physics parameter is set to some default value at the start of Blender. All parameters have a range of either discrete or continuous values. Parameters such a *gravity* and *mass* are intended to reflect the real-world phenomena with the same names. Other parameters are more obscure such as:

1. *use material physics*—determines whether or not a material's physical properties (such as its friction coefficient and its collision elasticity) are taken into account during simulation;
2. *material force*—specifies an upward repellent spring like force;
3. *material damping*—dampens a material's spring force;
4. *material distance*—the distance at which a material's physical properties have an affect;
5. *material align to normal*—align physics objects along their surface normal;
6. *use actor*—determines if a physics object is seen by near and/or radar sensors;
7. *use ghost*—determines whether or not a physics object registers a collision when colliding with other physics objects;
8. *no sleeping*—if set, a physics object's position and orientation is still calculated by the physics engine even if the physics object is at rest;
9. *form factor*—the higher the value, the lower the likelihood a rigid body will roll when acted upon by some outside force;
10. *use collision bounds*—if set to false, a physics object's collision bounds is defaulted to a sphere shape;
11. *max physics steps*—specifies the maximum number of physics engine iterations per rendered frame;
12. *physics sub-steps*—specifying a higher value results in a more precise physical simulation model;

13. *FPS*—specifies the fixed physics time step such that the time step equals $\frac{1}{FPS}$ and is independent of the rendering frame rate; and
14. *deactivation time*—specifies the amount of time at which the physics engine will no longer calculate the position and orientation of a physics object that has a (angular or linear) velocity below some threshold [web].

See Table 4.1 for the full 42 parameter set complete with each parameter’s valid range and default value.

4.2.4 Database Manager

Running within Blender, the database manager opens a connection to a local MySQL database. For each evaluated genetic algorithm generation, the database manager stores the generation number, the highest fitness, the average fitness, the lowest fitness, the crossover probability, and the mutation probability in the database.

4.2.5 Robot Monitor

Running within the Blender game engine, the robot monitor records the position and rotation state of the simulated robot’s base throughout the duration of running the game engine. At the very start of the game engine, the robot monitor records the position and rotation¹ state S of the robot’s base with a time stamp T . After one second has passed, the robot monitor records the updated position and rotation state S' of the robot’s base with a time stamp T' . At this point, if the robot’s base has come to a rest, the robot monitor exits the game engine. Otherwise, if the robot’s base is still moving, the robot monitor will update S' and T' every half second for the rest of the evaluation period. After 16 seconds have elapsed, the robot monitor exits the game engine regardless of whether or not the robot’s base is still moving. Every time the robot monitor records S' and T' , it writes S , T , S' , and T' to a file that will be later read by the fitness function.

4.2.6 Progress Monitor

The progress monitor is an external and self-contained Python HTTP-CGI server that listens on port 8000. By visiting <http://localhost:8000/index.py>, a user can track the GA’s progress concerning the highest

¹Position meaning its world position in the x, y, and z dimensions and rotation meaning its world orientation around the x, y, and z axes.

Parameter	Range	Default Value
Gravity	[0.0 $\frac{m}{s^2}$,10000.0 $\frac{m}{s^2}$]	9.8 $\frac{m}{s^2}$
Max Physics Steps	[1,5]	5
Physics Sub-steps	[1,50]	1
FPS	[1,10000]	60
Linear Deactivation Threshold	[0.001,10000.0]	0.8
Angular Deactivation Threshold	[0.001,10000.0]	1.0
Deactivation Time	[0.0s,60.0s]	2.0s
Use Material Physics	[False,True]	True
Material Friction	[0.0,100.0]	0.5
Material Elasticity	[0.0,1.0]	0.0
Material Force	[0.0,1.0]	0.0
Material Damping	[0.0,1.0]	0.0
Material Distance	[0.0,20.0]	0.0
Material Align to Normal	[False,True]	False
Physics Type	[NO_COLLISION, STATIC, DYNAMIC, RIGID_BODY, SOFT_BODY, OCCLUDE, SENSOR, NAVMESH, CHARACTER]	STATIC
Use Actor	[False,True]	True
Use Ghost	[False,True]	False
Use Material Force Field	[False,True]	False
Rotate From Normal	[False,True]	False
No Sleeping	[False,True]	False
Mass	[0.0,10000.0]	1.0
Radius	[0.01m,inf]	1m
Form Factor	[0.0,1.0]	0.4
Use Anisotropic Friction	[False,True]	False
Anisotropic Friction X,Y,Z	[0.0,1.0]	1.0
Velocity Minimum/Maximum	[0.0,1000.0]	0.0
Lock Translation X,Y,Z	[False,True]	False
Lock Rotation X,Y,Z	[False,True]	False
Damping Translation	[0.0,1.0]	0.025
Damping Rotation	[0.0,1.0]	0.159
Use Collision Bounds	[False,True]	False
Collision Bounds Type	[BOX, SPHERE, CYLINDER, CONE, CONVEX_HULL, TRIANGLE_MESH, CAPSULE]	BOX
Collision Margin	[0.0m,1.0m]	6cm
Force	[-inf,inf]	0.0
Torque	[-inf,inf]	0.0
Linear Velocity	[-inf,inf]	0.0
Angular Velocity	[-inf,inf]	0.0
Use Local Force	[False,True]	True
Use Local Torque	[False,True]	True
Use Local Linear Velocity	[False,True]	True
Use Local Angular Velocity	[False,True]	True
Damping Frames	[-32768,32767]	0

TABLE 4.1: The various physics parameters, their ranges, and their default values. Note that inf=340,282,346,638,528,859,811,704,183,484,516,925,440.0 in Blender.

fitness, average fitness, lowest fitness, crossover probability, and the mutation probability. See Figure 4.4. Once the user presses start on the GUI panel, BBAutoTune starts the server as an external process with the option of opening a browser to the progress page. Once every minute, the progress monitor retrieves the most current GA run information from the local MySQL database which was populated by the database manager.

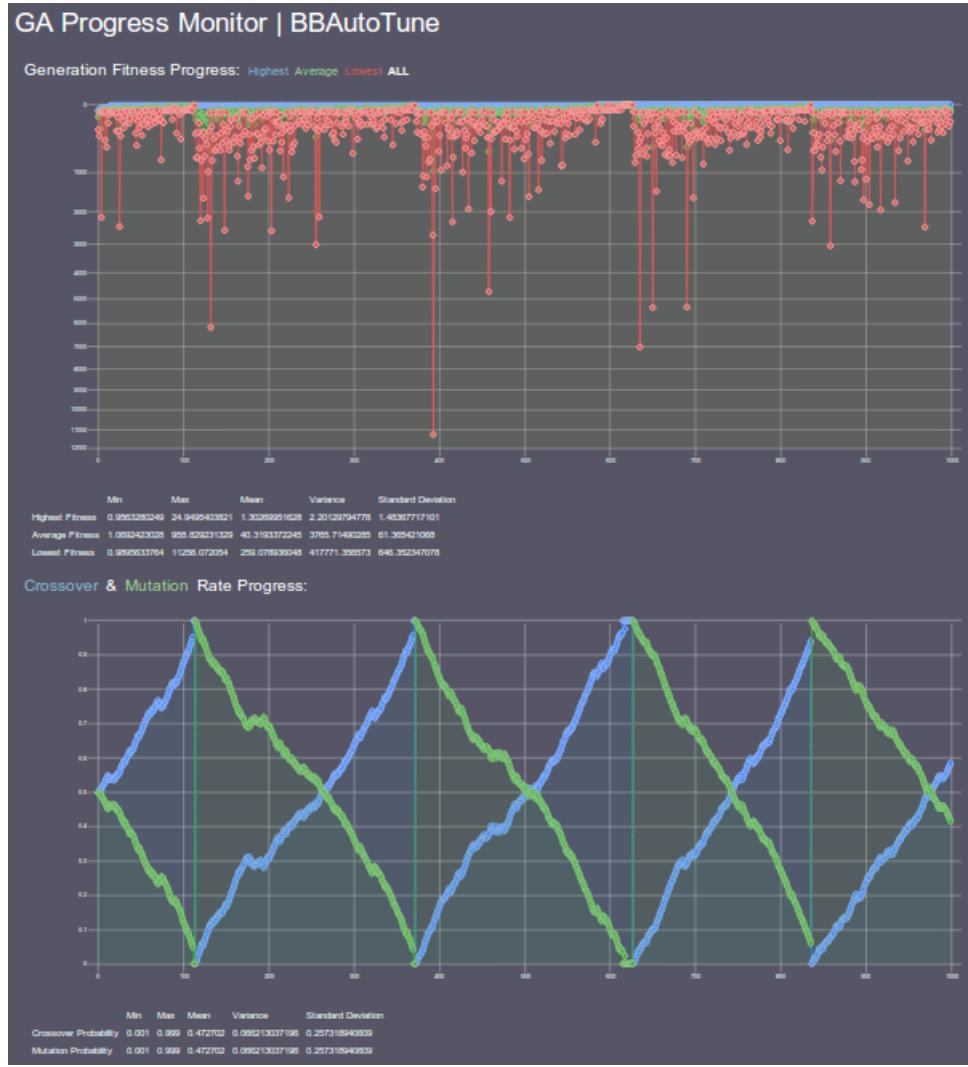


FIGURE 4.4: The external GA progress monitor.

4.2.7 Genetic Algorithm

The genetic algorithm for BBAutoTune was borrowed from the SimPL project and ported to Python with some aspects of the GA being altered to suit the needs of BBAutoTune. Since lower values of fitness are considered better than those of higher values of fitness, the population sorting function needed to be altered. Other portions altered were the selection operator, the population metrics calculator, and the self-adaptation algorithm.

4.2.7.1 Encoding Scheme

The physics parameters selected for tuning were a mixed set of floats, integers, string arrays, and boolean values (see Table 4.1). To ease the process of crossover and mutation, all genome genes were homogenized to a normalized range of [0.0, 1.0]. Let any given genome's gene value be g_i and any given physics parameter be p_i . For a float type with a maximum range value r_{max} and minimum range value r_{min} , the decoding function was $p_i = (g_i * (r_{max} - r_{min})) + r_{min}$. For an integer type, the decoding function was the same as for a float type except the whole value was floored. For an array A of strings type with size n (for example the collision bounds type parameter), the decoding function was $p_i = A[\lfloor g_i * (n - 1) \rfloor]$. Finally for a boolean type, the decoding function was

$$p_i = \begin{cases} \text{True} & \text{if } g_i \geq 0.5, \\ \text{False} & \text{if } g_i < 0.5. \end{cases}$$

4.2.7.2 Operators

The operators used include selection, elitism, crossover, and mutation. All of these operators work together to generate a new population once the current population has been fully evaluated by the fitness function.

The selection operator includes two variants: tournament selection and rank fitness selection. The user can indicate on the GUI panel if rank fitness selection is to be used—otherwise tournament selection will be used. Tournament selection works by gathering a sub-portion of the total population where the fittest genome among the sub-portion is selected thereby winning the tournament [18]. While gathering the sub-portion, all genomes in the population have a uniform probability of being included in the tournament,

regardless of their respective fitness values. There is the possibility that the same genome may be included in the tournament more than once. For crossover, two tournaments of size three are run, thereby giving two genomes to be crossed. For mutation, one tournament of size two is run, thereby giving one genome to be mutated. Rank fitness selection works by first sorting the population in non-increasing order according to fitness and then selects a genome at random where the probability of a genome being selected is proportional to its rank fitness. With the population in sorted order, the first genome is given a rank fitness of 1, the second genome is given a rank fitness of 2, ..., and the last genome is given a rank fitness of n which is the population size. The rank fitness prefix-sum for each genome is calculated in an array such that the first index value in the prefix-sum array is 1 while the last index value in the prefix-sum array is $\frac{n(n-1)}{2}$. A uniform random number is selected in the range $[0, \frac{n(n-1)}{2}]$. The genome selected G is the one in which the random number is greater than the previous prefix-sum for genome G_{i-1} and less than or equal to the prefix-sum for G_i . Genomes with a higher fitness will have a higher rank fitness and thus will have a higher probability of being selected for either crossover or mutation. See Figures 4.5 and 4.6.

```

BEGIN
    Population  $P$  with size  $n$  has been evaluated
    Sort  $P$  in non-increasing order
    For i=1 to  $n$  do
         $P[i-1].rankFitness = i$ 
    End for
    For i=0 to  $n - 1$  do
         $P[i].prefixSum = \sum_{k=0}^i (P[k].rankFitness)$ 
    End for
    Select a random number  $r = unif \left( 0, \frac{n(n-1)}{2} \right)$ 
    Genome selected  $G$ 
    For i=0 to  $n - 1$  do
        If  $P[i].prefixSum \geq r$  then
             $G = P[i]$ 
            Break
        End if
    End for
    Return  $G$ 
END

```

FIGURE 4.5: The rank fitness selection algorithm.

Rank Fitness Selection Example

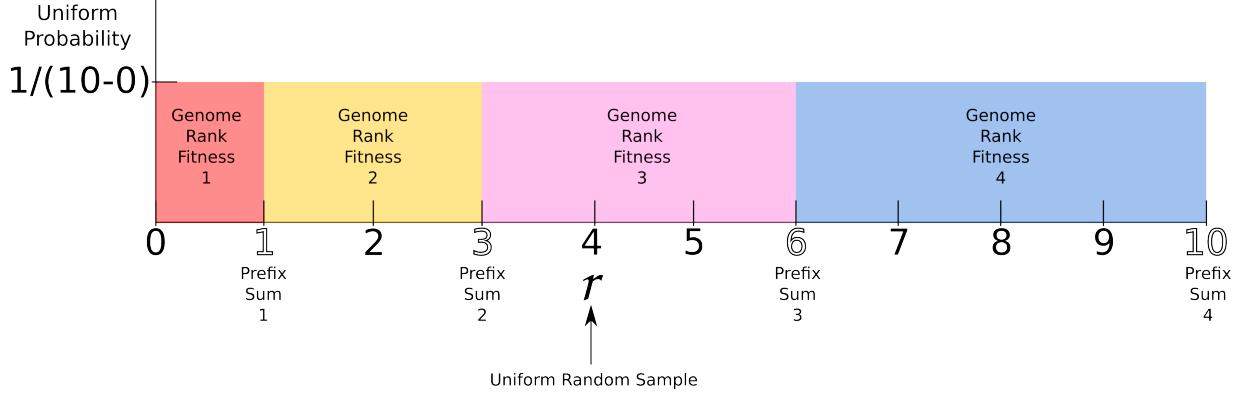


FIGURE 4.6: An illustrative rank fitness selection example. The population consists of four genomes where the rank fitnesses are one, two, three, and four. The prefix-sums are one, three, six, and 10. A random integer is sampled from a uniform distribution between zero and 10. Since the random number was four, the genome with a rank fitness of 3 would be selected. Notice that genomes with a higher rank fitness, have a greater uniform probability of being selected.

4.2.7.3 Fitness Function

To construct the fitness function, real robot motion data was collected which included 1040 sample points. Each sample point consisted of the x-position, y-position, and heading (z-orientation) of the robot before it moved and the x-position, y-position, and heading after the robot moved. With a camera overhead, the real robot was placed in the arena and was repeatedly commanded to go forward (relative from its current position and orientation) 25 centimeters. Care was taken to avoid having the robot collide with the arena walls. Once the robot consecutively moved forward three times, the robot rotated in place by 135 degrees and was not recorded during this period of rotation.

Using the camera, the robot’s position and orientation before and after performing each forward command was recorded. The robot’s position and orientation were not reset each time the robot performed a forward command. Instead, the robot was allowed to continue forward from its current position and orientation as it traveled around the arena. Thus each recorded pair of initial and final states was translated and rotated to be in the same reference frame such that the robot was always at the arena origin facing down the global positive x-axis before performing the forward command. See Figures 4.7 and 4.8. Note that from

the robot's perspective, it is always facing down its local positive x-axis no matter its position or orientation as seen from some other reference point. With all of the data transformed and rotated, each initial state had a x-position of 0.0, a y-position of 0.0, and an initial orientation of 0.0 degrees.

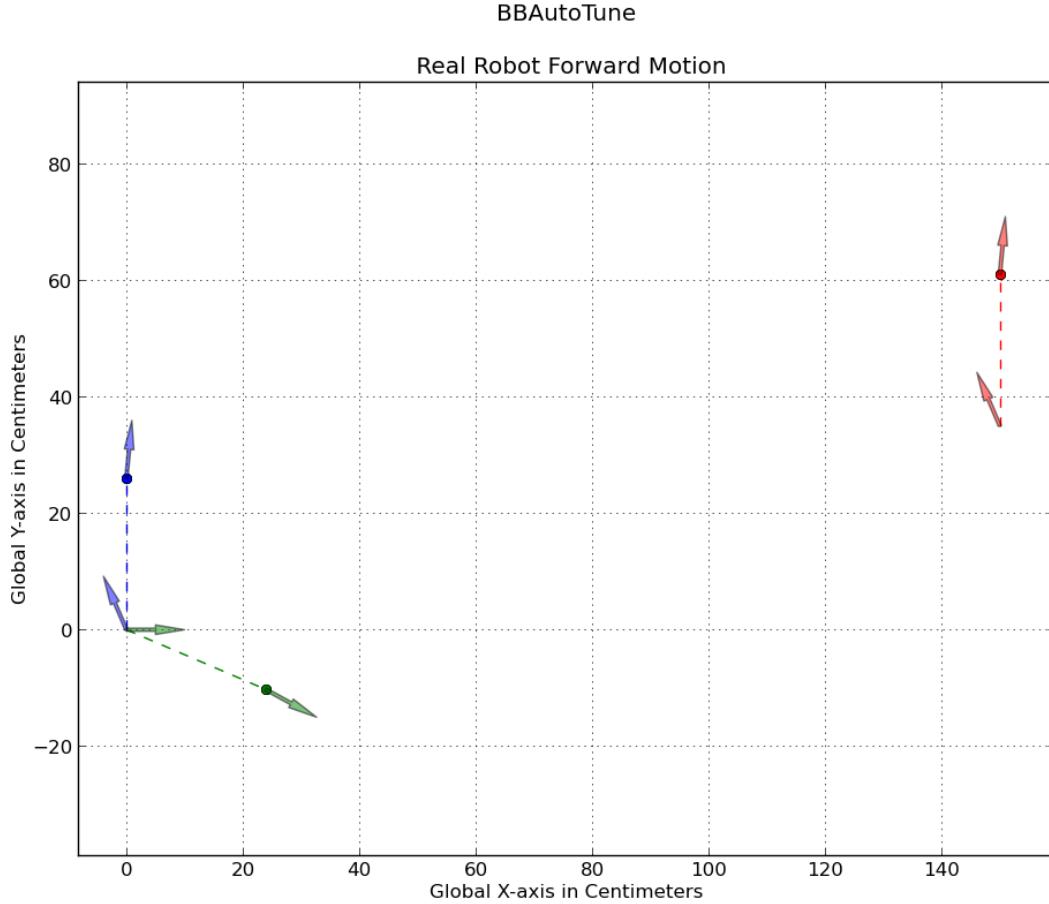


FIGURE 4.7: A specific instance of how the raw real robot forward motion data was translated and rotated such that each pair of initial and final states have the same reference frame. The red arrows, dot, and line represent the raw initial and final state of the robot recorded from the overhead camera before and after it performed the forward command. The blue arrows, dot, and line represent the initial and final state translated to the origin. The green arrows, dot, and line represent the initial and final state rotated by the amount needed to align the initial orientation with the positive global x-axis. For each colored group, the dot and arrow pair represent the position and orientation of the robot after having performed the forward command, while the arrow without a dot represents the position and orientation state of the robot before it performed the forward command.

Analyzing the distribution of final state x-positions, y-positions, and headings separately, all are unimodal and nearly symmetric with only a slight skew from their respective means. See Table 4.2 and Figure 4.9. When viewing the dimensions together, a large mass is centered around the point: 23.8644631679cm,

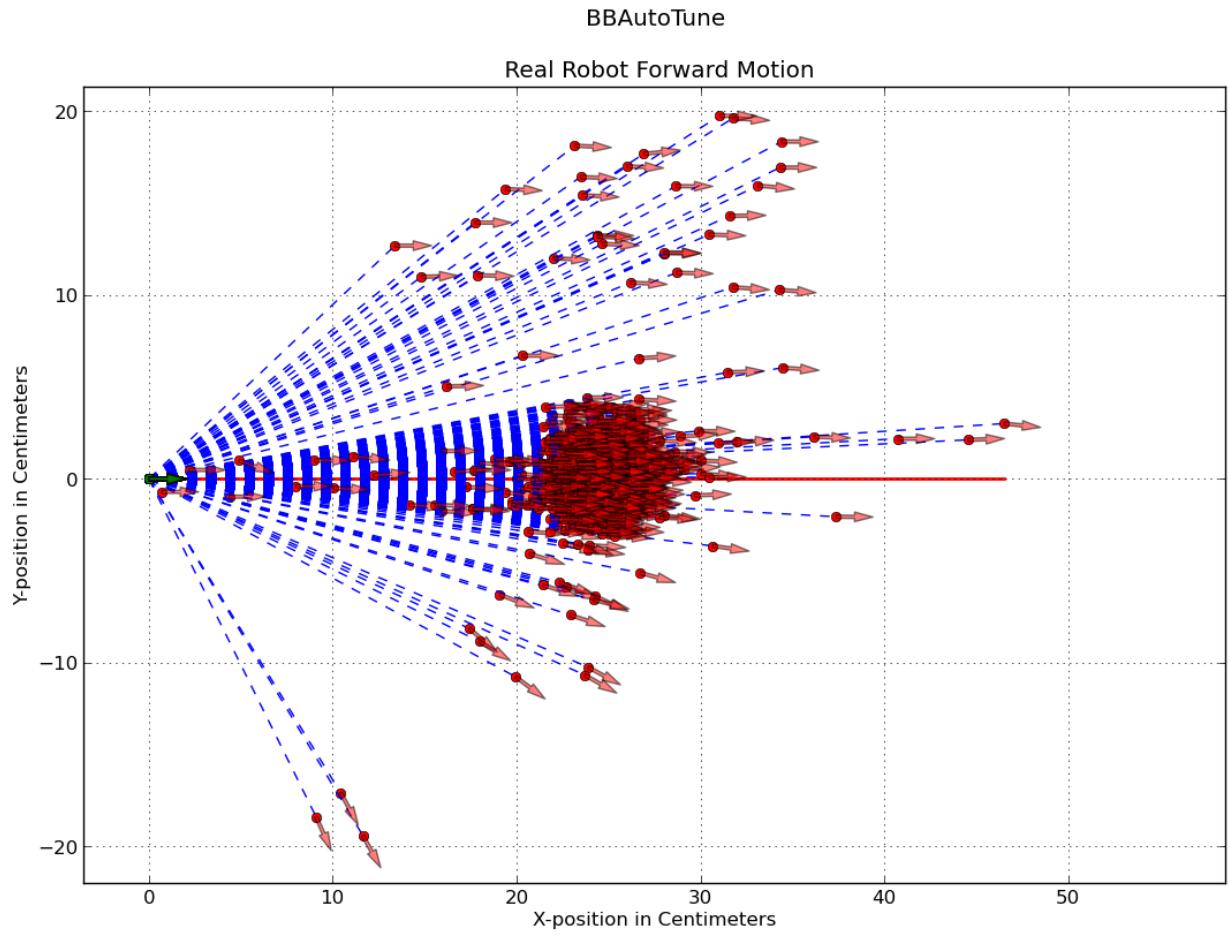


FIGURE 4.8: The collected real robot forward motion plotted from the same reference point. The green dots and arrows indicate the starting position and orientation of the real robot before the forward command was performed. The red dots and arrows indicate the ending position and orientation of the real robot after the forward command was performed. The dots represent position and the arrows represent orientation. The broken blue lines connect the initial states to their corresponding final states.

0.338269853117cm, and -0.00417473025048rad. See Figure 4.10. Based on the variance-covariance matrix, all three dimensions vary together and are not independent of one another.

	X-position	Y-position	Heading
Maximum	46.5183415482cm	19.7486813209cm	6.23776rad
Minimum	0.0cm	-19.4028539247cm	-1.148163rad
Mean/Centroid	23.8644631679cm	0.338269853117cm	-0.00417473025048rad
Mode	25.0cm	-1.0cm	0.0rad
Variance	10.3960320996	9.46441502772	0.152467827567
Standard Deviation	3.22428784378	3.07642894079	0.390471289043
Covariance with X-position	10.4060572	2.3348963	0.0685591
Covariance with Y-position	2.3348963	9.47354175	0.08654865
Covariance with Heading	0.0685591	0.08654865	0.15261486

TABLE 4.2: The distribution metrics of final state x-positions, y-positions, and headings after the real robot moved forward.

With the real robot motion data collected and analyzed, a metric was needed for the fitness function. This metric would need to indicate how different or dissimilar the movement of the simulated robot was from the real robot while running the GA. The intuition was that as the simulated robot motion moved closer to the centroid of the real robot motion, the simulated motion would become increasingly indistinguishable from the real motion. Various distance functions were considered and the Mahalanobis distance (MD) was chosen as the basis for the fitness function. The MD is a generalized form of the Euclidean distance, such that the MD accounts for the correlation in the data set since it is computed using the inverse of the variance-covariance matrix [19]. For uncorrelated data, the MD reduces to the Euclidean distance [20].

Noise introduced by the overhead camera and the timing at which the position and orientation state of the real robot was captured could have potentially skewed the real robot motion model with outliers, ultimately resulting in a skewed multivariate mean location and a skewed inverse variance-covariance matrix, making the MD skewed. To account for the potential outliers in the real motion data set, a robust² mean location and a robust variance-covariance matrix was computed from the data set using the Fast-MCD algorithm implemented in the Scikit-learn Python module [22][23]. The classical mean location was 23.8644632cm, 0.338269853cm, and -0.00417473025rad for final state x-positions, y-positions, and headings respectively while the robust mean location was 23.9934044cm, 0.0351240536cm, and -0.0189964938rad for

²Robust meaning the robustness of an estimator's resistance to outliers or data point contamination [21].

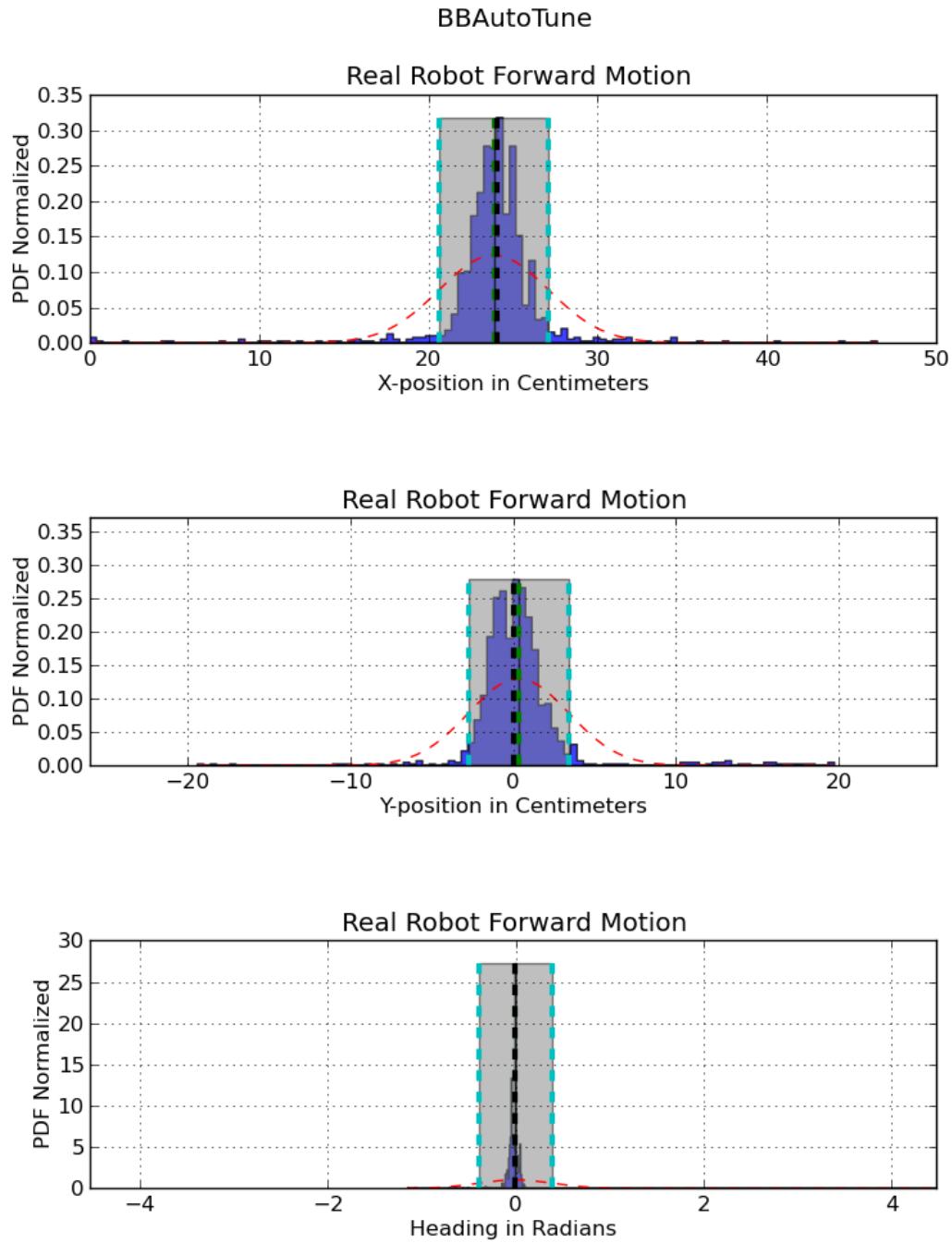


FIGURE 4.9: The distributions of final state x-positions, y-positions, and headings (after being translated and rotated to the same reference frame) recorded for the real robot forward motion. The broken black bar represents the mode, the green broken bar represents the mean, the cyan broken bars represent one standard deviation from the mean, and the red broken curve represents the best fit normal curve.

BBAutoTune
Real Robot Forward Motion

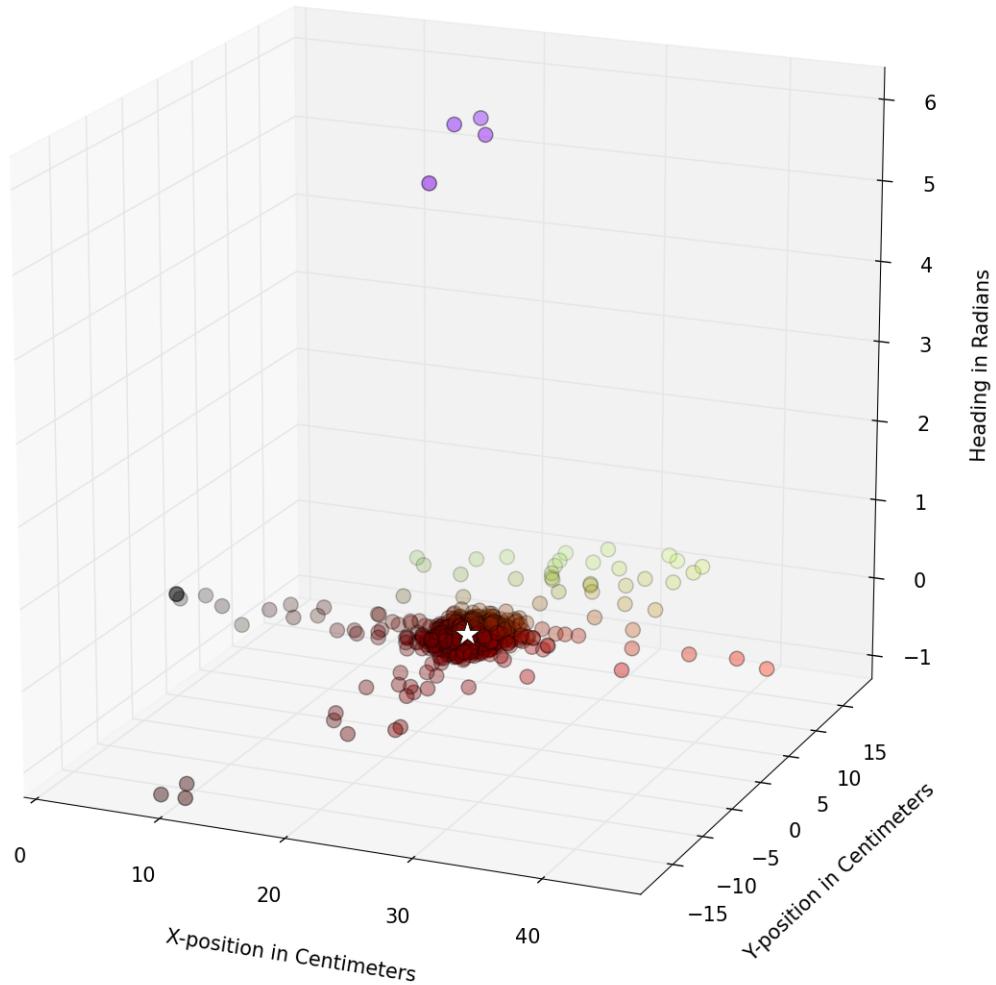


FIGURE 4.10: A 3D scatter plot of final state x-positions, y-positions, and heading values for the real robot after it performed the forward command. Positive values of x-position, y-position, and heading contribute a portion of red, green, and blue respectively to each scatter plot. The star located at the center of the large mass of points is the centroid.

final state x-positions, y-positions, and headings respectively. The left matrix below is the classical variance-covariance matrix, while on the right is the robust variance-covariance matrix returned by the Fast-MCD algorithm.

$$\left(\begin{array}{ccc} 10.3960321 & 2.33264688 & 0.06849305 \\ 2.33264688 & 9.46441503 & 0.08646527 \\ 0.06849305 & 0.08646527 & 0.15246783 \end{array} \right) \left(\begin{array}{ccc} 1.46298445 & 0.13924542 & 0.00223493 \\ 0.13924542 & 1.64197605 & 0.0168499 \\ 0.00223493 & 0.0168499 & 0.00173777 \end{array} \right)$$

The resulting samples weighted higher than others by the Fast-MCD algorithm are shown in Figure 4.11. These samples were used to calculate the robust mean and the robust variance-covariance matrix returned by the algorithm. By substituting the robust mean and the inverse of the robust variance-covariance matrix into the MD calculation, the robust distance (RD) for any sample point can be computed [21]. Comparisons between the MD and the RD for each of the 1040 real robot motion data points are shown in Figure 4.12. As the data points travel away from the centroid, the RD increases more rapidly than the MD.

Only three out of the total six degrees of freedom were recorded for the real robot. However, in Blender there were an additional three degrees of freedom (pitch, roll, and heave or up and down) to contend with. Thus, the simulated-robot base's x-rotation, y-rotation, and z-translation were constrained. Additionally, all wheels had their z-translation constrained. As an added precaution, penalties were added onto the robust distance by the absolute amount the simulated robot's base violated any rotation around the global x-axis, any rotation around the global y-axis, and/or any translation up or down the global z-axis. Additionally, a time penalty was added onto the robust distance by the amount of time in seconds the simulated robot took to evaluate (or rather took to come to a complete stop) greater than one second with a maximum penalty of 15 seconds since any given evaluation period only lasted a total of 16 seconds. This time penalty was necessary since it was observed that the real robot never took more than one second to come to a complete stop after moving forward. Without a time penalty, for example, a simulated robot could move just as the real robot and it would be given an erroneously high fitness even though it took 16 seconds to come to a complete stop. This undesirable scenario was avoided by using a time penalty.

Once the simulated robot was run through the game engine evaluation period (using the physics parameter settings decoded from the currently being evaluated genome G_i 's genes), 14 pieces of data was

BBAutoTune
Real Robot Forward Motion Robust Support Samples

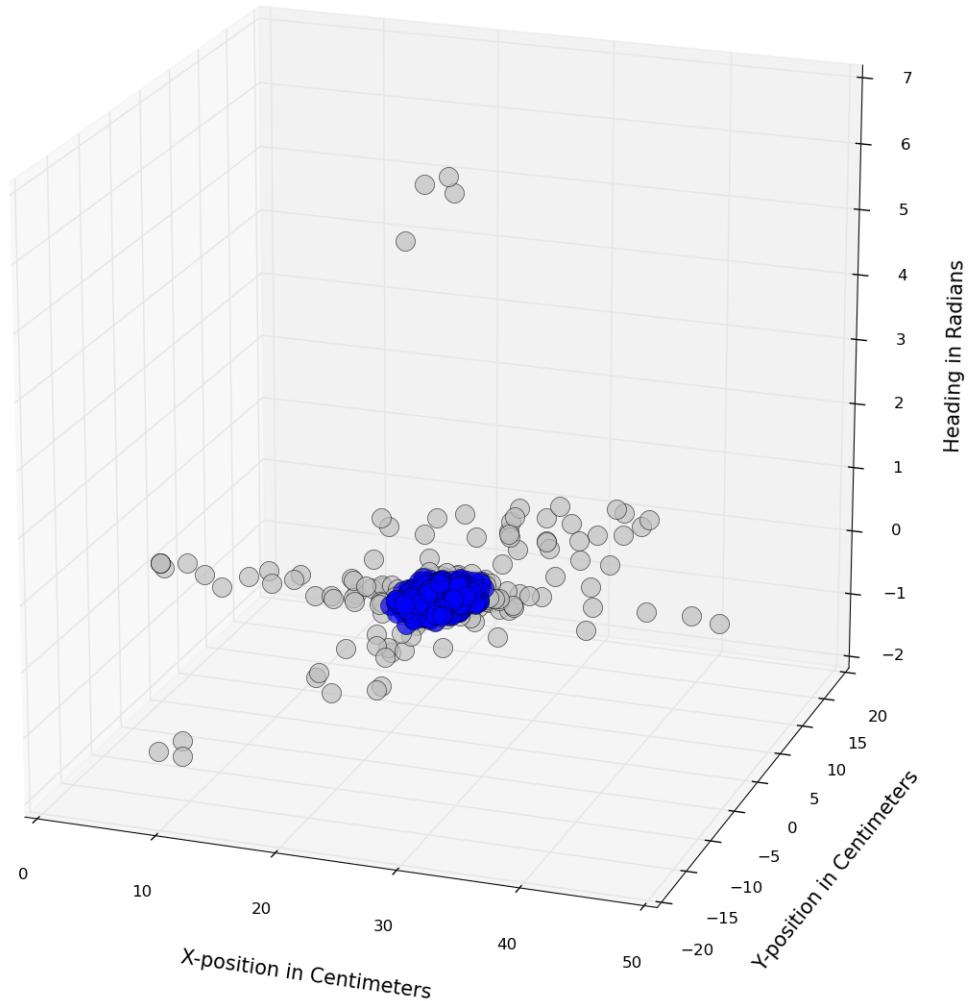


FIGURE 4.11: A 3D scatter plot of the support samples in blue used to calculate the robust mean location and the robust variance-covariance matrix as returned by the Fast-MCD algorithm.

BBAutoTune

Real Robot Forward Motion MD versus RD

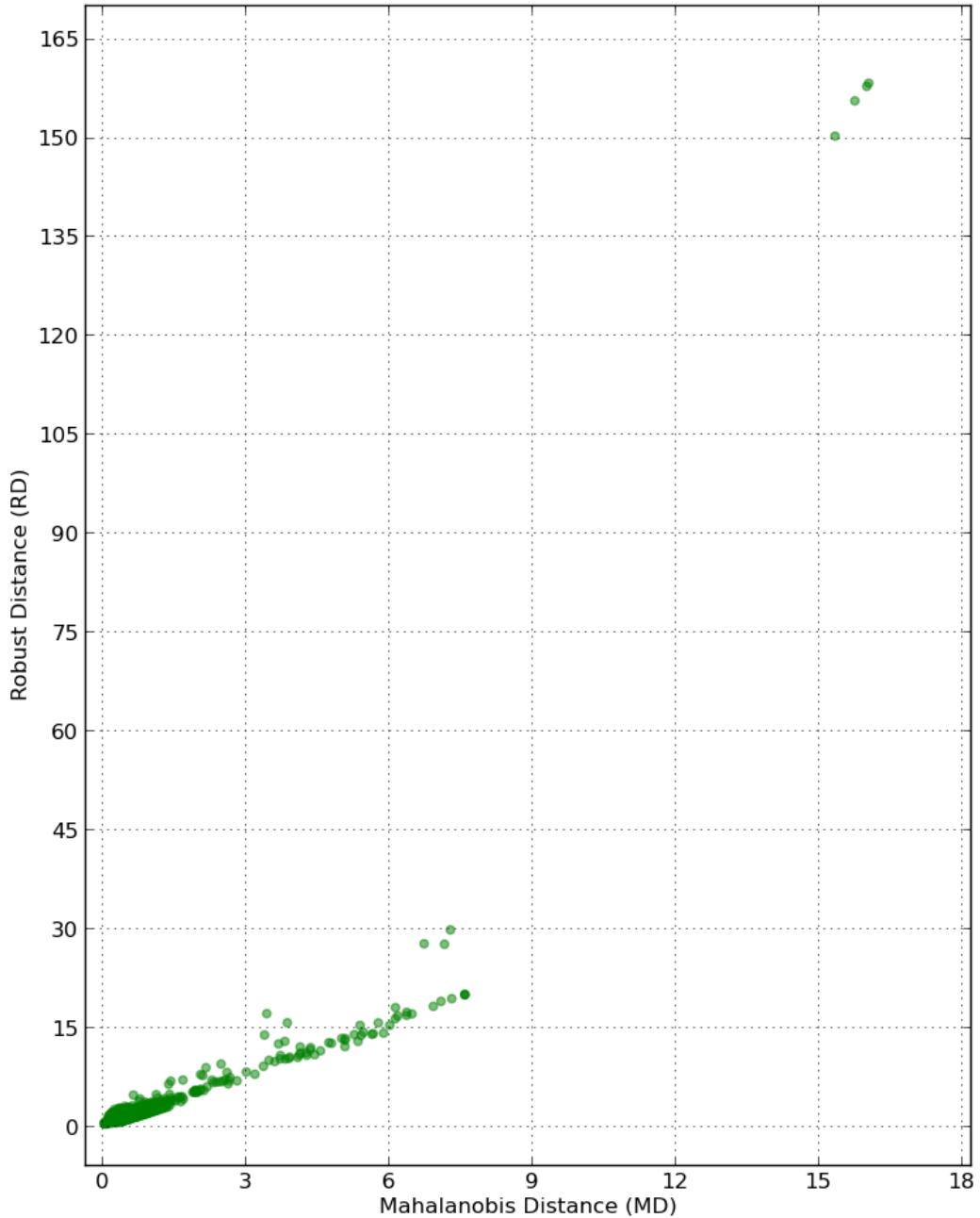


FIGURE 4.12: A scatter plot comparing the Mahalanobis distance versus the robust distance for each data point collected of the real robot motion.

collected by the robot monitor for use in the fitness function. Let $S = [x_p, y_p, z_p, x_o, y_o, z_o, T]$ be the starting state of the simulated robot at the beginning of the evaluation period at time $S[6] = T$ where the subscript p refers to position and the subscript o refers to orientation. Let $S' = [x_p, y_p, z_p, x_o, y_o, z_o, T']$ be the ending state of the simulated robot at the end of the evaluation period at time $S'[6] = T'$. Also, let $RD(x - \text{position}, y - \text{position}, z - \text{orientation})$ be the robust distance. The fitness of G_i was defined as $Fitness(S, S') = RD(S'[0], S'[1], S'[5]) + |S'[4] - S[4]| + |S'[3] - S[3]| + |S'[2] - S[2]| + ((S'[6] - S[6]) - 1) = G_i$'s fitness. The range of this function is $[0, \infty)$. Since the goal of this thesis was to have the simulated robot move as the real robot, the desired output of this function was 0.0 implying that three objectives were met:

- The simulated robot's x-position, y-position, and z-orientation (heading) after moving forward was 23.9934044cm, 0.0351240536cm, and -0.0189964938rad respectively.
- The simulated robot came to a complete stop after one second.
- The simulated robot did not fall through the floor, flip over, roll over, and/or launch upward.

Thus the goal of the GA was to minimize this function whereby lower output values were a higher fitness than higher output values.

4.2.7.4 Evaluation Setup

For each evaluation period (the running of the game engine), the 3D robot model's local coordinate system was axis aligned with the world coordinate system, the robot was faced forward looking down the positive global x-axis, and its local origin was placed at the world origin. See Figure 4.13. Before each evaluation period, the physics engine parameters were set to the values decoded from the genes of the currently being evaluated genome. All evaluation periods lasted no more than 16 seconds. If the robot stopped moving before 16 seconds, then the evaluation period ended immediately. The only applied force to the robot was the wheel torque, where each wheel received the same amount of applied torque for the same duration. The duration of applied torque was roughly 16 milliseconds after which no further force was applied to the robot.

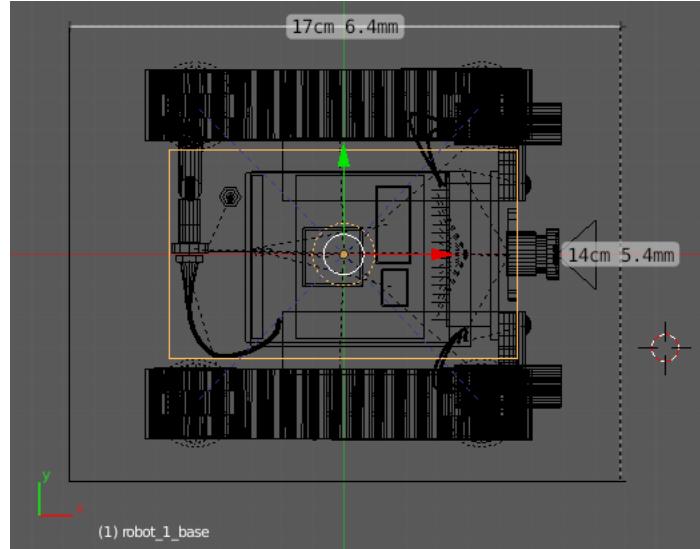


FIGURE 4.13: The simulated robot’s local coordinate system axis aligned with the world coordinate system.

4.3 Platform

For all experiments, BBAutoTune was run on a 64bit Linux operating system with 32GB of RAM and an Intel Core i7-4770K four core processor running at 3.9GHz.

4.4 Experimental Designs

The purpose for experiment one was to determine a base set of physics parameters that have significant influence over the physics simulation. Experiments two through five involved actually tuning the physics engine and comparing the simulated versus real robot motion. Self-adaptation and tournament versus rank fitness selection were the experimental GA parameters for experiments two through five.

4.4.1 Experiment one: physics engine parameter influence.

The potential Blender physics engine parameter candidates—to be tuned by the GA—were analyzed for their influence over the physics simulation. To accomplish this goal, a racquetball-like environment was constructed in Blender which consisted of a ball, an enclosed arena, and an automated racquet controlled via a Python script. See Figure 4.14. Note that the ball was allowed to travel in all three dimensions and was completely physics based.



FIGURE 4.14: The racquetball environment used to test the physics engine parameter candidates' influence over the physics simulation.

Fourty-four candidate parameters were selected for testing in the racquetball environment (see Table 4.3). All parameters tested were only associated with the ball. Before all of these parameters were tested for their influence, *nice* values were selected for each such that the ball’s behavior appeared normal based on visual observation. A standard was established where the ball was allowed to run for five seconds (with all parameters being set to their nice values) during which its location was recorded at roughly 60 times per second. With the standard established—with which all other runs would be compared to—a parameter was selected (from the candidate pool), its value was tweaked, the ball was run for five seconds with its location being recorded at roughly 60 times per second, and after the run was over, the tweaked parameter’s value was set back to its nice value. This sequence was repeated for all 44 candidate parameters.

4.4.2 Experiment two: tournament selection with self-adaptation.

Very early runs of BBAutoTune attempted to tune physics parameters: gravity, sub-steps, FPS, use material physics, material friction, material elasticity, mass, form factor, velocity maximum, damping translation, damping rotation, use collision bounds, collision bounds type, and torque, where the search space for each parameter was its entire valid range. This proved to be problematic since some of the valid ranges are quite large, especially torque with a maximum upper bound of 3.40×10^{38} . While running the game engine, if the genome’s genes decoded to relatively high physics engine parameter values, world coordinates would return the Python values “NaN” or “inf”.

To rectify this issue, the set of physics parameters selected for tuning was pruned and for the parameters left, their ranges were shortened to reasonable upper and lower bounds found manually. The resulting set of tunable physics parameters and their ranges for experiment two were: gravity [0.0,15.0], sub-steps [1,5], FPS [30,10000], material friction [0.0,100.0], material elasticity [0.0,1.0], mass [0.010,15.0], velocity maximum [0.0,1000.0], damping translation [0.0,1.0], damping rotation [0.0,1.0], collision bounds type [TRIANGLE_MESH,CONVEX_HULL,CYLINDER,SPHERE], and torque [0.0,100.0]. Use material physics and use collision bounds were set to true and held constant. Form factor was set to 1.0 and was held constant.

The GA was run for 500 generations, tournament selection was used, the population size was set to 10, elitism was set to 2, crossover and mutation were performed separately, and the crossover and mutation

probabilities were self-adapted over time.

4.4.3 Experiment three through five.

Experiments three through five had the exact same setup as experiment two, except for the selection method and whether or not self-adaptation was used. Experiment three used tournament selection without self-adaptation. Experiment four used rank fitness selection with self-adaptation. Lastly, experiment five used rank fitness selection without self-adaptation.

4.5 Experimental Results

Experiment two had the highest performing genome out of experiments two through five. Experiments three through five had similar highest fitnesses. Using self-adaptation with tournament selection resulted in the highest fitness observed among experiments two through five. Comparing experiment two to three, self-adaptation was beneficial, but was not beneficial when comparing experiment five to four.

4.5.1 Experiment one: physics engine parameter influence.

To compare the recorded tweaked-parameter ball paths with the recorded standard, four methods were utilized to give an indication as to how much influence any one candidate parameter had over the simulation. The first method was visual inspection. All 44 tweaked-parameter ball paths were plotted against the standard. See Figure 4.15 and Figure 4.16. The second method was an algorithm developed by the author, titled the *Lettier distance*, which gives the maximum Euclidean distance between two discrete curves P and Q . Informally, imagine holding a rubber band in your hands where the left hand affixes the left end of the rubber band to the first point in P and the right hand affixes the right end of the rubber band to the first point in Q . During each iteration, you advance the left end of the rubber band to the next point in P and you advance the right end of the rubber band to the next point in Q . If the distance grows between point $p_i \in P$ and point $q_j \in Q$, the rubber band stretches but never shrinks. If $|P| < |Q|$ then you hold the left end of the rubber band to the last point in P and continue advancing to the last point in Q and vice versa. Once you reach the last point in P and the last point in Q , the resulting length of the rubber band is the maximum Euclidean distance between P and Q . See Figure 4.17. The third method was the discrete Fréchet

distance and the fourth method was the Hausdorff distance [24] [25].

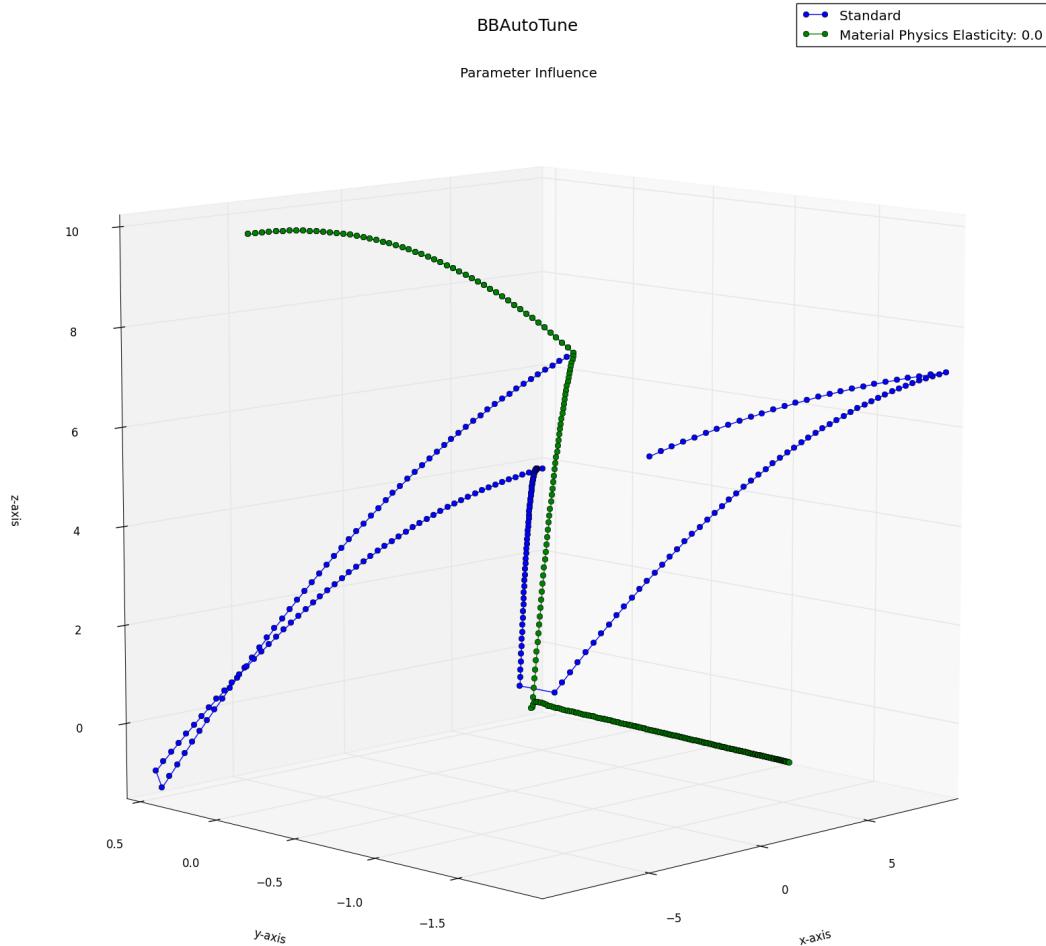


FIGURE 4.15: The dissimilarity of the ball paths between the tweaked, material-physics elasticity parameter and the standard (where no parameters were tweaked).

Twenty parameters out of the initial 44 showed no significant influence over the 3D physics simulation in Blender. Thus, the resulting 24 parameters which did have a significant influence were targeted for tuning by the genetic algorithm. See Table 4.3.

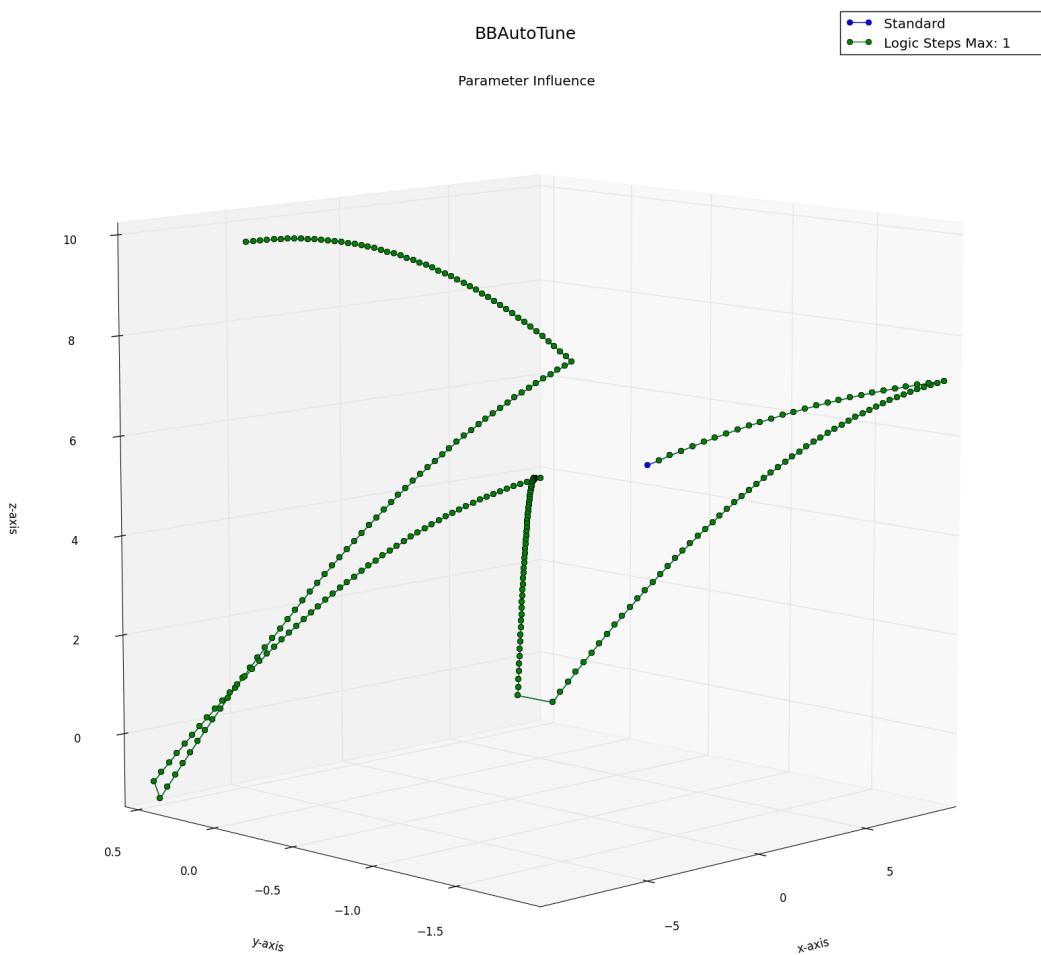


FIGURE 4.16: The similarity of the ball paths between the tweaked, logic-steps maximum parameter and the standard (where no parameters were tweaked).

Tweaked Parameter: Value	Lettier Distance	Discrete Fréchet Distance	Hausdorff Distance
Gravity: $1.0 \frac{m}{s^2}$	12.7741189989	20.948159542	9.86343687719
Physics Steps Max: 1	0.329232644023	0.329232644023	0.329232644023
Physics Sub-steps: 50	19.3073641073	17.0708640308	11.3180046289
Physics FPS: 1	218.037284056	211.287842927	205.848670021
Logic Steps Max: 1	0.329232644023	0.329232644023	0.329232644023
Physics Deactivation Linear Threshold: 10000.0	0.329232644023	0.329232644023	0.329232644023
Physics Deactivation Angular Threshold: 10000.0	0.329232644023	0.329232644023	0.329232644023
Physics Deactivation Time: 0.0	0.329232644023	0.329232644023	0.329232644023
Occlusion Culling: False	0.329232644023	0.329232644023	0.329232644023
Occlusion Culling Resolution: 1024	0.329232644023	0.329232644023	0.329232644023
Material Physics: False	18.0830473811	18.0830473811	18.0830473811
Material Physics Friction: 100.00	4.93924881608	4.94095279557	3.8109066203
Material Physics Elasticity: 0.0	17.3874844829	17.0233755244	11.3180046289
Force Field Force: 1.00	0.329232644023	0.329232644023	0.329232644023
Force Field Damping: 1.00	0.329232644023	0.329232644023	0.329232644023
Force Field Distance: 20.00	0.329232644023	0.329232644023	0.329232644023
Force Field Align to Normal: True	0.329232644023	0.329232644023	0.329232644023
Physics Type: Dynamic	3.55513601614	18.1217630973	3.275450812
Use Actor: False	0.329232644023	0.329232644023	0.329232644023
Use Ghost: True	138.489494312	138.489494312	132.02387242
Use Material Force Field: True	0.329232644023	0.329232644023	0.329232644023
Rotate From Normal: True	0.329232644023	0.329232644023	0.329232644023
No Sleeping: True	0.329232644023	0.329232644023	0.329232644023
Mass: 10000.0	3.57800913743	3.30042073543	3.21534852885
Radius: 1cm	0.329232644023	0.329232644023	0.329232644023
Form Factor: 0.0	3.55513601614	18.1217630973	3.275450812
Velocity Minimum: 1.0	0.329232644023	0.329232644023	0.329232644023
Anisotropic Friction: True	0.329232644023	0.329232644023	0.329232644023
Velocity Maximum: 1.0	17.1034960114	17.130808295	16.8922077042
Damping Translation: 1.0	17.9729741832	17.9729741832	17.9729741832
Damping Rotation: 1.0	8.09457671285	5.47840838373	5.18331655137
Collision Bounds: False	8.81773036062	17.4044978663	2.80531111777
Collision Bounds Margin: 0m	18.740072391	9.79629223411	3.78119352088
Collision Bounds: False	4.28865271192	4.23797419961	3.72440427516
Launch Dynamic Object Settings Force X: 30.0	5.21169989737	5.21169989737	3.78308993247
Launch Dynamic Object Settings Torque X: 30.0	8.82943537929	8.70403741077	6.58255281735
Launch Dynamic Object Settings AngV X: 30.0	2.93219084728	2.63246279507	1.82341393368
Launch Dynamic Object Settings LinV X: 0.0	19.1625050915	19.1625050915	17.0670582483
Launch Damping Frames: -32768	0.329232644023	0.329232644023	0.329232644023
Collision Dynamic Object Settings Force X: 30.0	5.32618850819	18.9696056987	3.80913153981
Collision Dynamic Object Settings Torque X: 30.0	1.67496526126	1.52842619107	1.52842619107
Collision Dynamic Object Settings LinV X: 0.0	19.2801183238	19.1535557726	3.3918725084
Collision Dynamic Object Settings AngV X: 30.0	4.69097055763	18.7403224372	3.80913153981
Damping Frames: -32768	0.329232644023	0.329232644023	0.329232644023

TABLE 4.3: The distances between each tweaked-parameter ball path and the standard ball path for each of the three quantifiable measurement methods employed. The highlighted tweaked parameters were determined not to be influential.

```

BEGIN
     $P = \langle p_1, p_2, \dots, p_n \rangle$ 
     $Q = \langle q_1, q_2, \dots, q_m \rangle$ 
     $max = 0.0$ 
    For all  $p_i \in P$  and  $q_j \in Q$  do
         $d = ||p_i - q_j||$ 
        If  $max < d$  then
             $max = d$ 
        End if
    End for
    Return  $max$ 
END

```

FIGURE 4.17: The Lettier distance algorithm.

4.5.2 Experiment two: tournament selection with self-adaptation.

The minimum values reached for the highest, average, and lowest fitness were 0.9306191001, 1.024632475, and 0.9315692954 respectively. The minimum and maximum probability for both crossover and mutation obtained over the course of 500 generations was 0.001 and 0.999. Interestingly, as the highest, average, and lowest fitness began to converge, the crossover and mutation probability flipped, causing the population to be entirely mutated (with the exception of the elites) which resulted in essentially a randomly generated population and thereby destroying the high fitness solutions previously found. Notice that after the probabilities flipped, the average and lowest fitness diverged. This converging and then diverging occurred twice during the 500 generation run. Up to generation 376, the highest fitness steadily declined and then afterward remained fairly stable. See Figure 4.18. Table 4.4 lists the best and worst physics parameters found by the GA, corresponding to the best and worst fitness observed during the 500 generation run.

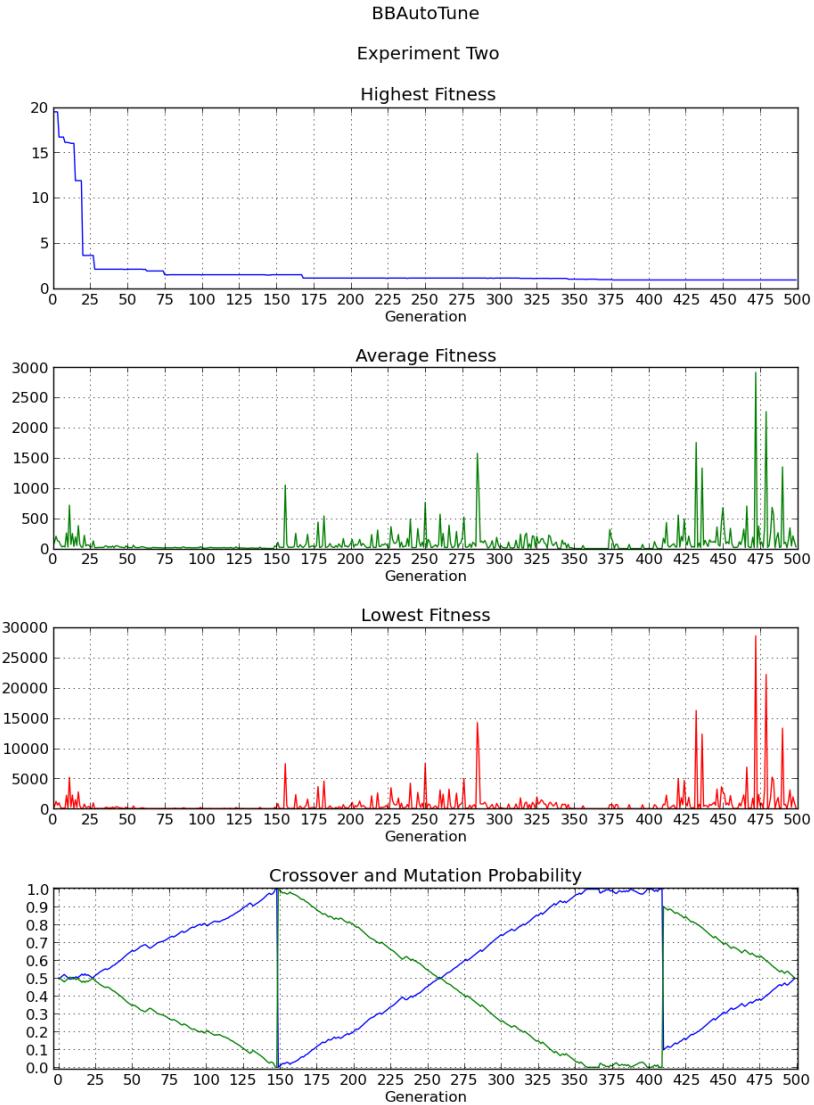


FIGURE 4.18: The highest, average, and lowest fitness in addition to the crossover and mutation probability over the course of 500 generations. For the bottom plot, the crossover probability is shown in blue while the mutation probability is shown in green.

	Best	Worst
Gravity	$2.89862416489 \frac{m}{s^2}$	$10.1989482496 \frac{m}{s^2}$
Sub-steps	5	5
FPS	30	30
Material Friction	59.5011814113	77.8151135094
Material Elasticity	0.0742521056997	0.279061300281
Mass	4.33392950881	1.76678194417
Velocity Maximum	900.11395466	647.638168514
Damping Translation	1.0	0.0
Damping Rotation	0.691143247902	0.648240602049
Collision Bounds Type	SPHERE	SPHERE
Torque	82.7271515601	100.0
Fitness	0.930619100106	28584.2244771

TABLE 4.4: The best and worst physics parameters found by the GA corresponding to the best and worst fitness observed during the 500 generation run for experiment two.

4.5.3 Experiment three: tournament selection without self-adaptation.

The minimum values reached for the highest, average, and lowest fitness were 1.0827696957, 2.892412821, and 7.7702053307 respectively. Up until generation 146, the highest fitness steadily declined and then afterwards remained fairly stable. See Figure 4.19. In contrast to experiment two, it would seem that the self-adaptation side effect of periodically randomizing the population helped experiment two obtain a better fitness than experiment three. Table 4.5 lists the best and worst physics parameters found by the GA, corresponding to the best and worst fitness observed during the 500 generation run.

	Best	Worst
Gravity	$14.09509165745291 \frac{m}{s^2}$	$0.8362602682788933 \frac{m}{s^2}$
Sub-steps	1	1
FPS	30	30
Material Friction	79.87292012678728	100.0
Material Elasticity	0.7331947746415657	0.6643893038716038
Mass	15.0	12.761484385447746
Velocity Maximum	0.0	250.88084935511978
Damping Translation	1.0	0.33429608723965537
Damping Rotation	0.14340109658364997	0.0
Collision Bounds Type	TRIANGLE_MESH	SPHERE
Torque	47.85677413931377	63.68300968863001
Fitness	1.0827696957	1617.02428027

TABLE 4.5: The best and worst physics parameters found by the GA corresponding to the best and worst fitness observed during the 500 generation run for experiment three.

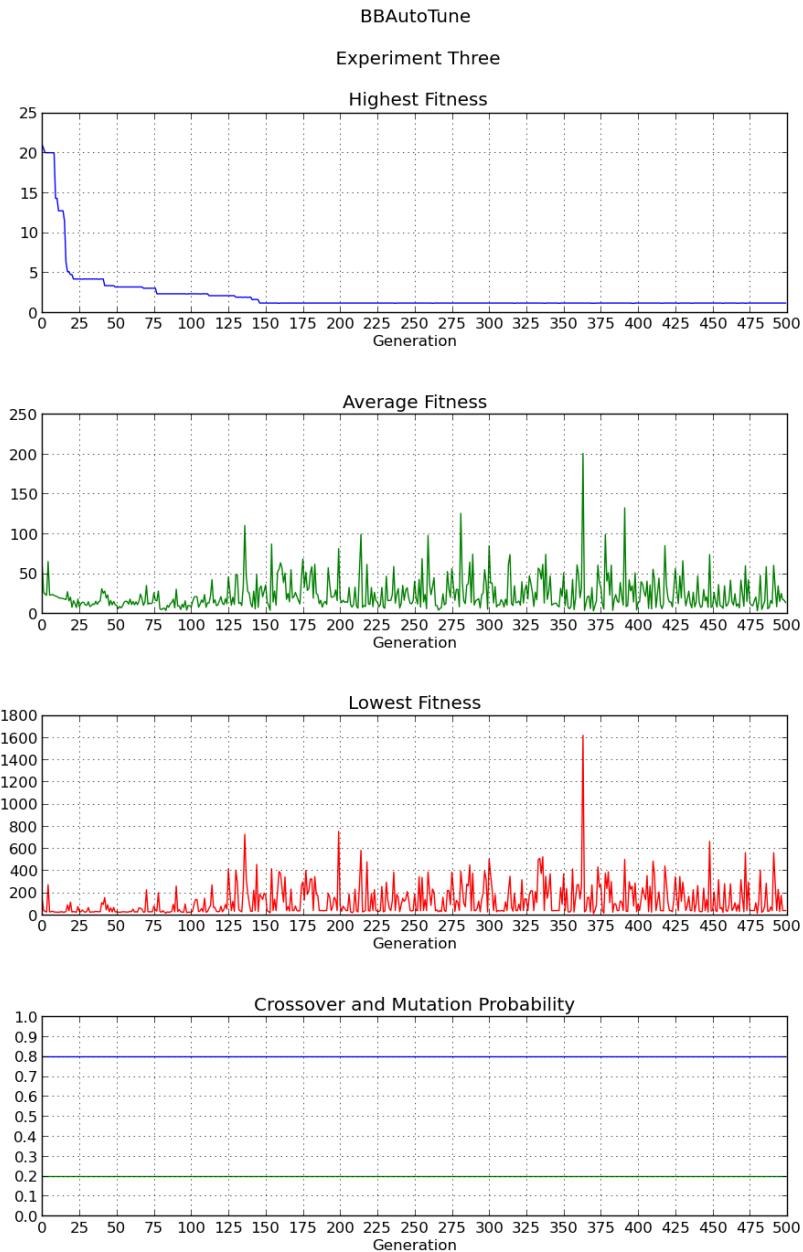


FIGURE 4.19: The highest, average, and lowest fitness in addition to the crossover and mutation probability over the course of 500 generations. For the bottom plot, the crossover probability is shown in blue while the mutation probability is shown in green.

4.5.4 Experiment four: rank fitness selection with self-adaptation.

The minimum values reached for the highest, average, and lowest fitness were 1.1309704845, 2.7714017205, and 2.5217479907 respectively. The minimum and maximum probabilities observed for crossover, during the 500 generation run, were 0.253 and 0.999 respectively. For mutation, the minimum and maximum probabilities observed were 0.001 and 0.747 respectively. From generation zero to 79, the highest fitness steadily declined and then fell more gradually afterwards for rest of the duration. The same periodic converging and then diverging seen in experiment two was observed again in experiment four. See Figure 4.20. Table 4.6 lists the best and worst physics parameters found by the GA, corresponding to the best and worst fitness observed during the 500 generation run.

	Best	Worst
Gravity	$13.8256917774 \frac{m}{s^2}$	$15.0 \frac{m}{s^2}$
Sub-steps	2	5
FPS	30	30
Material Friction	61.2749944576	0.0
Material Elasticity	0.171754015461	0.649745829218
Mass	15.0	0.158414320671
Velocity Maximum	1000.0	1000.0
Damping Translation	0.0	0.387362543282
Damping Rotation	0.984539067046	0.687852083808
Collision Bounds Type	SPHERE	CONVEX_HULL
Torque	6.70058480184	75.8262976514
Fitness	1.1309704845	16396.2145412

TABLE 4.6: The best and worst physics parameters found by the GA corresponding to the best and worst fitness observed during the 500 generation run for experiment four.

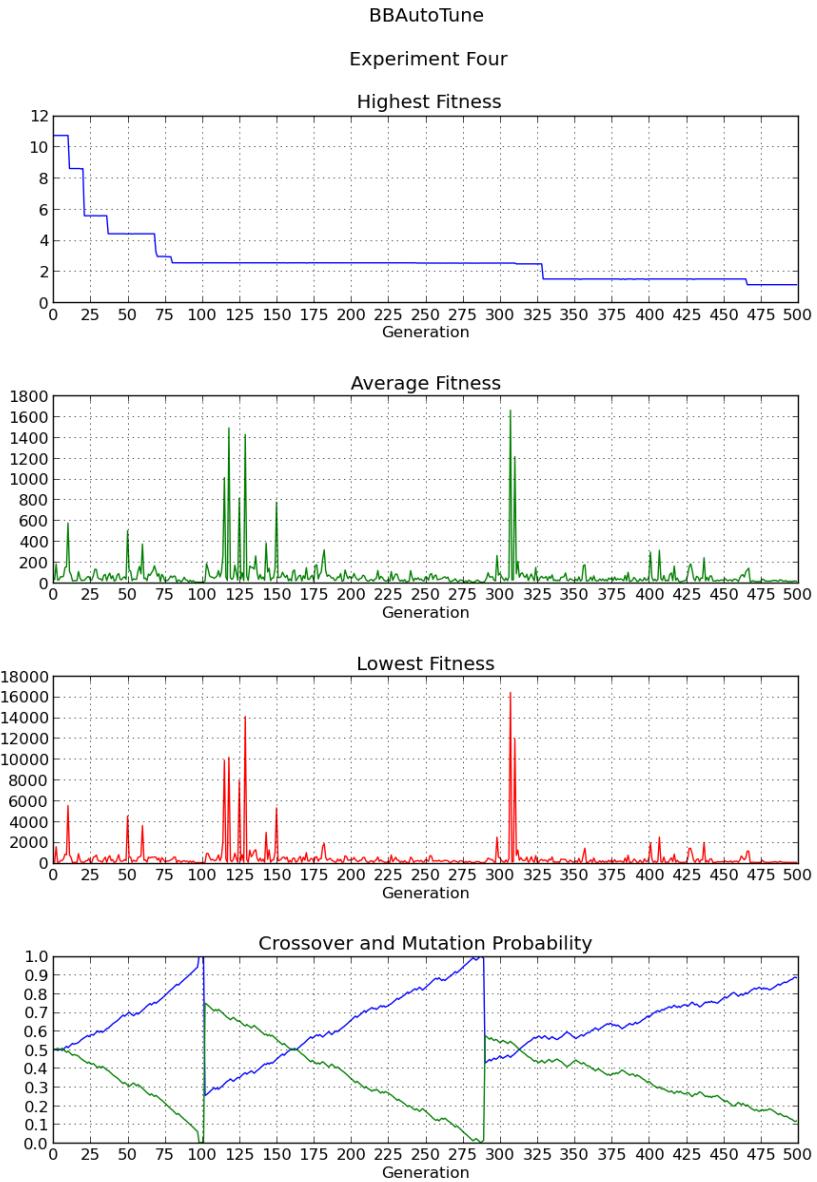


FIGURE 4.20: The highest, average, and lowest fitness in addition to the crossover and mutation probability over the course of 500 generations. For the bottom plot, the crossover probability is shown in blue while the mutation probability is shown in green.

4.5.5 Experiment five: rank fitness selection without self-adaptation.

The minimum values reached for the highest, average, and lowest fitness were 1.0638026764, 3.4974350451, and 11.6425679783 respectively. Throughout the 500 generation run, the highest fitness continued to decline reaching its lowest value at generation 469. See Figure 4.21. Table 4.7 lists the best and worst physics parameters found by the GA corresponding to the best and worst fitness observed during the 500 generation run.

	Best	Worst
Gravity	$0.0 \frac{m}{s^2}$	$12.803362098213498 \frac{m}{s^2}$
Sub-steps	3	2
FPS	30	30
Material Friction	60.71902294177607	15.76102238218593
Material Elasticity	0.5378313234044673	0.602617926833965
Mass	4.175314301157847	0.2111916960575379
Velocity Maximum	660.0787581868401	787.7673658611162
Damping Translation	1.0	0.6703819812309364
Damping Rotation	0.4031179325185546	0.10076651150002103
Collision Bounds Type	SPHERE	SPHERE
Torque	46.465508081185064	49.46737364841879
Fitness	1.0638026764	3257.00654843

TABLE 4.7: The best and worst physics parameters found by the GA corresponding to the best and worst fitness observed during the 500 generation run for experiment five.

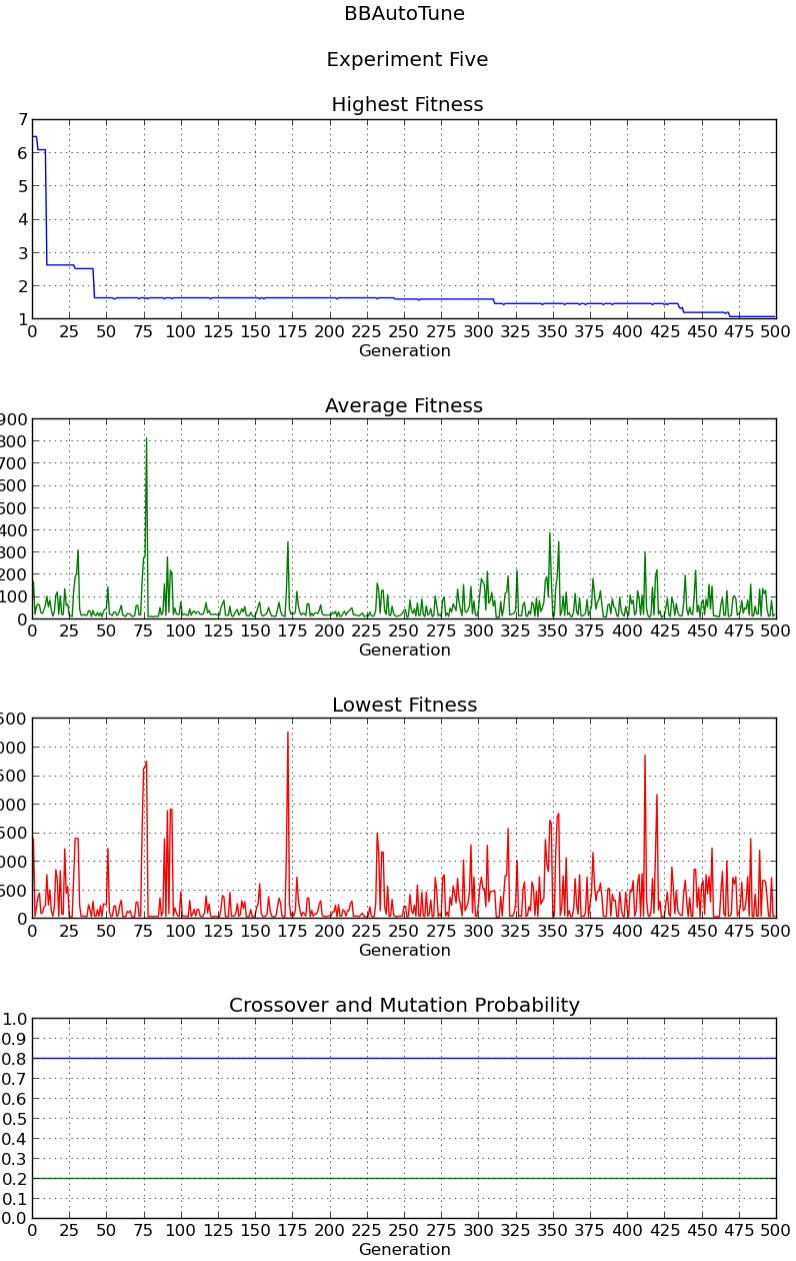


FIGURE 4.21: The highest, average, and lowest fitness in addition to the crossover and mutation probability over the course of 500 generations. For the bottom plot, the crossover probability is shown in blue while the mutation probability is shown in green.

4.6 Simulated versus Real Motion

The top phenotype for experiment two had the largest robust distance from the real robot robust mean, but suffered the least amount of penalty for not stopping at one second. The top phenotypes for experiments three through five had similar robust distances and stopping times over one second. See Table 4.8, Figure 4.22, and Figure 4.23.

	Final States of Highest Performing Phenotypes				Real Robot Robust Mean
	Exp. Two	Exp. Three	Exp. Four	Exp. Five	
X-position	23.12349975cm	23.95108938cm	23.49144816cm	24.05546605cm	23.9934044cm
Y-position	0.00953689cm	-0.34897618cm	-0.00286334cm	0.01641194cm	0.0351240cm
Heading (Z-orientation)	0.00203373rad	-0.00318596rad	-0.00428754rad	0.00118415rad	-0.0189964rad
Elapsed Time Until Coming to a Stop	1.0333563sec	1.5333535sec	1.5333476sec	1.5333496sec	
Resulting Genome Fitness	0.930619100106	1.0827696957	1.1309704845	1.0638026764	

TABLE 4.8: The comparison between the top phenotypes' final states (per experiment) and the robust mean of the real robot forward motion. The elapsed times indicate how long each top phenotype took before reaching its final at-rest state. The resulting genome fitnesses are included for reference.

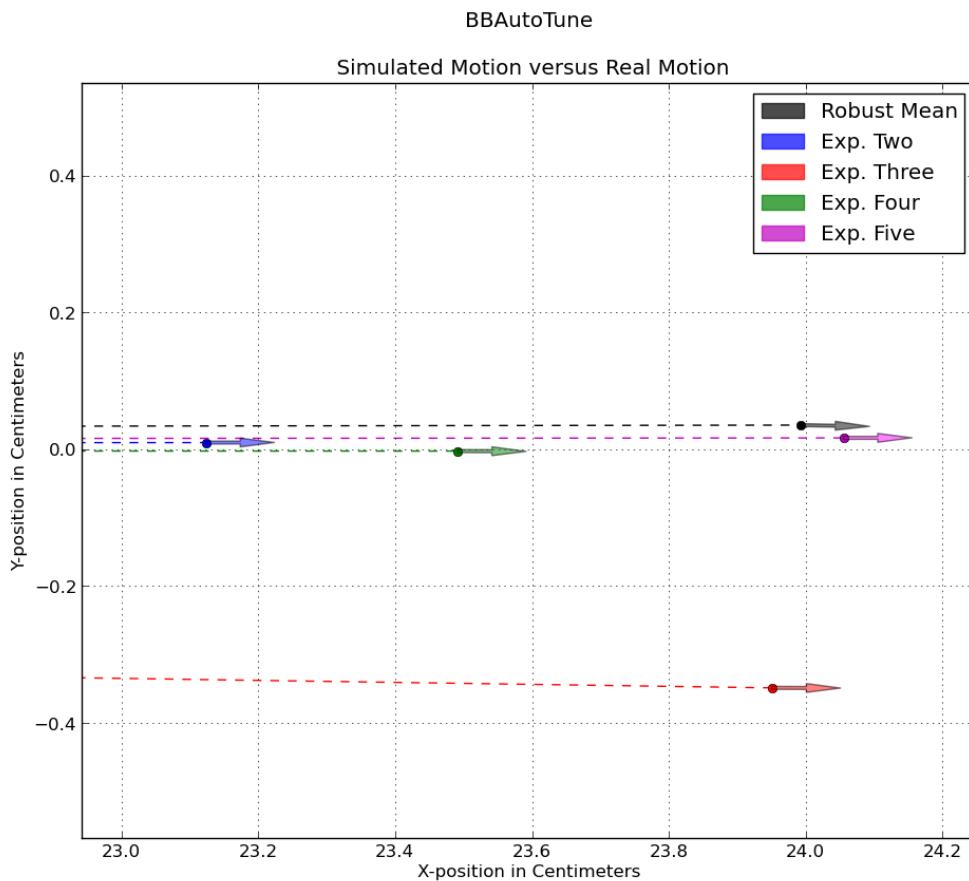


FIGURE 4.22: The final states of the top phenotypes from experiments two through five compared to the real robot robust mean.

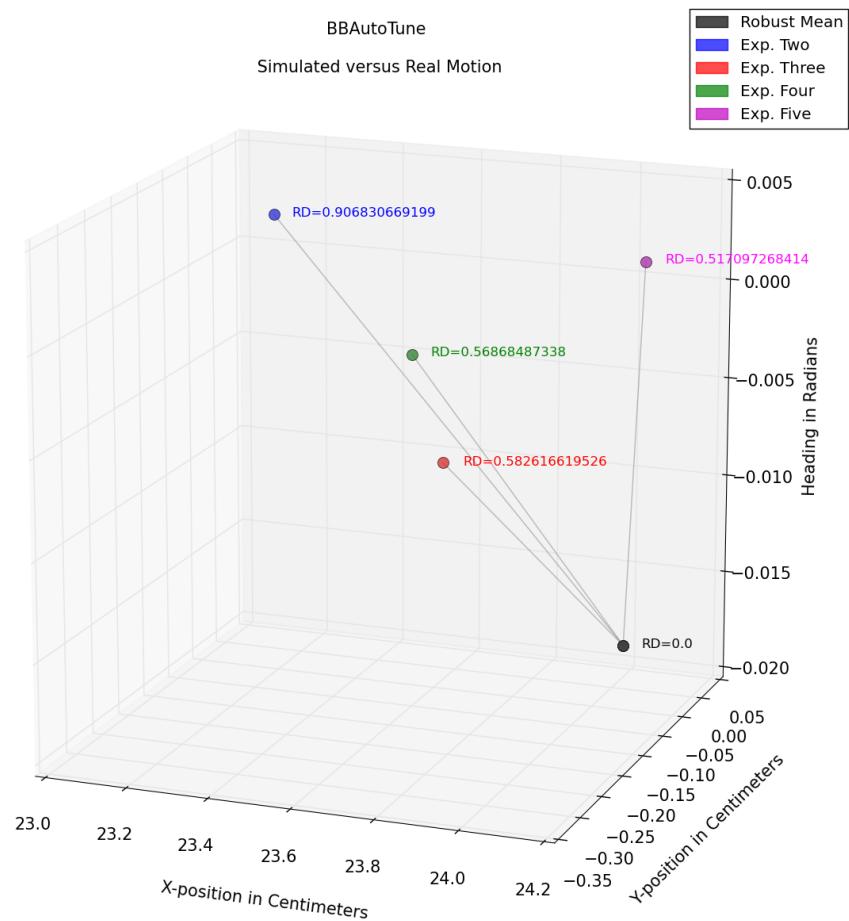


FIGURE 4.23: An alternate view of the final states of the top phenotypes from experiments two through five compared to the real robot robust mean. The robust distances are indicated near each data point.

Chapter 5

BlenderSim

5.1 Overview

Over the course of three months, a Blender based simulation was developed for HRTeam titled BlenderSim. Initially, BlenderSim was wholly physics based, but soon proved to be problematic on three fronts: time, scale, and intricacy. The problems faced by using the physics engine to model the locomotion of the robots gave way to the thesis of tuning the physics engine via a genetic algorithm. In the interim, the physics engine was abandoned and a constant linear motion model was used, in order to progress on the development of the BlenderSim 3D simulation environment.

As a proof of concept of the thesis, BlenderSim was revisited with the physics engine providing the motion model, using the best-fitness parameters learned by BBAutoTune. Using one robot, the motion of the simulated, physics-based robot was compared to the real robot by re-running a previously logged HRTeam experiment in BlenderSim.

5.2 Preliminary Work

Initial problems arose when the treads of the SRV-1 were recreated in the simulation. Even after numerous hours adjusting physics parameters and rigid-body configurations, the treads would consistently behave in erratic fashions. See Figure 5.1.

Scale was problematic as the Blender/Bullet physics engine has difficulty with collisions of objects that have a size outside of the assumed range of .05 to 10 meters [26]. Objects smaller than .05 (5cm) Blender/Bullet units, in any given dimension, erratically jitter despite having no force acting upon them.

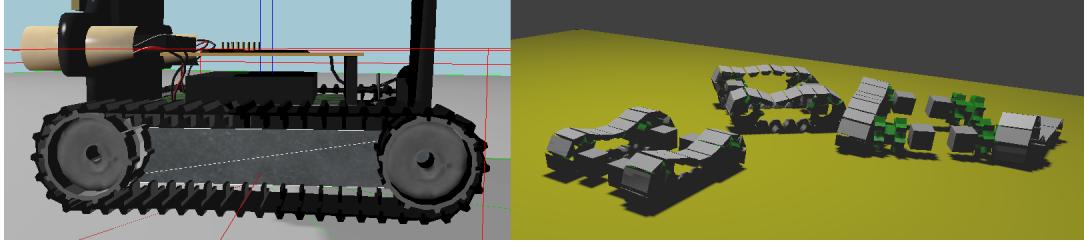


FIGURE 5.1: The to-scale treads modeled after the physical SRV-1 robot on the left and the physics-based rigid-body tracks in motion on the right.

As such, since the wheel dimensions of the real SRV-1 are 2.11cm x 2.45cm x 2.52cm, the to-scale 3D model of the SRV-1 was affected by this scale limitation of the physics engine.

To rectify these issues, the default physics engine was not used to provide a motion model—and was only kept to keep the robots from running through each other and the arena. In its place, a constant linear and angular velocity motion model was developed which only moves the 3D robot as if it were a single point body. See Figure 5.2 and Figure 5.3.

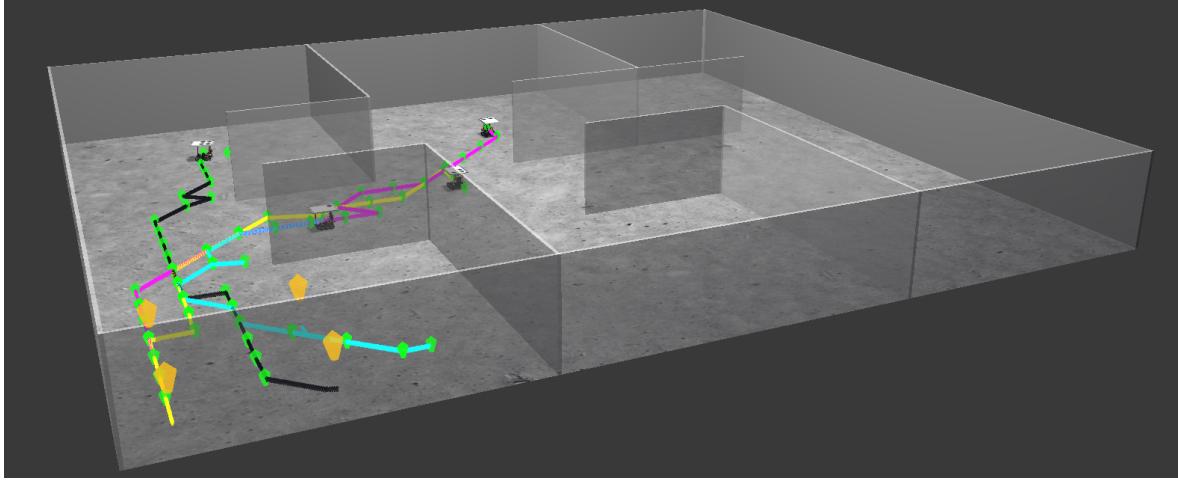


FIGURE 5.2: The constant velocity motion model in BlenderSim with four robots traversing their respective paths which consist of way-points logged in a previously recorded physical robot experiment.

5.3 Evaluation

For the purposes of the proof of concept, most of the original architecture of BlenderSim was simplified. The simulation contained one robot, one robot controller, one robot path planner, and the arena. The

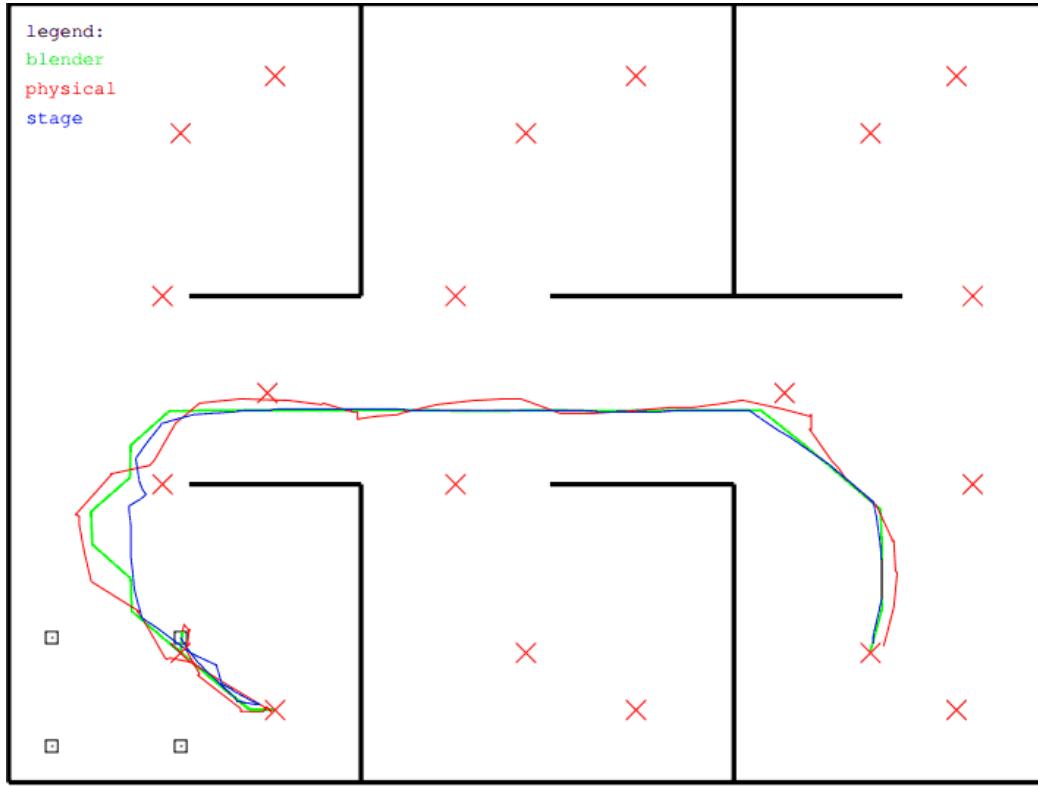


FIGURE 5.3: The path plots—as plotted by Dr. Elizabeth Sklar—of the BlenderSim robot, the physical robot, and the *Stage* (a 2D robot simulator already in use by HRTeam)[27] robot plotted in comparison.

purpose was to evaluate the efficacy of the physics parameters learned by BBAutoTune, when deployed in the simulated robot environment and measured in comparison with its physical robot counterpart.

5.3.1 Arena

The arena is a $602\text{cm} \times 538\text{cm}$ enclosure with a main hallway and six compartments. The floor and all of walls are physics based in BlenderSim and respond accordingly should any robot try to pass through them. See Figure 5.4. All dimensions and proportions of the simulated arena match the real arena used in HRTeam experiments.

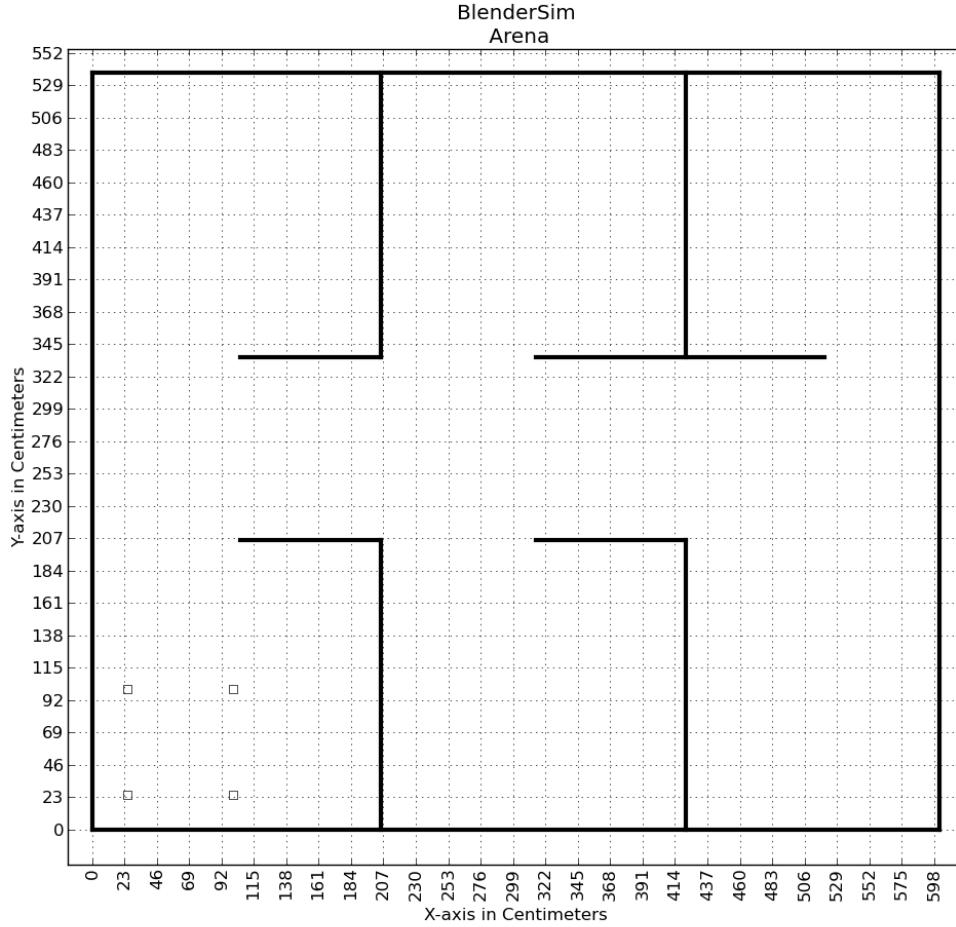


FIGURE 5.4: The layout and dimensions of the arena map both as it is in BlenderSim and in the real HRTeam lab. The smaller four squares in the lower left-hand corner represent the standard starting positions of the robots before any experiment. The grid shown in the plot is the same discrete grid used by HRTeam to calculate the A* generated paths of the robots.

5.3.2 Surveyor SRV-1 Blackfin 3D Model

The physics parameters governing the wheels were the same best-fitness parameters found by BBAutoTune in subsection 4.5.2. Residing 1.37cm off of the arena floor from their local origins in the positive global z-axis, the robot's base and wheels had their z-translation fixed. This distance between the wheels and the floor is important since this was the same height used to tune the physics engine parameters in BBAutoTune. Using any other height would result in different motion from the motion observed in section 4.6 for experiment two.

5.3.3 Robot Path Planner

Given a HRTeam experiment log and a robot number, the path planner extracts the waypoints that the real robot was instructed to go to during the HRTeam experiment. These waypoints come from an A* calculated path that runs from the robot's starting position to various points of interest or task points. With the waypoints extracted from the log file, the robot path planner populates the robot controller's waypoint queue.

5.3.4 Robot Controller

The robot controller is expressed in the simulation as the base of the SRV-1 3D model. See Figure 5.5. Contained in its logic is a path or waypoint queue that it runs through. This queue is populated by the robot path planner. For each waypoint in the queue, the robot controller will first rotate the robot towards the point and then move the robot forward to reach the point. Once the robot moves forward, the waypoint is removed from the queue.

For either rotating or moving the robot, the robot controller can only apply torque to the robot's wheels—no other force or mechanism is used. Recalling from subsection 4.5.2 and section 4.6, a torque setting of 82.7271515601 resulted in the simulated robot moving forward 23.12349975cm . Since turning had not been learned by BBAutoTune, there were no baseline values of torque versus rotation. To correct for this, the torque value for the robot's left wheels was set to -20.8 while the torque value for the right wheels was set to 20.8 resulting in an in-place rotation of 44.260811 degrees. Note that, the torque value ± 20.8 was chosen arbitrarily.

Using these torque versus displacement values, the robot controller linearly interpolates the amount of torque needed to first rotate the robot towards a waypoint (to within 1 degree) and then move the robot forward to reach the waypoint. While rotating, if the robot over or undershoots the orientation needed to face the waypoint, the robot controller will continuously interpolate the torque needed to get the robot facing the waypoint to within 1 degree. Depending on the sign of the angle needed to orient the robot towards the waypoint, the robot controller will either rotate the robot counter-clockwise or clockwise by applying the same magnitude but opposing signs of torque to either the left or right wheels. While moving forward, if the robot over or undershoots the position of the waypoint, the robot controller performs no correction but proceeds to orient and move the robot towards the next waypoint in the queue (if there is one). Note that for moving the robot forward, the robot controller applies the same torque value to all four wheels.

5.3.5 Task Points Manager

HRTeam experiments have five predefined sets of “interest points” or task points that the robots visit as they travel around the arena [28]. BlenderSim imitates this using its task points manager. At the start of the simulation, the task points manager reads the five configurations from the task points configuration directory. Controls include keys *a* through *e* where each key corresponds to five possible task point configurations. See Figures 5.5 and 5.6.

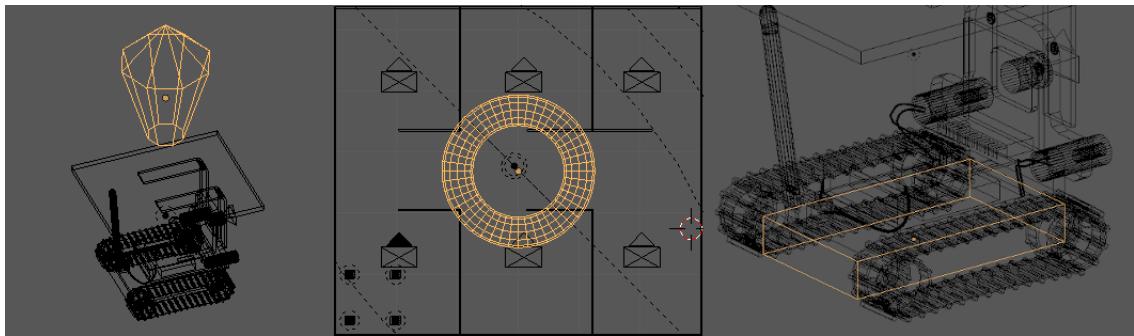


FIGURE 5.5: From left to right: the robot path planner, the task points manager, and the robot controller manifestations in the simulation.

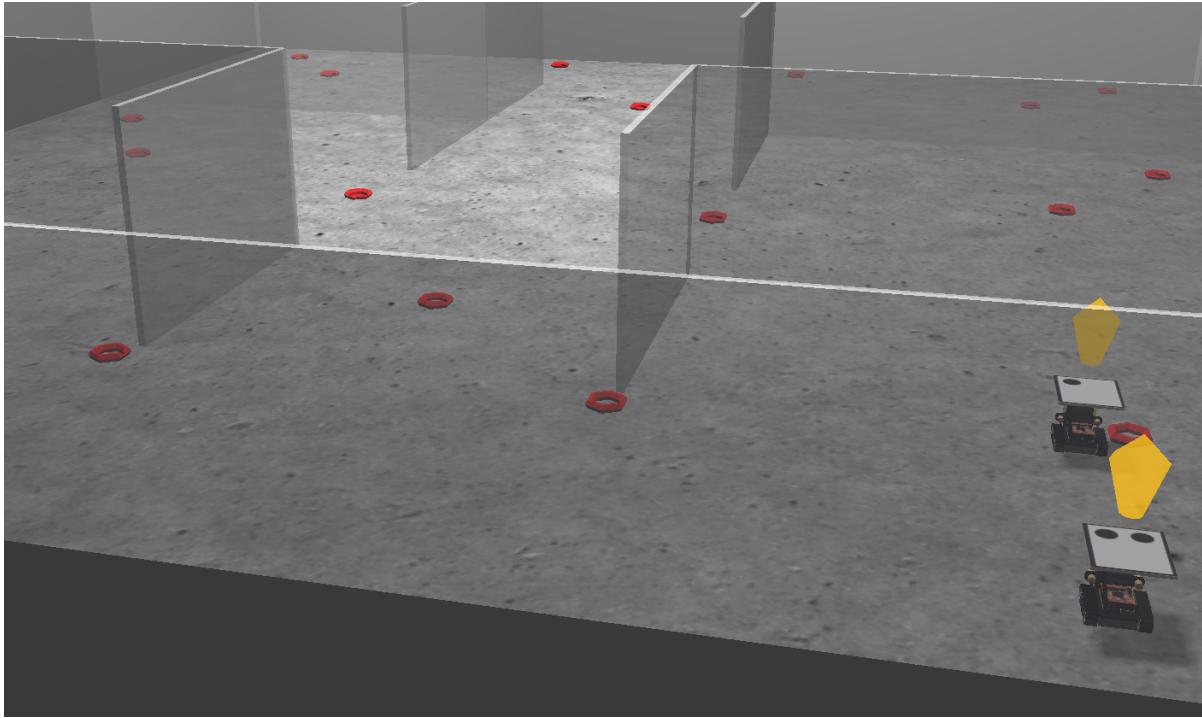


FIGURE 5.6: The red torus task points laid out in the arena.

5.4 Platform

BlenderSim was run on a 64bit Linux operating system with 32GB of RAM and an Intel Core i7-4770K four core processor running at 3.9GHz.

5.5 Experimental Design

To compare the simulated versus real robot motion (using the physics engine and the best-fitness physics parameters found by BBAutoTune), a HRTeam experiment was re-run in BlenderSim but for only one robot—specifically robot one with a starting position at $(100cm, 100cm)$. The A* path (the waypoints) and the task points that the real robot one was instructed to travel along were extracted from the experiment’s log file. Positioning the simulated robot at the same starting position as the real robot in the experiment, the simulated robot was instructed to travel along the same set of waypoints and task points as the real robot was instructed to. See Figure 5.7.

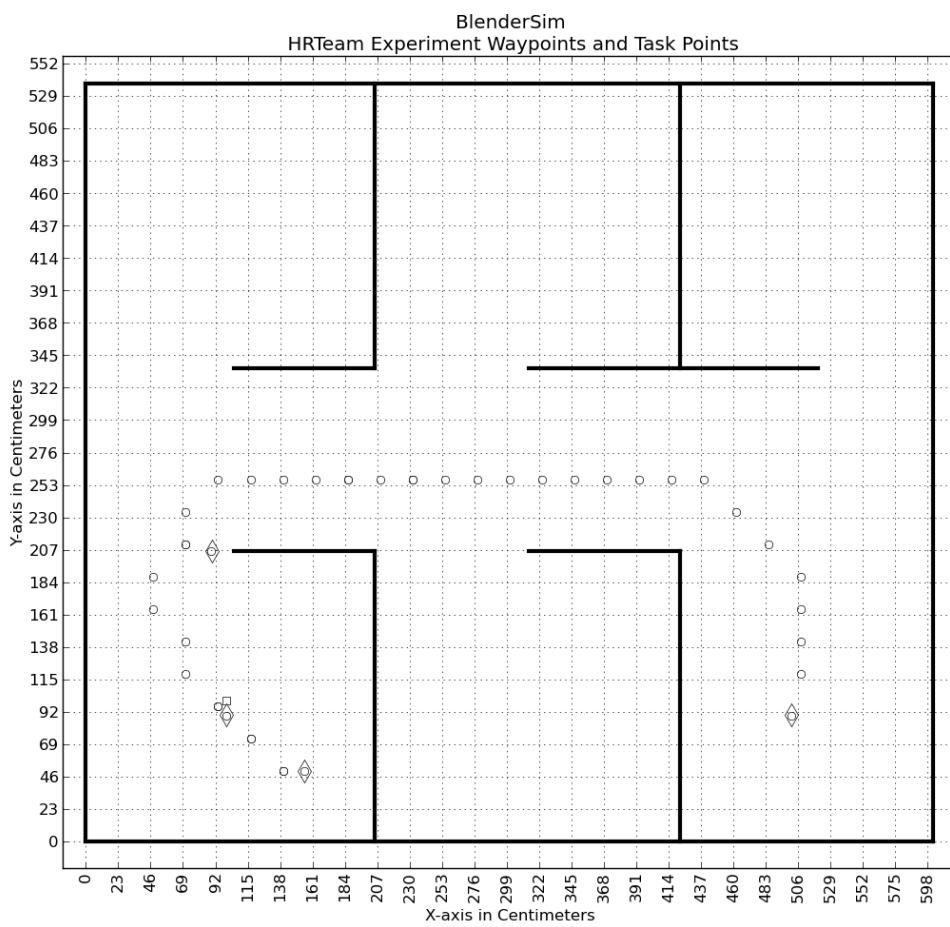


FIGURE 5.7: The arena layout with the experiment's waypoints and task points. The white square is the initial position of the robot before the experiment. The white circles are the waypoints and the white diamonds are the task points.

5.6 Experimental Result

Comparing the simulated versus real robot paths, the discrete Fréchet and Hausdorff distances between them were 40.575953633cm and 19.1208685021cm respectively. Between the simulated and real robot paths, the real robot path was the most dissimilar from the waypoint path¹. See Tables 5.1, 5.2, and Figure 5.8.

	Simulated	Real	Waypoint
Simulated	0.0cm	40.575953633cm	16.2376801625cm
Real	40.575953633cm	0.0cm	24.0208242989cm
Waypoint	16.2376801625cm	24.0208242989cm	0.0cm

TABLE 5.1: The discrete Fréchet distances between the various paths.

	Simulated	Real	Waypoint
Simulated	0.0cm	19.1208685021cm	16.2376801625cm
Real	19.1208685021cm	0.0cm	24.0208242989cm
Waypoint	16.2376801625cm	24.0208242989cm	0.0cm

TABLE 5.2: The Hausdorff distances between the various paths.

¹The waypoint path is the collection of waypoints that start at the robot's starting position and then travel to the four task points in the arena as seen in Figure 5.7.

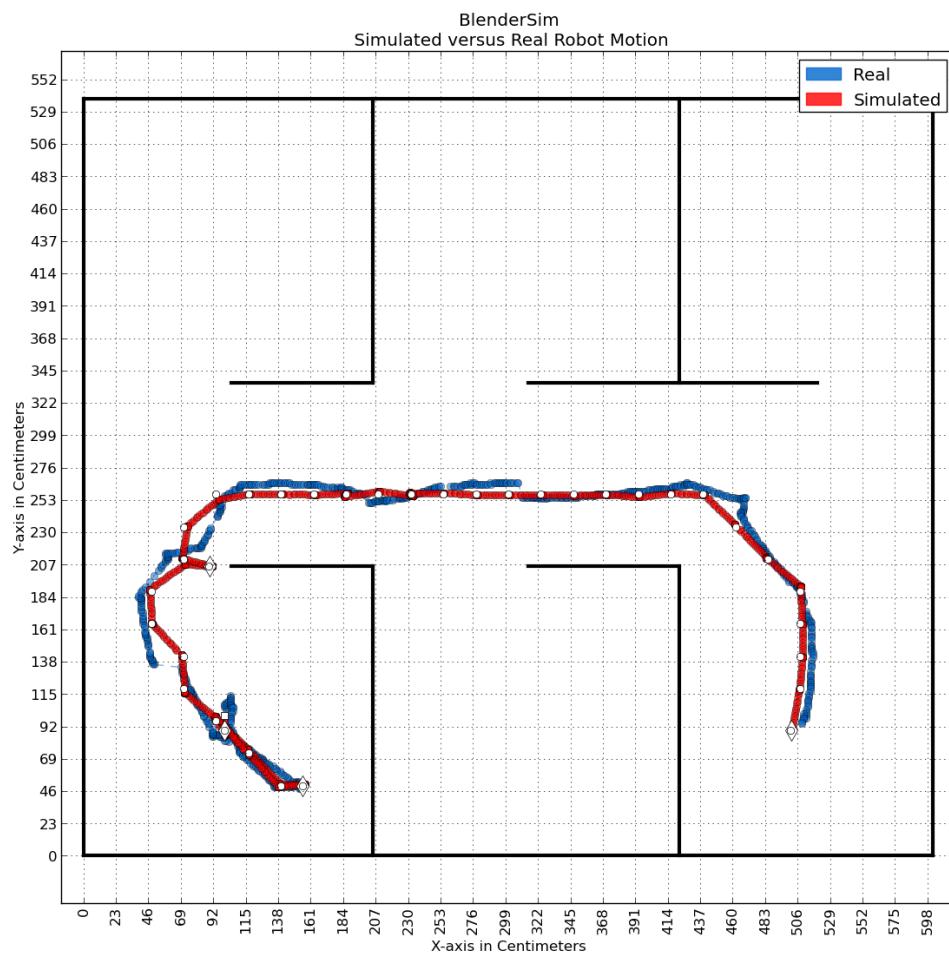


FIGURE 5.8: The simulated motion versus the real motion of the robot over the course of the experiment.

Chapter 6

Conclusion

6.1 Genetic Algorithms

The GA outlined in this thesis employed a wide variety of techniques presented by previous works. Unfortunately, there is no unanimously recognized theory of GAs [5]. Furthermore, there is no proven optimal set of GA parameters for any given problem being solved by a GA [4]. There are, however, a few schools of thought and generally accepted guidelines when developing a GA [4][5]. As to why GAs work, at least for BCGAs, a few ideas have been presented such as John Holland's schema theorem and David Goldberg's building block hypothesis [5].

6.2 SimPL

The GA developed for SimPL proved to be a robust basis for the GA needed to solve the harder problem of tuning a 3D physics engine (project BBAutoTune). The principles and techniques of evolutionary algorithms learned during the SimPL project certainly carried over to the more difficult project, BBAutoTune. And while the problem domain of SimPL and BBAutoTune were only somewhat similar, the problems faced and worked out during the development of SimPL alleviated problems faced while developing BBAutoTune. As the results show, the GA for SimPL performed well, producing neural network weight solutions that had the paddle keeping the ball in the arena for almost a minute. Had it not been for the round termination criteria of the ball's velocity magnitude dropping below 100, most of the paddles (with high fitnesses) would have kept the ball in the arena indefinitely. Thus, the goal to learn about and to cultivate an GA capable of tuning parameters with respect to a fitness landscape was certainly accomplished.

6.3 BBAutoTune

Using the real robot forward motion data, BBAutoTune was consistently able to tune the physics engine such that the reality gap between simulation and reality was extremely small. For all runs of the GA, BBAutoTune was able to find nearly optimal physics parameters in no more than five hours. This is particularly impressive considering the search space size was $(2^{53})^{11} = 2^{53*11} = 2^{583} = 3.165829139 \times 10^{175}$ possible states¹. It is even more impressive considering the many days lost trying to find reasonable parameters by hand (during preliminary work) only to abandon the physics engine altogether due to consistent instability issues. Interestingly, the physics parameters found were not necessarily intuitive nor did they coincide with their real world counterparts. For example, in experiment two, gravity was $\sim 2.89 \frac{m}{s^2}$ versus earth's gravitational constant $\sim 9.81 \frac{m}{s^2}$ and the collision bound type was sphere versus the cylindrical shape of the robot's wheels.

6.4 BlenderSim

Interpreting the plot of the simulated versus real robot motion along with the Fréchet and Hausdorff distances, one can see that the simulated motion was very close to the real robot motion. Considering the largest move the (simulated or real) robot can make at any one time on the discrete arena grid is $\sim 32.52cm^2$ and that the largest distance between the simulated and real robots paths was a Fréchet distance of $\sim 40.57cm$, the thesis was certainly demonstrated and its hypothesis was supported.

6.5 Future Work

Future work, concerning BBAutoTune and BlenderSim, could involve the following:

1. capture additional real-robot motion data on the SRV-1 by issuing it different commands (such as turning) instead of just forward;
 - (a) take this additional motion data and in BBAutoTune, learn the physics parameters needed to simulate these different robot commands in BlenderSim;

¹On a 64-bit computer architecture, there is approximately 2^{53} representable (double precision) floats between 0.0 and 1.0 [29][30]. Each genome in BBAutoTune contained an array of 11 floats which represented the 11 possible tunable physics parameters. The range of each float in the array was [0.0, 1.0].

²Overlaid on the robot arena is a grid spaced $23cm \times 23cm$ for both the simulated and real arenas. This discrete grid is used to compute the A* paths that take the robots from their starting positions to the task points in the arena. Moving diagonally from one grid square to another requires a distance of $\sqrt{23^2cm + 23^2cm} = 32.526911935cm$.

2. run new (or other previously logged) experiments in tandem between HRTeam and BlenderSim, making further comparisons between simulated and real robot paths; and
3. in BBAutoTune, learn the physics parameters necessary to simulate the motion of other robots (other than the SRV-1).

Appendix A

Physics Engine Parameters Governing Forward Motion Learned

Table A.1 lists every physics engine parameter that governed over the best-fitness forward motion learned in subsection 4.5.2. Some of the parameters only related to the physics engine as a whole, thus affect everything in simulation, while the other parameters effected only the robot’s base, the robot’s wheels, or just the floor. The highlighted values indicate the 11 GA tuned/learned physics engine parameters.

Parameter	Physics Engine	Wheels	Base	Floor
Gravity	$2.89862416489 \frac{m}{s^2}$	N/A	N/A	N/A
Max Steps	5	N/A	N/A	N/A
Sub-steps	5	N/A	N/A	N/A
FPS	30	N/A	N/A	N/A
Linear Deactivation Threshold	5.0	N/A	N/A	N/A
Angular Deactivation Threshold	5.0	N/A	N/A	N/A
Deactivation Time	0.5sec	N/A	N/A	N/A
Use Material Physics	N/A	True	True	True
Material Friction	N/A	59.5011814113	1.0	1.0
Material Elasticity	N/A	0.0742521056997	0.0	0.0
Material Force	N/A	0.0	0.0	0.0
Material Damping	N/A	0.0	0.0	0.0
Material Distance	N/A	0.0	0.0	0.0
Material Align to Normal	N/A	False	False	False
Physics Type	N/A	RIGID_BODY	RIGID_BODY	STATIC
Use Actor	N/A	True	True	False
Use Ghost	N/A	False	False	False
Use Material Force Field	N/A	False	False	N/A
Rotate From Normal	N/A	False	False	N/A
No Sleeping	N/A	False	False	N/A
Mass	N/A	4.33392950881	9.373	N/A
Radius	N/A	1.4cm	1cm	1cm
Form Factor	N/A	1.0	1.0	N/A
Use Anisotropic Friction	N/A	True	False	False
Anisotropic Friction X,Y,Z	N/A	0.0,1.0,1.0	N/A	N/A
Velocity Minimum	N/A	0.0	0.0	N/A
Velocity Maximum	N/A	900.11395466	0.0	N/A
Damping Translation	N/A	1.0	0.0	N/A
Damping Rotation	N/A	0.691143247902	0.0	N/A
Lock Translation X,Y,Z	N/A	False,False,True	False,False,True	N/A
Lock Rotation X,Y,Z	N/A	False,False,False	True,True,False	N/A
Use Collision Bounds	N/A	True	True	True
Collision Bounds Type	N/A	SPHERE	BOX	BOX
Collision Bounds Margin	N/A	0.0m	0.0m	0.0m
Force	N/A	0.0	N/A	N/A
Torque	N/A	82.7271515601	N/A	N/A
Linear Velocity	N/A	0.0	N/A	N/A
Angular Velocity	N/A	0.0	N/A	N/A
Use Local Force	N/A	N/A	N/A	N/A
Use Local Torque	N/A	True	N/A	N/A
Use Local Linear Velocity	N/A	N/A	N/A	N/A
Use Local Angular Velocity	N/A	N/A	N/A	N/A
Damping Frames	N/A	0	N/A	N/A

TABLE A.1: The physics engine parameters governing the best-fitness forward motion learned in subsection 4.5.2.
The highlighted cells indicate the GA tuned/learned values.

Appendix B

Source Code

B.1 SimPL

LISTING B.1: Index.js

```
1  /*
2   *
3   * David Lettier (C) 2013.
4   *
5   * http://www.lettier.com/
6   *
7   * Simple Pong Learner or SimPL.
8   *
9   * Single sided pong clone with only one paddle which learns to follow and collide with the ball.
10  */
11
13 var request_animation_id = null;
15 var take_control = false;
16 var pause = true;
17 var show_debug = false;
19 var use_neural_network_paddle = true;
20 var use_perfect_paddle = false;
21 var use_random_paddle = false;
23 var run_experiment = true;
25 var top_wall = new Static_Object( "top_wall" );
26 var right_wall = new Static_Object( "right_wall" );
27 var bottom_wall = new Static_Object( "bottom_wall" );
28 var left_wall = new Static_Object( "left_wall" );
29
30 var ball_slot = document.getElementById( "ball_slot" );
31 var paddle_slot = document.getElementById( "paddle_slot" );
33 var ball_reset_center = { x: ball_slot.offsetLeft + ( ( ball_slot.offsetWidth || ball_slot.clientWidth ) / 2 ),
34                           y: ball_slot.offsetTop + ( ( ball_slot.offsetHeight || ball_slot.clientHeight ) / 2 ) };
35 var paddle_reset_center = { x: paddle_slot.offsetLeft + ( ( paddle_slot.offsetWidth || paddle_slot.clientWidth ) / 2 ),
36                            y: paddle_slot.offsetTop + ( ( paddle_slot.offsetHeight || paddle_slot.clientHeight ) / 2 ) };
37
38 var paddle_path = document.getElementById( "paddle_path" );
39 var ball_in_paddle_path_color = "rgba( 200, 255, 136, .2 )";
40 var ball_not_in_paddle_path_color = "rgba( 255, 98, 98, .2 )";
41 var paddle_path_background_color = ball_in_paddle_path_color;
43 var random_angle_range = { min: 135, max: 225 };
44 var random_angle = random_angle_range.min + ( random_angle_range.max - random_angle_range.min ) * Math.random();
45
46 var starting_magnitude = 1000.0;
47 var starting_ball_magnitude = starting_magnitude;
48 var starting_paddle_magnitude = starting_magnitude;
49 var starting_paddle_angle = 90.0;
51 var ball = new Physics_Object( new Dynamic_Object( "ball" ), random_angle, starting_ball_magnitude );
53 var paddle = new Physics_Object( new Dynamic_Object( "paddle", [ paddle_path, "t" ] ),
54                               starting_paddle_angle, starting_paddle_magnitude );
55 var physics_engine = new Physics_Engine( collision_handler, paddle, ball, top_wall, right_wall,
56                                       bottom_wall, left_wall );
57 var time_delta = 0.0;
```

```

59 var fps_monitor = new FPS_Monitor();
61 var debug_manager = new Debug_Manager( "debug" );
63 var database_manager = new Database_Manager();
65 var neural_net_parameters = {
66   nInputs:           6,
67   nOutputs:          1,
68   nHiddenLayers:     1,
69   nNeuronsPerHiddenLayer: 5,
70   bias:              -1
71 };
73 };
75 var genetic_algorithm_parameters = {
76   popSize:            10,
77   nGenesPerGenome:    null,
78   useRankFitness:      true,
79   useSelfAdaptation:  true,
80   pCrMuSeq:           false,
81   iCProb:              0.8,
82   iMProb:              0.2,
83   nElite:             2
84 };
85 };
87 var learner_parameters = {
88   neural_net:          neural_net_parameters,
89   genetic_algorithm:   genetic_algorithm_parameters
90 };
93 };
95 var learner = {
96   parameters:         learner_parameters,
97   neural_net:          null,
98   neural_net_output:   null,
99   genetic_algorithm:   null,
100 evaluation_start_time: 0,
101 evaluation_end_time:   0,
102 evaluate_current_genome: false,
103 current_genome_fitness_tracking: new Array(),
104 current_genome_paddle_hits: 0,
105 current_genome_being_evaluated: 0
106 };
107 };
109 learner.neural_net = new Neural_Net( learner.parameters.neural_net );
111 learner.parameters.genetic_algorithm.nGenesPerGenome = learner.neural_net.get_number_of_weights();
113 learner.genetic_algorithm = new Genetic_Algorithm( learner.parameters.genetic_algorithm );
115 learner.neural_net_output = 0;
117 // Attempt to load in the last generation from the database.
119 var last_generation_data_string = "population_size=" + learner.genetic_algorithm.get_population_size();
121 last_generation_data_string += "&number_of_genes_per_genome=" + learner.genetic_algorithm.get_number_of_genes_per_genome();
123 database_manager.send_and_receive( "assets/scripts/retrieve_genomes.php", last_generation_data_string,
124                                     database_manager, "last_generation", false );
125 var last_generation = database_manager.responses[ "last_generation" ];
127 if ( last_generation.charAt( 0 ) != ";" )
128 {
129   if ( window.confirm( "Start from previous generation?" ) )
130   {
131     // String received from server is generation_number;crossover_probability;mutation_probability;
132     // population_genes.
133     var generation_number = parseInt( last_generation.split( ";" )[ 0 ] );
134     learner.genetic_algorithm.set_generation_number( generation_number );
135     var crossover_probability = parseFloat( last_generation.split( ";" )[ 1 ] );
136     learner.genetic_algorithm.set_crossover_probability( crossover_probability );
137     var mutation_probability = parseFloat( last_generation.split( ";" )[ 2 ] );
138     learner.genetic_algorithm.set_mutation_probability( mutation_probability );
139     var population_genes = last_generation.split( ";" )[ 3 ];
140     population_genes = population_genes.split( "," );
141     for ( var i = 0; i < population_genes.length; ++i )
142     {
143       population_genes[ i ] = parseFloat( population_genes[ i ] );
144     }
145   }
146 }
147 
```

```

159     learner.genetic_algorithm.replace_population_genes( population_genes );
160     // Set neural network weights to the first genome's genes.
161     learner.neural_net.put_weights( learner.genetic_algorithm.get_genome_genes( learner.
162         current_genome_being_evaluated ) );
163     pause = false;
164 }
165 }
166 else
167 {
168     learner.neural_net.put_weights( learner.genetic_algorithm.get_genome_genes( learner.
169         current_genome_being_evaluated ) );
170     pause = false;
171 }
172 }
173 }
174 else
175 {
176     learner.neural_net.put_weights( learner.genetic_algorithm.get_genome_genes( learner.
177         current_genome_being_evaluated ) );
178     pause = false;
179 }
180 }
181 }
182 }
183 }
184 }
185 var ball_style = window.getComputedStyle( ball.dynamic_object.object, null );
186 var ball_style_transform = ball_style.getPropertyValue( "-webkit-transform" ) ||
187     ball_style.getPropertyValue( "-moz-transform" ) ||
188     ball_style.getPropertyValue( "-ms-transform" ) ||
189     ball_style.getPropertyValue( "-o-transform" ) ||
190     ball_style.getPropertyValue( "transform" );
191 var ball_div_transform_angle = 360;
192 var ball_div_transform_angle_by = 20;
193
194 function draw( time_stamp )
195 {
196     request_animation_id = window.requestAnimationFrame( draw );
197     time_delta = fps_monitor.get_time_delta( time_stamp );
198     if ( !pause )
199     {
200         debug_manager.add_or_update( "FPS", fps_monitor.get_fps( time_stamp ) );
201         debug_manager.add_or_update( "Paddle", paddle );
202         debug_manager.add_or_update( "Ball", ball );
203         handle_neural_network_ouput();
204         debug_manager.add_or_update( "Current Genome", learner.current_genome_being_evaluated );
205         debug_manager.add_or_update( "NN", learner.neural_net );
206         debug_manager.add_or_update( "NN Weights", learner.neural_net.get_weights() );
207         debug_manager.add_or_update( "GA", learner.genetic_algorithm );
208         physics_engine.update( time_delta );
209         // Spin the ball div to give the illusion of flying through the air.
210         if ( ball_style_transform != undefined && ball.get_magnitude() != 0 )
211         {
212             ball.dynamic_object.style.webkitTransform = "rotate(" + ball_div_transform_angle + "deg)";
213             ball.dynamic_object.style.MozTransform = "rotate(" + ball_div_transform_angle + "deg)";
214             ball.dynamic_object.style.msTransform = "rotate(" + ball_div_transform_angle + "deg)";
215             ball.dynamic_object.style.OTransform = "rotate(" + ball_div_transform_angle + "deg)";
216             ball.dynamic_object.style.transform = "rotate(" + ball_div_transform_angle + "deg)";
217             if ( ball.get_angle() >= 90 && ball.get_angle() <= 270 )
218             {
219                 // Spin counter clock-wise if it is going towards the left of the screen.
220                 ball_div_transform_angle = ball_div_transform_angle < 0 ? 360 : ball_div_transform_angle - (
221                     ball_div_transform_angle_by * ( ball.get_magnitude() / starting_ball_magnitude ) );
222             }
223             else
224             {
225                 ball_div_transform_angle = ball_div_transform_angle > 360 ? 0 : ball_div_transform_angle + (
226                     ball_div_transform_angle_by * ( ball.get_magnitude() / starting_ball_magnitude ) );
227             }
228         }
229     }
230     // Time to evaluate the current genome?
231     if ( learner.evaluate_current_genome )
232     {

```

```

255     handle_genome_evaluation( );
257   }
259   debug_manager.print( );
261 }
263 }
265 // The following stub was taken from https://gist.github.com/paulirish/1579671.
267 ( function ( )
269 {
  var lastTime = 0;
271  var vendors = [ 'ms', 'moz', 'webkit', 'o' ];
272  for( var x = 0; x < vendors.length && !window.requestAnimationFrame; ++x )
273  {
275    window.requestAnimationFrame = window[ vendors[ x ] + 'RequestAnimationFrame' ];
276    window.cancelAnimationFrame = window[vendors[x] + 'CancelAnimationFrame'] || window[ vendors[ x ] + 'CancelRequestAnimationFrame' ];
277  }
279  if ( !window.requestAnimationFrame )
281  {
283    window.requestAnimationFrame = function ( callback, element )
285  {
286    var currTime = new Date( ).getTime( );
287    var timeToCall = Math.max( 0, 16 - ( currTime - lastTime ) );
288    var id = window.setTimeout( function ( ) { callback( currTime + timeToCall ); }, timeToCall );
289    lastTime = currTime + timeToCall;
290    return id;
291  };
293  }
295  if ( !window.cancelAnimationFrame )
297  {
299    window.cancelAnimationFrame = function ( id )
301  {
302    clearTimeout( id );
303  };
305  }
307 } () );
309 draw( );
311 function reset( )
313 {
  random_angle = random_angle_range.min + ( random_angle_range.max - random_angle_range.min ) * Math.
  random( );
315 ball.dynamic_object.set_center( ball_reset_center.x, ball_reset_center.y );
316 ball.set_magnitude( starting_ball_magnitude );
317 ball.set_angle( random_angle );
319 paddle.dynamic_object.set_center( paddle_reset_center.x, paddle_reset_center.y );
320 paddle.set_magnitude( starting_ball_magnitude );
321 paddle.set_angle( starting_paddle_angle );
323 take_control = false;
324 pause = false;
325 }
327 document.onkeyup = handle_key;
329 function handle_key( kevent )
331 {
  var key = ( window.event ) ? event.keyCode : kevent.keyCode;
333  switch ( key )
335  {
337    case 68: // [d] key.
338      show_debug = !show_debug
339      if ( show_debug ) debug_manager.show_debug( );
340      else debug_manager.hide_debug( );
343      break;
345    case 70: // [f] key.
346      debug_div = document.getElementById( "debug" );
347      debug_div_font_size = parseInt( window.getComputedStyle( debug_div, null ).getPropertyValue( 'font-
348 size' ), 10 );
350      if ( window.event.shiftKey )
351      {

```

```

355     debug_div_font_size -= 1;
357     debug_div.style.fontSize = debug_div_font_size + "px";
359 }
361 {
363     debug_div_font_size += 1;
365     debug_div.style.fontSize = debug_div_font_size + "px";
367 }
369     break;
371 case 77: // [m] key.
373     ball.set_magnitude( ball.get_magnitude() + 100 );
375     break;
377 case 80: // [p] key.
379     pause = !pause;
381     break;
383 case 82: // [r] key.
385     reset();
387     break;
389 case 84: // [t] key.
391     take_control = !take_control;
393     break;
395 }
397 document.onmousemove = handle_mouse_move;
399 function handle_mouse_move( mevent )
401 {
403 if ( !take_control ) return null;
405 mevent = ( window.event ) ? window.event : mevent;
407 if ( ( mevent.clientY - ( paddle.dynamic_object.get_height() / 2 ) ) >= ( window.innerHeight - paddle.
408     dynamic_object.get_height() ) )
409 {
410     paddle.dynamic_object.set_left_top( paddle.dynamic_object.get_left(), window.innerHeight - paddle.
411         dynamic_object.get_height() );
411     return null;
413 }
415 else if ( ( mevent.clientY - ( paddle.dynamic_object.get_height() / 2 ) ) <= 0 )
416 {
417     paddle.dynamic_object.set_left_top( paddle.dynamic_object.get_left(), 0 );
419     return null;
421 }
423 paddle.dynamic_object.set_left_top( paddle.dynamic_object.get_left(), mevent.clientY - ( paddle.
424     dynamic_object.get_height() / 2 ) );
425 }
427 function handle_neural_network_ouput( )
429 {
431 if ( take_control )
432 {
433     paddle.set_magnitude( 0 );
435     paddle.set_angle( starting_paddle_angle );
437     return null;
439 }
441 // To help with fitness testing, keep track of if the ball
443 // is in the path of the paddle.
444 // 1 for in the path of the ball.
445 // Nothing for not in the path of the ball.
446 //
447 // In the path:
448 // -----
449 // |      0
450 // |
451 // |-----
452 //

```

```

453 // Not in the path:
454 // 0
455 // -----
456 // |
457 // | -----
458 // |
459 // | -----
460 // |
461 // |
462 // | -----
463 // |
464 // | -----
465 // |
466 // 0
467

469 if ( !( ( ball.dynamic_object.get_top( ) > paddle.dynamic_object.get_bottom( ) ) || ( ball.
    dynamic_object.get_bottom( ) < paddle.dynamic_object.get_top( ) ) ) )
{
471     learner.current_genome_fitness_tracking.push( 1 );
473     // Adjust paddle path visual.
475     paddle_path.style.background = ball_in_paddle_path_color;
477

479 }
481 else
{
483     // Add nothing.
485     // Adjust paddle path visual.
487     paddle_path.style.background = ball_not_in_paddle_path_color;
489 }
491 /*
493 // Experiment one tracking.
495 learner.current_genome_fitness_tracking.push( Math.abs( paddle.dynamic_object.get_center( ).y - ball.
    dynamic_object.get_center( ).y ) );
497 */
499 // Get input values for the neural network.

501 var x = ball.dynamic_object.get_center( ).x - paddle.dynamic_object.get_center( ).x;
var y = ball.dynamic_object.get_center( ).y - paddle.dynamic_object.get_center( ).y;
503
504 var paddle_offset_from_ball = { x: x,
505     y: y,
506     h: Math.sqrt( ( x * x ) + ( y * y ) )
507 };
508
509 x = paddle.dynamic_object.get_center( ).x - 0;
y = paddle.dynamic_object.get_center( ).y - 0;
511
512 var paddle_offset_from_screen_origin = { x: x,
513     y: y,
514     h: Math.sqrt( ( x * x ) + ( y * y ) )
515 };
516
517 var ball_velocity = deep_copy( ball.get_velocity( ) );
518
519 // Normalize input in [-1,1].
520
521 paddle_offset_from_ball.x = paddle_offset_from_ball.x / paddle_offset_from_ball.h;
paddle_offset_from_ball.y = paddle_offset_from_ball.y / paddle_offset_from_ball.h;
523
524 paddle_offset_from_screen_origin.x = paddle_offset_from_screen_origin.x /
    paddle_offset_from_screen_origin.h;
paddle_offset_from_screen_origin.y = paddle_offset_from_screen_origin.y /
    paddle_offset_from_screen_origin.h;
526
527 // Turn the velocity into unit vectors.
528
529 ball_velocity.x = ball_velocity.x / ball.get_magnitude( );
ball_velocity.y = ball_velocity.y / ball.get_magnitude( );
531
532 // Send in the input and get out the output which is an array.
533
534 learner.neural_net_output = learner.neural_net.update( [ paddle_offset_from_ball.x,
    paddle_offset_from_ball.y, ball_velocity.x, ball_velocity.y, paddle_offset_from_screen_origin.x,
    paddle_offset_from_screen_origin.y ] );
535
536 debug_manager.add_or_update( "NN Input", paddle_offset_from_ball.x.toFixed( 3 ) + " " +
    paddle_offset_from_ball.y.toFixed( 3 ) + " " + ball_velocity.x.toFixed( 3 ) + " " + ball_velocity.y.
   toFixed( 3 ) + " " + paddle_offset_from_screen_origin.x.toFixed( 3 ) + " " +
    paddle_offset_from_screen_origin.y.toFixed( 3 ) );
537
538 debug_manager.add_or_update( "NN Output", learner.neural_net_output );
539
540 if ( use_neural_network_paddle )
{
541
542     if ( learner.neural_net_output[ 0 ] < 0.0 )
{
545

```

```

547     // Output indicates that we must go down the screen
548     // by some magnitude in the range (0,MAG_MAX).
549
550     // Don't set a negative magnitude so multiply the output by -1 to
551     // make it positive and multiply this result by the starting paddle
552     // magnitude.
553
554     paddle.set_magnitude( starting_paddle_magnitude * ( -1 * learner.neural_net_output[ 0 ] ) );
555
556     paddle.set_angle( 270 );
557
558 }
559 else if ( learner.neural_net_output[ 0 ] == 0.0 )
{
560
561     // Don't move.
562
563     paddle.set_magnitude( 0.0 );
564
565     paddle.set_angle( starting_paddle_angle );
566
567 }
568 else if ( learner.neural_net_output[ 0 ] > 0.0 )
{
569
570     // Go up by some portion of the starting paddle magnitude.
571
572     paddle.set_magnitude( starting_paddle_magnitude * learner.neural_net_output[ 0 ] );
573
574     paddle.set_angle( 90.0 );
575
576 }
577
578 }
579 else if ( use_perfect_paddle )
{
580
581     /*
582
583     var difference = paddle.dynamic_object.get_center( ).y - ball.dynamic_object.get_center( ).y;
584     debug_manager.add_or_update( "Perfect Output", difference );
585
586     if ( difference < 0 )
587     {
588         paddle.set_magnitude( 10.0 * ( -1 * difference ) );
589         paddle.set_angle( 270 );
590     }
591     else if ( difference == 0.0 )
592     {
593         paddle.set_magnitude( 0.0 );
594         paddle.set_angle( starting_paddle_angle );
595     }
596     else if ( difference > 0 )
597     {
598         paddle.set_magnitude( 10.0 * difference );
599         paddle.set_angle( 90.0 );
600     }
601
602     */
603
604     paddle.set_magnitude( 0.0 );
605
606     paddle.set_angle( starting_paddle_angle );
607
608 }
609
610 else if ( use_random_paddle )
{
611
612     var random_float = get_random_float( -1, 1 );
613     debug_manager.add_or_update( "Random Output", random_float );
614
615     if ( random_float < 0.0 )
616     {
617
618         paddle.set_magnitude( starting_paddle_magnitude * ( -1 * random_float ) );
619         paddle.set_angle( 270.0 );
620
621     }
622     else if ( random_float == 0.0 )
623     {
624
625         paddle.set_magnitude( 0.0 );
626         paddle.set_angle( starting_paddle_angle );
627
628     }
629
630 }
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647

```

```

649     }
650     else if ( random_float > 0.0 )
651     {
653         paddle.set_magnitude( starting_paddle_magnitude * random_float );
655         paddle.set_angle( 90.0 );
657     }
659 }
661 }

663 /* Experiment one fitness function.

665 function handle_genome_evaluation( )
666 {
667     pause = true;
668     var fitness = 0.0;
669     for( var i = 0; i < learner.current_genome_fitness_tracking.length - 1; ++i )
670     {
671         if ( learner.current_genome_fitness_tracking[ i ] < learner.current_genome_fitness_tracking[ i + 1 ] )
672         {
673             fitness = fitness - 0.1;
674         }
675         else if ( learner.current_genome_fitness_tracking[ i ] == learner.current_genome_fitness_tracking[ i + 1 ] )
676         {
677             if ( learner.current_genome_fitness_tracking[ i ] == 0 && learner.current_genome_fitness_tracking[ i + 1 ] == 0 )
678             {
679                 fitness = fitness + 0.1;
680             }
681             else
682             {
683                 fitness = fitness - 0.1;
684             }
685         }
686     }
687     else if ( learner.current_genome_fitness_tracking[ i ] > learner.current_genome_fitness_tracking[ i + 1 ] )
688     {
689         fitness = fitness + 0.1;
690     }
691 }
692 }

693     fitness = fitness + 0.1;
694 }

695 }

696 }

697 }

698 }

699 }

700 }

701 }

702 }

703 }

704 }

705 }

706 }

707 learner.current_genome_fitness_tracking = [ ];
708 fitness = fitness + ( 1 * learner.current_genome_paddle_hits );
709 learner.current_genome_paddle_hits = 0;
710 if ( fitness < 0.0 ) fitness = 0.0;
711 debug_manager.add_or_update( "Last Genome Fitness", fitness );
712 learner.genetic_algorithm.set_genome_fitness( learner.current_genome_being_evaluated, fitness );
713 if ( ( learner.current_genome_being_evaluated + 1 ) == learner.genetic_algorithm.get_population_size( )
714 )
715 {
716     // Evaluated all the genomes in the population.
717     // Calculate population metrics.
718     // Adjust crossover and mutation probabilities if using self-adaptation.
719     learner.genetic_algorithm.sort_population( );
720     learner.genetic_algorithm.evaluate_population( );
721     if ( learner.parameters.genetic_algorithm.useSelfAdaptation )
722     {
723         learner.genetic_algorithm.adjust_crossover_and_mutation_probabilities( );
724     }
725     // Package up this population and send it to the database if its generation number is higher than
726     // the highest generation number already in the database.
727     var data_string = "generation_number=" + learner.genetic_algorithm.get_generation_number( )
728     ;
729     data_string += "&best_fitness=" + learner.genetic_algorithm.get_best_fitness( );
730     data_string += "&average_fitness=" + learner.genetic_algorithm.get_average_fitness( );
731     data_string += "&worst_fitness=" + learner.genetic_algorithm.get_worst_fitness( );
732     data_string += "&population_size=" + learner.genetic_algorithm.get_population_size( );

```

```

745     data_string      += "&number_of_genes_per_genome=" + learner.genetic_algorithm.
746     get_number_of_genes_per_genome( );
747     data_string      += "&crossover_probability="      + learner.genetic_algorithm.
748     get_crossover_probability( );
749     data_string      += "&mutation_probability="    + learner.genetic_algorithm.get_mutation_probability
750     ( );
751     data_string      += "&population_genes="       + learner.genetic_algorithm.
752     get_population_genes_flattened( );
753
754     database_manager.send_and_receive( "assets/scripts/store_genomes.php", data_string, database_manager,
755     "adding_genome_population" );
756
757     if ( run_experiment )
758     {
759
760         // Experiment of first 100 generations.
761
762         if ( learner.genetic_algorithm.get_generation_number( ) < 100 )
763         {
764
765             var experiment_record_data_string = "action=record";
766             experiment_record_data_string += "&generation_number="      + learner.genetic_algorithm.
767             get_generation_number( );
768             experiment_record_data_string += "&best_fitness="        + learner.genetic_algorithm.
769             get_best_fitness( );
770             experiment_record_data_string += "&average_fitness="   + learner.genetic_algorithm.
771             get_average_fitness( );
772             experiment_record_data_string += "&worst_fitness="     + learner.genetic_algorithm.
773             get_worst_fitness( );
774             experiment_record_data_string += "&crossover_probability=" + learner.genetic_algorithm.
775             get_crossover_probability( );
776             experiment_record_data_string += "&mutation_probability=" + learner.genetic_algorithm.
777             get_mutation_probability( );
778
779             database_manager.send_and_receive( "assets/scripts/experiment.php", experiment_record_data_string,
780             database_manager, "experiment_record" );
781
782             if ( ( learner.genetic_algorithm.get_generation_number( ) + 1 ) % 10 == 0 )
783             {
784
785                 var experiment_store_data_string = "action=store";
786                 experiment_store_data_string += "&generation_number="      + learner.genetic_algorithm.
787                 get_generation_number( );
788                 experiment_store_data_string += "&fitness="           + learner.genetic_algorithm.
789                 get_genome_fitness( learner.genetic_algorithm.get_fittest_genome_index( ) );
790                 experiment_store_data_string += "&crossover_probability=" + learner.genetic_algorithm.
791                 get_crossover_probability( );
792                 experiment_store_data_string += "&mutation_probability=" + learner.genetic_algorithm.
793                 get_mutation_probability( );
794                 experiment_store_data_string += "&genes="            + learner.genetic_algorithm.
795                 get_genome_genes_flattened( learner.genetic_algorithm.get_fittest_genome_index( ) );
796
797                 database_manager.send_and_receive( "assets/scripts/experiment.php", experiment_store_data_string
798                 , database_manager, "experiment_store" );
799
800             }
801         }
802     }
803
804     else
805     {
806
807         // Test the next genome in the population.
808
809         learner.current_genome_being_evaluated += 1;
810
811         learner.neural_net.put_weights( learner.genetic_algorithm.get_genome_genes( learner.
812             current_genome_being_evaluated ) );
813
814     }
815
816     learner.evaluate_current_genome = false;
817
818     reset( );
819
820 }
821 */
822
823 function handle_genome_evaluation( )
824 {
825     pause = true;

```

```

827     var fitness = 0.0;
829     for( var i = 0; i < learner.current_genome_fitness_tracking.length; ++i )
830     {
831         fitness += learner.current_genome_fitness_tracking[ i ];
833     }
835     learner.current_genome_fitness_tracking = [ ];
837     if ( fitness < 0.0 ) fitness = 0.0;
839     debug_manager.add_or_update( "Last Genome Fitness", fitness );
841     learner.genetic_algorithm.set_genome_fitness( learner.current_genome_being_evaluated, fitness );
843     if ( ( learner.current_genome_being_evaluated + 1 ) == learner.genetic_algorithm.get_population_size( ) )
844     {
845
847         // Evaluated all the genomes in the population.
848         // Calculate population metrics.
849         // Adjust crossover and mutation probabilities if using self-adaptation.
851         learner.genetic_algorithm.sort_population( );
853         learner.genetic_algorithm.evaluate_population( );
855         if ( learner.parameters.genetic_algorithm.useSelfAdaptation )
856         {
857             learner.genetic_algorithm.adjust_crossover_and_mutation_probabilities( );
859         }
861         // Package up this population and send it to the database if its generation number is higher than
862         // the highest generation number already in the database.
863         //data_string = "generation_number=" + learner.genetic_algorithm.get_generation_number( );
864         data_string += "&best_fitness=" + learner.genetic_algorithm.get_best_fitness( );
865         data_string += "&average_fitness=" + learner.genetic_algorithm.get_average_fitness( );
866         data_string += "&worst_fitness=" + learner.genetic_algorithm.get_worst_fitness( );
867         data_string += "&population_size=" + learner.genetic_algorithm.get_population_size( );
868         data_string += "&number_of_genes_per_genome=" + learner.genetic_algorithm.
869             get_number_of_genes_per_genome( );
870         data_string += "&crossover_probability=" + learner.genetic_algorithm.
871             get_crossover_probability( );
872         data_string += "&mutation_probability=" + learner.genetic_algorithm.get_mutation_probability
873             ();
874         data_string += "&population_genes=" + learner.genetic_algorithm.
875             get_population_genes_flattened( );
876
877         database_manager.send_and_receive( "assets/scripts/store_genomes.php", data_string, database_manager,
878             "adding_genome_population" );
879
880         if ( run_experiment )
881         {
882             // Experiment of first 100 generations.
883             if ( learner.genetic_algorithm.get_generation_number( ) < 100 )
884             {
885                 var experiment_record_data_string = "action=record";
886                 experiment_record_data_string += "&generation_number=" + learner.genetic_algorithm.
887                     get_generation_number( );
888                 experiment_record_data_string += "&best_fitness=" + learner.genetic_algorithm.
889                     get_best_fitness( );
890                 experiment_record_data_string += "&average_fitness=" + learner.genetic_algorithm.
891                     get_average_fitness( );
892                 experiment_record_data_string += "&worst_fitness=" + learner.genetic_algorithm.
893                     get_worst_fitness( );
894                 experiment_record_data_string += "&crossover_probability=" + learner.genetic_algorithm.
895                     get_crossover_probability( );
896                 experiment_record_data_string += "&mutation_probability=" + learner.genetic_algorithm.
897                     get_mutation_probability( );
898
899                 database_manager.send_and_receive( "assets/scripts/experiment.php", experiment_record_data_string,
900                     database_manager, "experiment_record" );
901
902             if ( ( learner.genetic_algorithm.get_generation_number( ) + 1 ) % 10 == 0 )
903             {
904                 var experiment_store_data_string = "action=store";
905                 experiment_store_data_string += "&generation_number=" + learner.genetic_algorithm.
906                     get_generation_number( );
907                 experiment_store_data_string += "&fitness=" + learner.genetic_algorithm.
908                     get_genome_fitness( learner.genetic_algorithm.get_fittest_genome_index( ) );
909                 experiment_store_data_string += "&crossover_probability=" + learner.genetic_algorithm.
910                     get_crossover_probability( );
911                 experiment_store_data_string += "&mutation_probability=" + learner.genetic_algorithm.
912                     get_mutation_probability( );
913                 experiment_store_data_string += "&genes=" + learner.genetic_algorithm.
914                     get_genome_genes_flattened( learner.genetic_algorithm.get_fittest_genome_index( ) );
915
916                 database_manager.send_and_receive( "assets/scripts/experiment.php", experiment_store_data_string
917                     , database_manager, "experiment_store" );
918             }

```

```

909     }
911   }
913   // Generate a new generation.
915   learner.genetic_algorithm.generate_new_generation();
917   // Get the makeup of the population.
919   learner.genetic_algorithm.compute_population_makeup();
921   // Load in the first genome's genes.
923   learner.current_genome_being_evaluated = 0;
925   learner.neural_net.put_weights(learner.genetic_algorithm.get_genome_genes(learner.
926                                 current_genome_being_evaluated));
927 }
928 else
929 {
930   // Test the next genome in the population.
931   learner.current_genome_being_evaluated += 1;
932   learner.neural_net.put_weights(learner.genetic_algorithm.get_genome_genes(learner.
933                                 current_genome_being_evaluated));
934 }
935
936 learner.evaluate_current_genome = false;
937 reset();
938
939 }
940
941 var ball_magnitude_reduction_threshold = 100;
942 var ball_magnitude_reduce_by_percentage = .5;
943
944 function collision_handler(colliding_objects)
945 {
946   learner.evaluate_current_genome = false;
947
948   for (var i = 0; i < colliding_objects.length; ++i)
949   {
950     // Ball collisions
951
952     if (colliding_objects[i][0].id == "ball" && colliding_objects[i][1].id == "paddle" || (
953       colliding_objects[i][0].id == "paddle" && colliding_objects[i][1].id == "ball"))
954     {
955
956       ball.set_magnitude((ball.get_magnitude() - (ball.get_magnitude() *
957                           ball_magnitude_reduce_by_percentage)) > ball_magnitude_reduction_threshold ? (ball.get_magnitude(
958                             ) - (ball.get_magnitude() * .1)) : 0);
959
960       learner.current_genome_paddle_hits = learner.current_genome_paddle_hits + 1;
961
962       if (ball.get_magnitude() == 0)
963       {
964
965         learner.evaluate_current_genome = true;
966
967       }
968
969     }
970
971     // Wind the ball's position back, going along the direction opposite of the angle it was traveling
972     // along when it collided with
973     // the paddle until it no longer collides with the paddle.
974     // This is easier to calculate than finding the intersection of a line along the direction of the
975     // ball's vector with that of
976     // the paddle's top, right, bottom, and left boundary lines.
977
978     var reverse_angle = ball.mod_degrees((ball.get_angle() + 180));
979     var dx = 5 * Math.cos(ball.degrees_to_radians(reverse_angle));
980     var dy = -5 * Math.sin(ball.degrees_to_radians(reverse_angle)); // Negative one because of the
981     // mirrored coordinate system.
982
983     /*
984      while (physics_engine.rectangle_intersection(paddle.dynamic_object, ball.dynamic_object))
985      {
986
987        console.log("x");
988
989        ball.dynamic_object.move_left_top(dx, dy);
990
991      }
992
993    */
994
995    // There are two cases:
996    // 1. The ball hits the paddle from the top or bottom.
997    // 2. The ball hits the paddle from either the left or right.
998
999    if ((ball.dynamic_object.get_top() > paddle.dynamic_object.get_bottom()) || (ball.
1000         dynamic_object.get_bottom() < paddle.dynamic_object.get_top()))
1001    {
1002
1003      // Top or bottom side case.

```



```

1093     ball.set_magnitude( ( ball.get_magnitude( ) - ( ball.get_magnitude( ) *
1094         ball.magnitude_reduce_by_percentage ) > ball_magnitude_reduction_threshold ? ( ball.get_magnitude(
1095             ) - ( ball.get_magnitude( ) * .1 ) ) : 0 );
1096
1097     if ( ball.get_magnitude( ) == 0 )
1098     {
1099         learner.evaluate_current_genome = true;
1100     }
1101
1102     ball.dynamic_object.move_left_top( 0, ( -1 * ( ball.dynamic_object.get_bottom( ) - window.
1103         innerHeight ) ) -1 );
1104
1105     var reflection_angle = ball.mod_degrees( -1 * ball.get_angle( ) );
1106     ball.set_angle( reflection_angle );
1107
1108 } else if ( colliding_objects[ i ][ 0 ].id == "ball" && colliding_objects[ i ][ 1 ].id == "left_wall" ||
1109 { colliding_objects[ i ][ 0 ].id == "left_wall" && colliding_objects[ i ][ 1 ].id == "ball" ) )
1110
1111     ball.set_magnitude( ( ball.get_magnitude( ) - ( ball.get_magnitude( ) *
1112         ball.magnitude_reduce_by_percentage ) > ball_magnitude_reduction_threshold ? ( ball.get_magnitude(
1113             ) - ( ball.get_magnitude( ) * .1 ) ) : 0 );
1114
1115     learner.evaluate_current_genome = true;
1116
1117     ball.dynamic_object.move_left_top( ( -1 * ( ball.dynamic_object.get_left( ) ) ) + 1, 0 );
1118
1119     var reflection_angle = -1 * ( ball.get_angle( ) - 180.0 );
1120     ball.set_angle( reflection_angle );
1121
1122 // Paddle collisions.
1123
1124 if ( colliding_objects[ i ][ 0 ].id == "paddle" && colliding_objects[ i ][ 1 ].id == "top_wall" || (
1125 { colliding_objects[ i ][ 0 ].id == "top_wall" && colliding_objects[ i ][ 1 ].id == "paddle" )
1126
1127     paddle.dynamic_object.move_left_top( 0, ( -1 * paddle.dynamic_object.get_top( ) ) + 1 );
1128
1129 } else if ( colliding_objects[ i ][ 0 ].id == "paddle" && colliding_objects[ i ][ 1 ].id == "bottom_wall"
1130 " || ( colliding_objects[ i ][ 0 ].id == "bottom_wall" && colliding_objects[ i ][ 1 ].id == "paddle"
1131 ) )
1132
1133     paddle.dynamic_object.move_left_top( 0, ( -1 * ( paddle.dynamic_object.get_bottom( ) - window.
1134         innerHeight ) ) -1 );
1135
1136 }
1137 }
1138 }
```

LISTING B.2: Genetic_Algorithm.js

```

/*
2  *
3  * David Lettier (C) 2013.
4  *
5  * http://www.lettier.com/
6  *
7  * Code ported to JS and HEAVILY modified from original C++ source
8  * found at http://www.ai-junkie.com/ann/evolved/nnt1.html and
9  * written by Mat Buckland.
10 *
11 * Implements a genetic algorithm for NN weight tuning.
12 *
13 */
14
15 function Genome( genes, fitness )
16 {
17
18     this.genes = null;
19     this.fitness = null;
20
21     if ( genes == undefined ) this.genes = new Array();
22     else this.genes = genes;
23
24     if ( fitness == undefined ) this.fitness = 0.0;
25     else this.fitness = fitness;
26
27     // Used to calculate either the crossover progress or mutation progress.
28     // If this genome is created via crossover, use the weighted average
29     // based on the cross over point.
30     // So if the crossover point is say 9 and the genome length is 10,
31     // then the weighted average pf = (p1.f*.9) + (p2.f*.1).
32     // In other words the offspring received 90% of its genes from parent one
33     // and it received 10% of its genes from parent two so its parent fitness is
34     // 90% of parent one's fitness and 10% of parent two's fitness.
35
36     this.parent_fitness = 0.0;
37
38     // Created by means if this genome was generated either by randomness, crossover,
39     // mutation, both crossover and mutation, or elitism.
40     // Initially it is created from nothing so set it to -1.
```

```

    // 0 = randomness, 1 = crossover, 2 = mutation, 3 = crossover & mutation, 4 = elitism
42    // This encoding is to facilitate crossover's and mutation's progress at producing fitter offspring than
43    // the offspring's parents.
44    this.created_by = 0;
46  }
48  function Genetic_Algorithm( params )
50 {
52    // Size of population.
54    this.population_size = params.popSize;
56    // Amount of genes per genome.
58    this.number_of_genes_per_genome = params.nGenesPerGenome;
60    // Use rank in selection?
62    this.use_rank_fitness = params.useRankFitness;
64    // Perform crossover and mutation sequentially or separately?
66    this.perform_crossover_and_mutation_sequentially = params.pCrMuSeq;
68    // Probability of genome's crossing over bits.
69    // 0.7 is pretty good.
70    this.crossover_probability      = params.iCProb;
72    this.crossover_probability_minimum = 0.001;
73    this.crossover_probability_adjustment = 0.01;
74    this.crossover_operator_progress_average = 0.0;
75    this.observed_crossover_rate = 0.0;
76    this.total_number_of_crossovers = 0;
77    this.total_number_of_crossover_attempts = 0;
78
79    // Probability that a genomes bits will mutate.
80    // Try figures around 0.05 to 0.3-ish.
81    this.mutation_probability      = params.iMProb;
82    this.mutation_probability_minimum = 0.001;
83    this.mutation_probability_adjustment = 0.01;
84    this.mutation_operator_progress_average = 0.0;
85    this.observed_mutation_rate = 0.0;
86    this.total_number_of_mutations = 0;
87    this.total_number_of_mutation_attempts = 0;
88
89    // Set the number of elite that go on to the next generation.
90    this.number_of_elite = params.nElite;
91
92    // This holds the entire population of genomes.
93    this.population = new Array();
94
95    // Total fitness of population.
96
97    this.total_fitness = 0;
98
99    // Average fitness.
100   this.average_fitness = 0;
101
102   // Best fitness this population.
103   this.best_fitness = 0;
104
105   // Worst fitness.
106   this.worst_fitness = 0;
107
108   // Keeps track of the best genome.
109   this.fittest_genome_index = -1;
110
111   // Keep track of the worst genome.
112   this.weakest_genome_index = -1;
113
114   // Generation number.
115   this.generation_number = 0;
116
117   // Current population makeup of randoms, crossovers, mutants, crossover mutants, elites.
118   this.population_makeup = "";
119
120   // Initialize population with genomes consisting of random
121   // genes and all fitness's set to zero.
122   for ( var i = 0; i < this.population_size; ++i )
123   {
124
125     this.population.push( new Genome() );
126
127     for ( var j = 0; j < this.number_of_genes_per_genome; ++j )
128     {
129
130       this.population[ i ].genes.push( get_random_float( -1.0, 1.0 ) );
131
132     }
133
134   }
135
136
137
138
139
140

```

```

142     }
144   }
146   this.replace_population_genes = function ( replacement_population_genes )
148   {
150     if ( replacement_population_genes === undefined ||
151         replacement_population_genes.length === 0 ||
152         replacement_population_genes.length != ( this.population_size * this.number_of_genes_per_genome ) )
154     {
155       console.error( "[Genetic_Algorithm:replace_population_genes] Replacement population genes invalid." );
156       return null;
158     }
160   // Assumes replace_population_genes is one big array.
162   // Splices the big array based on the number of genes
163   // per genome.
164
166   // Big array: [ 1,1,1,1,1,1,1,1,1 ] >>
167   // Population: [ [ 1, 1 ] G0
168   //                [ 1, 1 ] G1
169   //                [ 1, 1 ] ...
170   //                [ 1, 1 ] ...
171   //                [ 1, 1 ] ...
172   //                ]
174   var k = 0;
176   for ( var i = 0; i < this.population_size; ++i )
178   {
179     this.population[ i ].genes = [ ];
180     for ( var j = 0; j < this.number_of_genes_per_genome; ++j )
181     {
182       this.population[ i ].genes.push( replacement_population_genes[ k ] );
183       k += 1;
184     }
185   }
186 }
192 }
194 this.selection_operator = function ( number_of_indexes )
195 {
196   // Assumes population has been evaluated.
197   // Assumes population is sorted in ascending order according to fitness.
198   // Roulette selection of n genome indexes in the population.
199   if ( !this.use_rank_fitness )
200   {
201     // Say we have a population of 4 with these fitness values:
202     // G-1: 1
203     // G-2: 2
204     // G-3: 3
205     // G-4: 4
206     // Total fitness: 10
207     // Probabilities:
208     // G-1: .1
209     // G-2: .2
210     // G-3: .3
211     // G-4: .4
212     //
213     // Now shift them over by the running sum.
214     // This give them a portion on the number line [0.0,1.0] proportional to their
215     // fitness.
216     //
217     // G-1: .1
218     // G-2: G-1 + .2 = .3
219     // G-3: G-2 + .3 = .6
220     // G-4: G-3 + .4 = 1.0
221     //
222     // 0.0----.10----.20----.30----.40----.50----.60----.70----.80----.90----1.0
223     //          G-1           G-2           G-3           G-4
224     //
225     // Now selected a random float in [0.0,1.0]:
226     // RF: .51
227     //
228     // 0.0----.10----.20----.30----.40----.50----.60----.70----.80----.90----1.0
229     //          G-1           G-2           RF  G-3           G-4
230     //
231     // G-3 gets selected for mating.
232
233   var probabilities = new Array( );
234   var genome_indexes_selected = new Array( );
235   if ( this.total_fitness == 0 )
236

```

```

244     {
245         // So that we don't divide by zero.
246         // This means genomes all have zero fitness
247         // so just select random genome indexes.
248
249         for ( var i = 0; i < number_of_indexes; ++i )
250         {
251
252             genome_indexes_selected.push( get_random_integer( 0, this.population_size - 1 ) );
253
254         }
255
256         return genome_indexes_selected;
257     }
258
259     probabilities.push( this.population[ 0 ].fitness / this.total_fitness );
260
261     for ( var i = 1; i < this.population_size; ++i )
262     {
263
264         probabilities.push( probabilities[ i - 1 ] + ( this.population[ i ].fitness / this.total_fitness ) );
265
266     }
267
268     while ( genome_indexes_selected.length < number_of_indexes )
269     {
270
271         var random_number = get_random_float( 0.0, 1.0 );
272
273         for ( var i = 0; i < this.population_size; ++i )
274         {
275
276             if ( random_number <= probabilities[ i ] )
277             {
278
279                 genome_indexes_selected.push( i );
280
281             }
282
283         }
284
285     }
286
287     return genome_indexes_selected;
288 }
289
290 else
291 {
292
293     // Give the worst genome a rank fitness of 1.
294     // Give the second worst genome a rank fitness of 2.
295     // ...
296     // Give the best genome a rank fitness of the population size.
297
298     // Now, based on rank fitness, do a roulette selection where the
299     // probabilities are based on the rank fitness.
300
301     var probabilities = new Array( );
302
303     var genome_indexes_selected = new Array( );
304
305     // Rank fitness of the first is 1.
306     // Probability is 1/(n(n+1)/2).
307     // Where n is population size.
308     // (n(n+1)/2) = the total rank fitness.
309     // Summing the numbers from 1 to population size.
310     // Say population size is 10.
311     // Rank fitness: G-1 = 1, G-2 = 2, ..., G-10 = 10.
312     // Total rank fitness is 1+2+3+...+10 = n(n+1)/2 = (10*11)/2 = 55
313     // Probabilities:
314     // G-1: 1/55
315     // G-2: G-1 + 2/55
316     // ...
317     // G-10: G-9 + 10/55
318
319     var total_rank_fitness = ( this.population_size * ( this.population_size + 1 ) ) / 2;
320
321     probabilities.push( 1 / total_rank_fitness ); // First rank fitness probability.
322
323     // Rest of the rank fitness probabilities.
324
325     for ( var i = 1; i < this.population_size; ++i )
326     {
327
328         probabilities.push( probabilities[ i - 1 ] + ( ( i + 1 ) / total_rank_fitness ) );
329
330     }
331
332     while ( genome_indexes_selected.length < number_of_indexes )
333     {
334
335         var random_number = get_random_float( 0.0, 1.0 );
336
337         for ( var i = 0; i < this.population_size; ++i )
338         {
339
340             if ( random_number <= probabilities[ i ] )
341             {

```

```

344         genome_indexes_selected.push( i );
346     }
348   }
350 }
352   return genome_indexes_selected;
354 }
356 }
358 this.elitism_operator = function ( new_population )
{
360   if ( this.number_of_elite > this.population_size ) this.number_of_elite = this.population_size;
362   // Assumes the population is sorted in ascending order of fitness.
364   // A = [ 0, 1, 2, 3, 4, 5, 6, 7, 8, 9 ]
366   // |A| = 10
367   // i = 2 check.
368   // A[ ( 10 - 1 = 9 ) - i ] = 8 ]
369   // i = 1 check.
370   // i = 0 decrement.
371   // A[ ( 10 - 1 = 9 ) - i ] = 9 ]
372   // i = 0 check.
373   // Stop.
374
375   var i = this.number_of_elite;
376   while( i-- )
377   {
378     var genome_temp = deep_copy( this.population[ ( this.population_size - 1 ) - i ] );
379     genome_temp.fitness = 0;
380     genome_temp.parent_fitness = 0;
381     genome_temp.created_by = 4;
382     new_population.push( genome_temp );
383     if ( new_population.length == this.population_size ) return;
384   }
385 }
386 this.crossover_operator = function ( parent_one_index, parent_two_index )
{
387   // One point crossover operator.
388   // Do we crossover?
389   if ( get_random_float( 0.0, 1.0 ) <= this.crossover_probability )
390   {
391     // If the parents are the same genome then this is not a true crossover.
392     if ( parent_one_index === parent_two_index ) return 0;
393     // Only returns one crossed offspring.
394     var offspring = new Genome();
395     // Determine a crossover point.
396     // Let the uniform sample be in the range of [1,n-1].
397     // If the crossover point was zero than no true crossover takes place
398     // as all of one parent's genes get copied into the offspring.
399     // If the cp = n-1 then at least you get n-1 from one parent and 1
400     // from another parent.
401     var crossover_point = get_random_integer( 1, ( this.number_of_genes_per_genome - 1 ) );
402     // Cross the parent's genes in the offspring.
403     offspring.genes = [ ];
404     offspring.fitness = 0;
405     offspring.parent_fitness = 0;
406     for ( var i = 0; i < crossover_point; ++i )
407     {
408       offspring.genes.push( deep_copy( this.population[ parent_one_index ].genes[ i ] ) );
409     }
410     for ( var i = crossover_point; i < this.number_of_genes_per_genome; ++i )
411     {
412       offspring.genes.push( deep_copy( this.population[ parent_two_index ].genes[ i ] ) );
413     }
414   }
415   // Determine if a crossover actually took place.

```

```

446     // The offspring should not match the parent one's genes and
448     // it should not match parent two's genes as the offspring
449     // should be a combination of the two.
450
450     if ( ( offspring.genes.toString( ) != this.population[ parent_one_index ].genes.toString( ) ) &&
451         ( offspring.genes.toString( ) != this.population[ parent_two_index ].genes.toString( ) ) )
452     {
453
454         // Weighted average fitness of the parents based on crossover point
455         // determining percentage of genes received from parent one and parent two.
456         // Let the number of genes per genome be 41 and let the crossover point be 1.
457         // Offspring gets [0,1) = 1 gene from parent one and [1,41) = 40 genes from parent two.
458         // PF = PF1 * (1/41) + PF2 * ((41-1)/41).
459
460         var parent_one_contribution = ( this.population[ parent_one_index ].fitness * ( (
461             crossover_point ) / ( this.number_of_genes_per_genome ) ) );
462         var parent_two_contribution = ( this.population[ parent_two_index ].fitness * ( ( this.
463             number_of_genes_per_genome - crossover_point ) / ( this.number_of_genes_per_genome ) ) );
464
465         offspring.parent_fitness = parent_one_contribution + parent_two_contribution;
466
467         offspring.created_by = 1;
468
469         return offspring;
470     }
471     else
472     {
473
474         return 0;
475     }
476 }
477 else
478 {
479
480     return 0;
481 }
482
483 }
484
485 }
486
487
488 this.mutation_operator = function ( parent_index )
489 {
490
491     // Mutates parent genome's genes on a whole genome basis based on the mutation probability.
492
493     // Gaussian distribution mutation.
494
495     // Do we mutate?
496
497     if ( get_random_float( 0.0, 1.0 ) <= this.mutation_probability )
498     {
499
500         // Reference: http://www.nashcoding.com/2010/07/07/evolutionary-algorithms-the-little-things-you-d-never-guess-part-1/
501
502         function gaussian_distribution( mean, standard_deviation )
503         {
504
505             // Two uniformly distributed random variable samples.
506
507             var x1 = Math.random();
508             var x2 = Math.random();
509
510             // The method requires sampling from a uniform random of (0,1]
511             // but Math.random() returns a sample of [0,1].
512
513             if ( x1 == 0.0 ) x1 = 1.0;
514             if ( x2 == 0.0 ) x2 = 1.0;
515
516             // Box-Muller transformation for Z_0.
517
518             var y1 = Math.sqrt( -2.0 * Math.log( x1 ) ) * Math.cos( 2.0 * Math.PI * x2 );
519
520             return ( y1 * standard_deviation ) + mean;
521         }
522
523
524         // Create an offspring blank.
525
526         var offspring = new Genome();
527
528         offspring.genes = [ ];
529
530         offspring.genes = deep_copy( this.population[ parent_index ].genes );
531
532         offspring.fitness = 0;
533
534         offspring.parent_fitness = 0;
535
536         // Begin to mutate.
537
538         var mutated = false;
539
540         for ( var i = 0; i < this.number_of_genes_per_genome; ++i )
541         {
542
543             // Mutate this gene by sampling a value from a normal distribution
544             // where the mean is the current gene value and the standard deviation

```

```

546     // the mutation step = mutation probability in the range [0,1].
547     // A low mutation probability will give a mutated gene value close to the original gene
548     // value (the mean) (most of the time) as the standard deviation is small and therefore the
549     // mutation step is small.
550     // A high mutation probability will give (or it can easily) a mutated gene value farther from the
551     // original gene
552     // value (the mean) as the standard deviation is large and therefore the mutation step is large.
553
554     // Note that gv = gv + *N(0,1) is the same as gv = N(gv, 1).
555
556     // Clamp the gene to range [-1,1].
557
558     var temp_gene_value = deep_copy( offspring.genes[ i ] );
559
560     offspring.genes[ i ] = gaussian_distribution( offspring.genes[ i ], this.mutation_probability );
561     offspring.genes[ i ] = get_clamped_value( offspring.genes[ i ], -1.0, 1.0 );
562
563     // Test if it was truly mutated.
564
565     if ( temp_gene_value != offspring.genes[ i ] )
566     {
567         mutated = true;
568     }
569
570     if ( mutated ) // If truly mutated.
571     {
572
573         offspring.parent_fitness = deep_copy( this.population[ parent_index ].fitness );
574
575         offspring.created_by = 2;
576
577         return offspring;
578     }
579     else
580     {
581
582         return 0;
583     }
584
585     else
586     {
587
588         return 0;
589     }
590
591     else
592     {
593
594         return 0;
595     }
596 }
597
598 this.crossover_then_mutate_operator = function ( parent_one_index, parent_two_index )
599 {
600
601     // Crossover and mutation done sequentially as in more traditional genetic algorithms.
602
603     // First attempts crossover and then attempts mutation.
604
605     var offspring_one = deep_copy( this.population[ parent_one_index ] );
606     var offspring_two = deep_copy( this.population[ parent_one_index ] );
607
608     offspring_one.fitness = 0.0;
609     offspring_two.fitness = 0.0;
610
611     offspring_one.parent_fitness = null;
612     offspring_two.parent_fitness = null;
613
614     offspring_one.created_by = 0;
615     offspring_two.created_by = 0;
616
617     // Attempt crossover.
618
619     var crossover_point = get_random_integer( 0, ( this.number_of_genes_per_genome - 1 ) );
620
621     if ( ( get_random_float( 0.0, 1.0 ) <= this.crossover_probability ) && ( parent_one_index != parent_two_index ) && ( crossover_point != 0 ) )
622     {
623
624         // Cross the parent's genes in the offspring.
625
626         offspring_one.genes = [ ];
627         offspring_two.genes = [ ];
628
629         for ( var i = 0; i < crossover_point; ++i )
630         {
631
632             offspring_one.genes.push( deep_copy( this.population[ parent_one_index ].genes[ i ] ) );
633             offspring_two.genes.push( deep_copy( this.population[ parent_two_index ].genes[ i ] ) );
634
635         }
636
637         for ( var i = crossover_point; i < this.number_of_genes_per_genome; ++i )
638         {
639
640             offspring_one.genes.push( deep_copy( this.population[ parent_two_index ].genes[ i ] ) );
641             offspring_two.genes.push( deep_copy( this.population[ parent_one_index ].genes[ i ] ) );
642
643         }
644
645     }
646
647 }
648

```

```

644     var parent_one_contribution = ( this.population[ parent_one_index ].fitness * ( (
645         crossover_point ) / ( this.number_of_genes_per_genome ) ) );
646     var parent_two_contribution = ( this.population[ parent_two_index ].fitness * ( ( this.
647         number_of_genes_per_genome - crossover_point ) / ( this.number_of_genes_per_genome ) ) );
648
649     offspring_one.parent_fitness = parent_one_contribution + parent_two_contribution;
650     offspring_one.created_by = offspring_one.created_by + 1;
651
652     parent_two_contribution = ( this.population[ parent_two_index ].fitness * ( (
653         crossover_point ) / ( this.number_of_genes_per_genome ) ) );
654     parent_one_contribution = ( this.population[ parent_one_index ].fitness * ( ( this.
655         number_of_genes_per_genome - crossover_point ) / ( this.number_of_genes_per_genome ) ) );
656
657     offspring_two.parent_fitness = parent_two_contribution + parent_one_contribution;
658     offspring_two.created_by = offspring_two.created_by + 1;
659
660     // Crossover may or may not have happened but now try to mutation.
661
662     // Normal distribution sample function.
663
664     function gaussian_distribution( mean, standard_deviation )
665     {
666
667         // Two uniformly distributed random variable samples.
668
669         var x1 = Math.random();
670         var x2 = Math.random();
671
672         // The method requires sampling from a uniform random of (0,1]
673         // but Math.random() returns a sample of [0,1).
674
675         if ( x1 == 0.0 ) x1 = 1.0;
676         if ( x2 == 0.0 ) x2 = 1.0;
677
678         // Box-Muller transformation for Z_0.
679
680         var y1 = Math.sqrt( -2.0 * Math.log( x1 ) ) * Math.cos( 2.0 * Math.PI * x2 );
681
682         return ( y1 * standard_deviation ) + mean;
683     }
684
685     // Attempt to mutate offspring one.
686
687     var mutated_one = false;
688
689     for ( var i = 0; i < this.number_of_genes_per_genome; ++i )
690     {
691
692         // Mutate this gene by sampling a value from a normal distribution
693         // where the mean is the current gene value and the standard deviation
694         // is the mutation step = mutation probability in the range [0,1].
695         // A low mutation probability will give a mutated gene value close to the original gene
696         // value (the mean) (most of the time) as the standard deviation is small and therefore the mutation
697         // step is small.
698         // A high mutation probability will give (or it can easily) a mutated gene value farther from the
699         // original gene
700         // value (the mean) as the standard deviation is large and therefore the mutation step is large.
701
702         // Note that gv = gv +    * N( 0, 1 ) is the same as gv = N( gv,    ).
703
704         // Clamp the gene to range [-1,1].
705
706         if ( get_random_float( 0.0, 1.0 ) <= this.mutation_probability ) // Mutate this gene?
707         {
708
709             var temp_gene_value_one = deep_copy( offspring_one.genes[ i ] );
710
711             offspring_one.genes[ i ] = gaussian_distribution( offspring_one.genes[ i ], this.
712                 mutation_probability );
713             // offspring_one.genes[ i ] = gaussian_distribution( offspring_one.genes[ i ], 0.5 );
714             // offspring_one.genes[ i ] = offspring_one.genes[ i ] + ( get_random_float( -1.0, 1.0 ) * .3 );
715             offspring_one.genes[ i ] = get_clamped_value( offspring_one.genes[ i ], -1.0, 1.0 );
716
717             // Test if it was truly mutated.
718
719             if ( temp_gene_value_one != offspring_one.genes[ i ] )
720             {
721
722                 mutated_one = true;
723             }
724         }
725
726         // Attempt to mutate offspring two.
727
728         var mutated_two = false;
729
730         for ( var i = 0; i < this.number_of_genes_per_genome; ++i )
731
732             // Mutate this gene by sampling a value from a normal distribution
733             // where the mean is the current gene value and the standard deviation
734             // is the mutation step = mutation probability in the range [0,1].
735             // A low mutation probability will give a mutated gene value close to the original gene

```

```

738     // value (the mean) (most of the time) as the standard deviation is small and therefore the mutation
739     // step is small.
740     // A high mutation probability will give (or it can easily) a mutated gene value farther from the
741     // original gene
742     // value (the mean) as the standard deviation is large and therefore the mutation step is large.
743
744     // Note that gv = gv +   * N( 0, 1 ) is the same as gv = N( gv,   ).  

745
746     if ( get_random_float( 0.0, 1.0 ) <= this.mutation_probability ) // Mutate this gene?
747     {
748
749         var temp_gene_value_two = deep_copy( offspring_two.genes[ i ] );
750
751         offspring_two.genes[ i ] = gaussian_distribution( offspring_two.genes[ i ], this.
752             mutation_probability );
753         // offspring_two.genes[ i ] = gaussian_distribution( offspring_two.genes[ i ], 0.5 );
754         // offspring_two.genes[ i ] = offspring_two.genes[ i ] + ( get_random_float( -1.0, 1.0 ) * .3 );
755         offspring_two.genes[ i ] = get_clamped_value( offspring_two.genes[ i ], -1.0, 1.0 );
756
757         // Test if it was truly mutated.
758
759         if ( temp_gene_value_two != offspring_two.genes[ i ] )
760         {
761             mutated_two = true;
762         }
763     }
764
765     if ( mutated_one ) // If truly mutated.
766     {
767
768         // Mutation = 2, crossover = 1, crossover + mutation = 3.
769
770         offspring_one.created_by = offspring_one.created_by + 2;
771
772         // If this offspring was only mutated, that is, it was not crossed then get its parent fitness.
773         // It it was crossed before being mutated then offspring_one.created would equal 3.
774
775         if ( offspring_one.created_by === 2 )
776         {
777
778             offspring_one.parent_fitness = deep_copy( this.population[ parent_one_index ].fitness );
779         }
780
781     }
782
783     if ( mutated_two ) // If truly mutated.
784     {
785
786         offspring_two.created_by = offspring_two.created_by + 2;
787
788         // If this offspring was only mutated, that is, it was not crossed then get its parent fitness.
789         // It it was crossed before being mutated then offspring_two.created would equal 3.
790
791         if ( offspring_two.created_by === 2 )
792         {
793
794             offspring_two.parent_fitness = deep_copy( this.population[ parent_two_index ].fitness );
795         }
796
797     }
798
799     // No parents->offspring not crossed and/or not mutated enter into the new population.
800     // Each offspring going into the new population must either crossed, mutated, or both.
801
802     if ( ( offspring_one.created_by === 0 ) || ( offspring_two.created_by === 0 ) )
803     {
804
805         return 0;
806     }
807
808     else if ( ( offspring_one.genes.toString( ) === this.population[ parent_one_index ].genes.toString( )
809             ) || ( offspring_two.genes.toString( ) === this.population[ parent_two_index ].genes.toString( ) ) )
810     {
811
812         return 0;
813     }
814
815     else
816     {
817
818         return { one: offspring_one, two: offspring_two };
819     }
820
821
822     this.evaluate_population = function ( )
823     {
824
825         this.reset_population_evaluation( );
826
827
828         var highest_so_far = this.population[ 0 ].fitness;
829         var lowest_so_far = this.population[ 0 ].fitness;

```

```

836     this.fittest_genome_index = 0;
838     this.weakest_genome_index = 0;
840     this.total_fitness = this.population[ 0 ].fitness;
841     this.best_fitness = this.population[ 0 ].fitness;
842     this.worst_fitness = this.population[ 0 ].fitness;
844     for ( var i = 1; i < this.population_size; ++i )
845     {
846         // Update fittest if necessary.
847         if ( highest_so_far < this.population[ i ].fitness )
848         {
849             highest_so_far = this.population[ i ].fitness;
850             this.fittest_genome_index = i;
851             this.best_fitness = highest_so_far;
852         }
853         // Update worst if necessary.
854         if ( lowest_so_far > this.population[ i ].fitness )
855         {
856             lowest_so_far = this.population[ i ].fitness;
857             this.weakest_genome_index = i;
858             this.worst_fitness = lowest_so_far;
859         }
860         this.total_fitness += this.population[ i ].fitness;
861     }
862     this.average_fitness = this.total_fitness / this.population_size;
863 }
864 this.reset_population_evaluation = function ( )
865 {
866     this.total_fitness = 0;
867     this.best_fitness = 0;
868     this.worst_fitness = 0;
869     this.average_fitness = 0;
870     this.fittest_genome_index = -1;
871     this.weakest_genome_index = -1;
872 }
873 this.compute_population_makeup = function ( )
874 {
875     var randoms = 0;
876     var crossovers = 0;
877     var mutants = 0;
878     var crossover_mutants = 0;
879     var elites = 0;
880     for ( var i = 0; i < this.population_size; ++i )
881     {
882         if ( this.population[ i ].created_by === 0 )
883         {
884             randoms = randoms + 1;
885         }
886         else if ( this.population[ i ].created_by === 1 )
887         {
888             crossovers = crossovers + 1;
889         }
890         else if ( this.population[ i ].created_by === 2 )
891         {
892             mutants = mutants + 1;
893         }
894         else if ( this.population[ i ].created_by === 3 )
895         {
896             crossover_mutants = crossover_mutants + 1;
897         }
898         else if ( this.population[ i ].created_by === 4 )
899         {
900             elites = elites + 1;
901         }
902     }

```

```

938     this.population_makeup = randoms + " " + crossovers + " " + mutants + " " + crossover_mutants + " " +
939     elites;
940 }
942 this.adjust_crossover_and_mutation_probabilities = function ( )
944 {
946     // Calculate the crossover and mutation operators' progress where
947     // their progress is based on how well they produced offspring that
948     // had a better fitness than their parent.
949
950     var crossover_operator_progress_sum = 0;
951     var number_of_crossovers = 0;
952
953     var mutation_operator_progress_sum = 0;
954     var number_of_mutations = 0;
955
956     // Sum all of the progresses.
957
958     for ( var i = 0; i < this.population_size; ++i )
959     {
960
961         if ( this.population[ i ].created_by === 1 ) // Created by crossover.
962         {
963
964             crossover_operator_progress_sum += ( this.population[ i ].fitness - this.population[ i ].parent_fitness );
965
966             number_of_crossovers += 1;
967
968         }
969         else if ( this.population[ i ].created_by === 2 ) // Created by mutation.
970         {
971
972             mutation_operator_progress_sum += ( this.population[ i ].fitness - this.population[ i ].parent_fitness );
973
974             number_of_mutations += 1;
975
976         }
977     }
978
979     // Now calculate the average crossover and mutation progress for the population.
980
981     this.crossover_operator_progress_average = 0.0;
982     this.mutation_operator_progress_average = 0.0;
983
984     if ( number_of_crossovers != 0 )
985     {
986
987         this.crossover_operator_progress_average = ( crossover_operator_progress_sum ) / (
988             number_of_crossovers );
989
990     }
991
992     if ( number_of_mutations != 0 )
993     {
994
995         this.mutation_operator_progress_average = ( mutation_operator_progress_sum ) / (
996             number_of_mutations );
997
998     }
999
1000    // Adjust crossover and mutation rate adjustments.
1001
1002    if ( this.best_fitness > this.worst_fitness )
1003    {
1004
1005        this.crossover_probability_adjustment = 0.01 * ( ( this.best_fitness - this.average_fitness ) / (
1006            this.best_fitness - this.worst_fitness ) );
1007
1008        this.mutation_probability_adjustment = 0.01 * ( ( this.best_fitness - this.average_fitness ) / (
1009            this.best_fitness - this.worst_fitness ) );
1010
1011    }
1012
1013    else if ( this.best_fitness == this.average_fitness )
1014    {
1015
1016        this.crossover_probability_adjustment = 0.01;
1017
1018        this.mutation_probability_adjustment = 0.01;
1019
1020    }
1021
1022    // Adjust crossover and mutation rates.
1023
1024    if ( this.crossover_operator_progress_average > this.mutation_operator_progress_average )
1025    {
1026
1027        this.crossover_probability = this.crossover_probability + this.crossover_probability_adjustment;
1028
1029        this.mutation_probability = this.mutation_probability - this.mutation_probability_adjustment;
1030
1031    }
1032    else if ( this.crossover_operator_progress_average < this.mutation_operator_progress_average )
1033    {
1034
1035        this.crossover_probability = this.crossover_probability - this.crossover_probability_adjustment;
1036
1037    }
1038
1039}

```

```

1034     this.mutation_probability = this.mutation_probability + this.mutation_probability_adjustment;
1035 }
1036 else if ( this.crossover_operator_progress_average == this.mutation_operator_progress_average )
1037 {
1038     // Do not adjust.
1039 }
1040
1041     this.crossover_probability = get_clamped_value( this.crossover_probability, this.
1042         crossover_probability_minimum, 1.0 );
1043
1044     this.mutation_probability = get_clamped_value( this.mutation_probability, this.
1045         mutation_probability_minimum, 1.0 );
1046
1047 }
1048
1049 this.sort_population = function ( descending )
1050 {
1051     if ( descending == undefined || descending == false )
1052     {
1053         this.population.sort( function ( a, b ) { return a.fitness - b.fitness; } );
1054     }
1055     else
1056     {
1057         this.population.sort( function ( a, b ) { return b.fitness - a.fitness; } );
1058     }
1059 }
1060
1061
1062 this.generate_new_generation = function ( )
1063 {
1064
1065     // Assumes population is sorted in ascending order.
1066
1067     // Assumes population is completely evaluated.
1068
1069     // Assumes crossover probability and mutation probability have been adjusted if using self-adaptation.
1070
1071     // Create a temporary population to store newly created generation.
1072
1073     var new_population = new Array( );
1074
1075     // Allow the top N elite to pass into the next generation.
1076
1077     this.elitism_operator( new_population );
1078
1079     // Perform crossover and mutation separately?
1080
1081     if ( !this.perform_crossover_and_mutation_sequentially )
1082     {
1083
1084         // Now we enter the GA loop.
1085
1086         // Repeat until a new population is generated.
1087
1088         while ( new_population.length < this.population_size )
1089         {
1090
1091             // Perform crossover and mutation separately.
1092
1093             // Try to generate an offspring via crossover first.
1094
1095             this.total_number_of_crossover_attempts += 1;
1096
1097             // Select two genome indexes.
1098
1099             var parents = this.selection_operator( 2 );
1100
1101             var crossover_offspring = this.crossover_operator( parents[ 0 ], parents[ 1 ] );
1102
1103             if ( crossover_offspring != 0 )
1104             {
1105
1106                 new_population.push( crossover_offspring );
1107
1108                 this.total_number_of_crossovers += 1;
1109             }
1110
1111             // There is the possibility of adding up to two
1112             // offspring per while loop.
1113             // Don't create more than the population size.
1114
1115             if ( new_population.length === this.population_size ) break;
1116
1117             // Try to generate an offspring via mutation second.
1118
1119             this.total_number_of_mutation_attempts += 1;
1120
1121             // Select one genome index.
1122
1123             var parent = this.selection_operator( 1 );
1124
1125             var mutation_offspring = this.mutation_operator( parent[ 0 ] );
1126
1127
1128
1129
1130
1131
1132

```

```

1134     if ( mutation_offspring != 0 )
1135     {
1136         new_population.push( mutation_offspring );
1137         this.total_number_of_mutations += 1;
1138     }
1139 }
1140 }
1141 }
1142 }
1143 if ( new_population.length > this.population_size )
1144 {
1145     console.warn( "[Genetic_Algorithm:generate_new_generation] New population larger than population size." );
1146 }
1147 }
1148 // Finished so assign new pop to the current population.
1149 this.population = [ ];
1150 this.population = deep_copy( new_population );
1151 new_population = [ ];
1152 }
1153 else // Perform crossover and mutation in sequence.
1154 {
1155     // Now we enter the GA loop.
1156     // Repeat until a new population is generated.
1157     while ( new_population.length < this.population_size )
1158     {
1159         // Attempt crossover and then mutation in sequence.
1160         var parents = this.selection_operator( 2 );
1161         var offspring = this.crossover_then_mutation_operator( parents[ 0 ], parents[ 1 ] );
1162         if ( offspring != 0 )
1163         {
1164             // First offspring.
1165             if ( offspring.one.created_by === 1 )
1166             {
1167                 this.total_number_of_crossovers += 1;
1168                 this.total_number_of_crossover_attempts += 1;
1169                 this.total_number_of_mutation_attempts += 1;
1170                 new_population.push( offspring.one );
1171             }
1172             else if ( offspring.one.created_by === 2 )
1173             {
1174                 this.total_number_of_mutations += 1;
1175                 this.total_number_of_crossover_attempts += 1;
1176                 this.total_number_of_mutation_attempts += 1;
1177                 new_population.push( offspring.one );
1178             }
1179             else if ( offspring.one.created_by === 3 )
1180             {
1181                 this.total_number_of_crossovers += 1;
1182                 this.total_number_of_mutations += 1;
1183                 this.total_number_of_crossover_attempts += 1;
1184                 this.total_number_of_mutation_attempts += 1;
1185                 new_population.push( offspring.one );
1186             }
1187         }
1188         // Old population size should match this new population size.
1189         if ( new_population.length === this.population_size ) break;
1190         // Second offspring.
1191         if ( offspring.two.created_by === 1 )
1192         {
1193             this.total_number_of_crossovers += 1;
1194             this.total_number_of_crossover_attempts += 1;
1195             this.total_number_of_mutation_attempts += 1;
1196             new_population.push( offspring.two );
1197         }
1198         else if ( offspring.two.created_by === 2 )
1199         {
1200             this.total_number_of_mutations += 1;
1201             this.total_number_of_crossover_attempts += 1;
1202             this.total_number_of_mutation_attempts += 1;
1203             new_population.push( offspring.two );
1204         }
1205     }
1206 }
1207 }
1208 }
1209 }
1210 }
1211 }
1212 }
1213 }
1214 }
1215 }
1216 }
1217 }
1218 }
1219 }
1220 }
1221 }
1222 }
1223 }
1224 }
1225 }
1226 }
1227 }
1228 }
1229 }
1230 }
1231 }
1232 }

```

```

1234         new_population.push( offspring.two );
1235     }
1236     else if ( offspring.two.created_by === 3 )
1237     {
1238
1239         this.total_number_of_crossovers += 1;
1240         this.total_number_of_mutations += 1;
1241         this.total_number_of_crossover_attempts += 1;
1242         this.total_number_of_mutation_attempts += 1;
1243
1244         new_population.push( offspring.two );
1245     }
1246 }
1247 }
1248 }
1249 }
1250 }
1251
1252 if ( new_population.length > this.population_size )
1253 {
1254
1255     console.warn( "[Genetic_Algorithm:generate_new_generation] New population larger than population size." );
1256
1257 }
1258
1259 // Finished so assign new pop to the current population.
1260
1261 this.population = [ ];
1262 this.population = deep_copy( new_population );
1263 new_population = [ ];
1264
1265 }
1266
1267 // Calculate the observed rates.
1268
1269 this.observed_crossover_rate = this.total_number_of_crossovers / this.
1270     total_number_of_crossover_attempts;
1271 this.observed_mutation_rate = this.total_number_of_mutations / this.
1272     total_number_of_mutation_attempts;
1273
1274 // Advance generation counter.
1275
1276 this.generation_number += 1;
1277 }
1278
1279 // Getter methods.
1280
1281 this.get_population = function ( )
1282 {
1283
1284     return deep_copy( this.population );
1285
1286 }
1287
1288 this.get_population_size = function ( )
1289 {
1290
1291     return deep_copy( this.population_size );
1292
1293 }
1294
1295 this.get_number_of_genes_per_genome = function ( )
1296 {
1297
1298     return deep_copy( this.number_of_genes_per_genome );
1299
1300 }
1301
1302 this.get_genome_fitness = function ( index )
1303 {
1304
1305     index = parseInt( index );
1306
1307     if ( ( index > ( this.population_size - 1 ) ) || ( index < 0 ) )
1308     {
1309
1310         console.error( "[Genetic_Algorithm:get_genome_fitness] Index out of bounds of population size." );
1311
1312         return;
1313
1314     }
1315
1316     return deep_copy( this.population[ index ].fitness );
1317
1318 }
1319
1320 this.get_genome_genes = function ( index )
1321 {
1322
1323     index = parseInt( index );
1324
1325     if ( ( index > ( this.population_size - 1 ) ) || ( index < 0 ) )
1326     {
1327
1328         console.error( "[Genetic_Algorithm:get_genome_genes] Index out of bounds of population size." );
1329
1330         return;
1331
1332     }

```

```

1334     return deep_copy( this.population[ index ].genes );
1336   }
1338   this.get_genome_genes_flattened = function ( index )
{
1340   index = parseInt( index );
1342   if ( ( index > ( this.population_size - 1 ) ) || ( index < 0 ) )
{
1346     console.error( "[Genetic_Algorithm:get_genome_genes_flattened] Index out of bounds of population
size." );
1348     return;
1350   }
1352   return deep_copy( this.population[ index ].genes.join( "," ) );
1354 }
1356 this.get_population_genes_flattened = function ( )
{
1358   var population_genes = "";
1360   for ( var i = 0; i < this.population_size - 1; ++i )
{
1364     population_genes += deep_copy( this.population[ i ].genes.join( "," ) + "," );
1366   }
1368   population_genes += deep_copy( this.population[ this.population_size - 1 ].genes.join( "," ) );
1370   return population_genes;
1372 }
1374 this.get_best_fitness = function ( )
{
1376   this.evaluate_population();
1378   return deep_copy( this.best_fitness );
1380 }
1382 this.get_average_fitness = function ( )
1384 {
1386   this.evaluate_population();
1388   return deep_copy( this.average_fitness );
1390 }
1392 this.get_worst_fitness = function ( )
{
1394   this.evaluate_population();
1396   return deep_copy( this.worst_fitness );
1398 }
1400 this.get_fittest_genome_index = function ( )
1402 {
1404   this.evaluate_population();
1406   return deep_copy( this.fittest_genome_index );
1408 }
1410 this.get_weakest_genome_index = function ( )
{
1412   this.evaluate_population();
1414   return deep_copy( this.weakest_genome_index );
1416 }
1418 this.get_crossover_probability = function ( )
1420 {
1422   return deep_copy( this.crossover_probability );
1424 }
1426 this.get_mutation_probability = function ( )
{
1428   return deep_copy( this.mutation_probability );
1430 }
1432 this.get_generation_number = function ( )

```

```

1434  {
1436      return deep_copy( this.generation_number );
1438  }
1440 // Setter methods.
1442 this.set_crossover_probability = function ( rate )
{
1444     this.crossover_probability = parseFloat( rate );
1446 }
1448 this.set_mutation_probability = function ( rate )
{
1450     this.mutation_probability = parseFloat( rate );
1452 }
1454 }
1456 this.set_generation_number = function ( number )
{
1458     number = parseInt( number );
1460     this.generation_number = number;
1462 }
1464 this.set_genome_fitness = function ( index, fitness )
{
1466     index = parseInt( index );
1468     fitness = parseFloat( fitness );
1470     if ( ( index > ( this.population_size - 1 ) ) || ( index < 0 ) )
1472     {
1474         console.error( "[Genetic_Algorithm:set_genome_fitness] Index out of bounds of population size." );
1476         return;
1478     }
1480     this.population[ index ].fitness = fitness;
1482 }

```

LISTING B.3: Neural_Network.js

```

1 /*
2 *
3 * David Lettier (C) 2013.
4 *
5 * http://www.lettier.com/
6 *
7 * Code ported to JS and HEAVILY modified from original C++ source
8 * found at http://www.ai-junkie.com/ann/evolved/nnt1.html and
9 * written by Mat Buckland.
10 *
11 * Implements a neural network for learning.
12 *
13 */
15
16 function Neuron( nInputs )
17 {
18     // Plus one for the bias/threshold.
19     // x_1*w_1+x_2*w_2+...+x_n*w_n >= t
20     // x_1*w_1+x_2*w_2+...+x_n*w_n+(-1)*t >= 0
21     // Where t=w_(n+1).
22
23     this.number_of_inputs = nInputs + 1;
24
25     if ( this.number_of_inputs < 0 ) this.number_of_inputs = 1;
26
27     this.weights = new Array( );
28
29     for ( var i = 0; i < this.number_of_inputs; ++i )
30     {
31
32         this.weights.push( get_random_float( -1.0, 1.0 ) );
33
34     }
35
36 }
37
38 function Neuron_Layer( nNumberNeurons, nNumberInputsPerNeuron )
39 {
40
41     this.number_of_neurons = nNumberNeurons;
42
43     this.neurons = new Array( );
44
45     for ( var i = 0; i < nNumberNeurons; ++i )
46     {
47

```

```

49     this.neurons.push( new Neuron( nNumberInputsPerNeuron ) );
51   }
53 }
55 function Neural_Net( params )
{
57   this.number_of_inputs = params.nInputs;
59   this.number_of_outputs = params.nOutputs;
61   this.number_of_hidden_layers = params.nHiddenLayers;
63   this.neurons_per_hidden_layer = params.nNeuronsPerHiddenLayer;
65   this.bias = params.bias;
67   this.layers = new Array( );
69   this.create_network = function ( )
71   {
73     // Create the layers of the network.
74     if ( this.number_of_hidden_layers > 0 )
75     {
77       // Create first hidden layer.
78       this.layers.push( new Neuron_Layer( this.neurons_per_hidden_layer, this.number_of_inputs ) );
79       // Create the subsequent hidden layers.
80       for ( var i = 0; i < this.number_of_hidden_layers - 1; ++i )
81       {
83         this.layers.push( new Neuron_Layer( this.neurons_per_hidden_layer, this.neurons_per_hidden_layer ) );
84       };
85     }
87     // Create output layer.
88     this.layers.push( new Neuron_Layer( this.number_of_outputs, this.neurons_per_hidden_layer ) );
89   }
91   else
93   {
95     // Create output layer.
96     this.layers.push( new Neuron_Layer( this.number_of_outputs, this.number_of_inputs ) );
97   }
99 }
101 this.create_network( );
103 this.get_weights = function ( )
105 {
107   var weights = new Array( );
109   // For each layer.
111   for ( var i = 0; i < this.number_of_hidden_layers + 1; ++i ) // Plus one for the output layer.
113   {
114     // For each neuron.
115     for ( var j = 0; j < this.layers[ i ].number_of_neurons; ++j )
117     {
118       // For each weight.
119       for ( var k = 0; k < this.layers[ i ].neurons[ j ].number_of_inputs; ++k )
121       {
122         weights.push( this.layers[ i ].neurons[ j ].weights[ k ] );
123       };
124     };
125   }
127 }
129 }
131 return weights;
133 }
135 this.get_number_of_weights = function ( )
137 {
139   var weights = 0;
141   // For each layer.
143   for ( var i = 0; i < this.number_of_hidden_layers + 1; ++i ) // Plus one for the output layer.
145   {
146     // For each neuron.
147     for ( var j = 0; j < this.layers[ i ].number_of_neurons; ++j )

```

```

149      {
151          // For each weight.
153          for ( var k = 0; k < this.layers[ i ].neurons[ j ].number_of_inputs; ++k )
155          {
156              weights += 1;
157          }
158      }
159  }
160 }
161
163     return weights;
164 }
165
166 this.put_weights = function ( weights )
167 {
168
169     var weight = 0;
170
171     // For each layer.
172     for ( var i = 0; i < this.number_of_hidden_layers + 1; ++i ) // Plus one for the output layer.
173     {
174
175         // For each neuron.
176         for ( var j = 0; j < this.layers[ i ].number_of_neurons; ++j )
177         {
178
179             // For each weight.
180             for ( var k = 0; k < this.layers[ i ].neurons[ j ].number_of_inputs; ++k )
181             {
182
183                 this.layers[ i ].neurons[ j ].weights[ k ] = weights[ weight++ ];
184
185             }
186
187         }
188     }
189 }
190
191 }
192
193     return null;
194 }
195
196 this.update = function ( inputs )
197 {
198
199     // Stores the resultant outputs from each layer.
200
201     var outputs = new Array( );
202
203     var weight = 0;
204
205     // First check that we have the correct amount of inputs.
206
207     if ( inputs.length != this.number_of_inputs )
208     {
209
210         console.error( "[Neural_Net:update] Passed inputs length does not equal neural network number of inputs setting." );
211
212         // Just return an empty vector if incorrect.
213         return outputs;
214     }
215
216     // For each layer.
217     for ( var i = 0; i < this.number_of_hidden_layers + 1; ++i )
218     {
219
220         if ( i > 0 )
221         {
222
223             inputs = deep_copy( outputs ); // Deep copy outputs.
224
225         }
226
227         outputs.length = 0;
228
229         weight = 0;
230
231         // For each neuron sum the ( inputs * corresponding weights ).
232         // Throw the total at our sigmoid function to get the output.
233
234         for ( var j = 0; j < this.layers[ i ].number_of_neurons; ++j )
235         {
236             var net_input = 0.0;
237
238             var number_of_inputs = this.layers[ i ].neurons[ j ].number_of_inputs;
239
240             // For each weight.
241
242             for ( var k = 0; k < number_of_inputs - 1; ++k )
243             {
244
245                 // Sum the weights x inputs.
246
247                 net_input += this.layers[ i ].neurons[ j ].weights[ k ] * inputs[ weight++ ];
248
249             }

```

```

251     // Add in the bias/threshold.
252     //  $x_1*w_1+x_2*w_2+\dots+x_n*w_n \geq t$ 
253     //  $x_1*w_1+x_2*w_2+\dots+x_n*w_n+(-1)*t \geq 0$ 
254     // Where  $t=w_{(n+1)}$ .
255
256     net_input += this.bias * this.layers[ i ].neurons[ j ].weights[ number_of_inputs - 1 ];
257
258     // We can store the outputs from each layer as we generate them.
259     // The combined activation is first filtered through the Sigmoid function.
260
261     outputs.push( this.sigmoid( net_input ) );
262
263     weight = 0;
264 }
265 }
266
267 return outputs;
268
269 }
270
271 this.sigmoid = function ( input )
272 {
273
274     // Use the hyperbolic tangent function to get a range of outputs [-1,1].
275
276     var math_exp = Math.exp;
277
278     var numerator = math_exp( 2 * input ) - 1;
279     var denominator = math_exp( 2 * input ) + 1;
280
281     return numerator / denominator;
282
283     /*
284     Old way.
285
286     // Returns [-1, 1].
287
288     var numerator = 1.0;
289     var denominator = 1.0 + Math.pow( Math.E, ( -input / response ) );
290
291     return ( ( numerator / denominator ) - 0.5 ) * 2.0;
292
293     */
294 }
295
296 }
297
298 }

```

B.2 BBAutoTune

LISTING B.4: GA.py

```

1  #! /usr/bin/env python
3  """
5  David Lettier (C) 2014.
7  http://www.lettier.com/
9  The main GA python file.
11 """
13 import sys;
14 import atexit;
15 import random;
16 import math;
17 import copy;
18 import signal;
19 import time;
20 import itertools;
21 import subprocess;
22 import mysql.connector
23 import os;
24 import bpy;
25 import pickle;
26 import scipy;
27 import numpy;
28 import sklearn.covariance;
29 from bpy.props import *
30
31 """
32 Helper functions.
33 """
34
35 def get_clamped_value( value, minimum, maximum ):
36     return max( min( maximum, value ), minimum );
37
38 def get_scripts_location( ):
39     current_working_directory = os.getcwd();

```

```

45     current_working_directory = current_working_directory.rsplit( "/", 1 )
47     while ( current_working_directory[ 1 ] != "bbautotune" ):
49         current_working_directory = current_working_directory[ 0 ].rsplit( "/", 1 );
51     return current_working_directory[ 0 ] + "/bbautotune/source/scripts/";
53     '',
55 Creates the Blender properties for the BBAutoTune UI panel.
57     '',
59 def initialize_bbautotune_parameter_properties( ):
61     bpy.types.Scene.GA_POPULATION_SIZE = IntProperty(
63         name = "Population Size",
64         description = "Population size.",
65         min = 0
66     );
67     bpy.context.scene[ "GA_POPULATION_SIZE" ] = 10;
69     bpy.types.Scene.GA_MAX_GENERATIONS = IntProperty(
71         name = "Max Generations",
72         description = "Max generations.",
73         min = 0
74     );
75     bpy.context.scene[ "GA_MAX_GENERATIONS" ] = 100;
79     bpy.types.Scene.GA_NUMBER_OF_ELITE = IntProperty(
81         name = "Number of Elite",
82         description = "Number of elite.",
83         min = 0
84     );
85     bpy.context.scene[ "GA_NUMBER_OF_ELITE" ] = 2;
87     bpy.types.Scene.GA_CROSSOVER_PROBABILITY = FloatProperty(
89         name
90             = "Crossover Probability",
91             description = "Crossover probability.",
92             default
93                 = 0.8,
94             min
95                 = 0.0,
96             max
97                 = 1.0
98     );
99     bpy.types.Scene.GA_MUTATION_PROBABILITY = FloatProperty(
100         name
101             = "Mutation Probability",
102             description = "Mutation probability.",
103             default
104                 = 0.2,
105             min
106                 = 0.0,
107             max
108                 = 1.0
109     );
110     bpy.types.Scene.GA_MAX_TORQUE = FloatProperty(
111         name
112             = "Max Torque",
113             description = "Maximum torque value possible during search.",
114             default
115                 = 50.0,
116             min
117                 = 0.0,
118             max
119                 = 340282346638528859811704183484516925440.0
120     );
121     bpy.types.Scene.GA_USE_RANK_FITNESS_SELECTION = BoolProperty(
122         name
123             = "Use Rank Fitness Selection",
124             description = "Use rank fitness selection otherwise tournament selection will be used."
125     );
126     bpy.context.scene[ "GA_USE_RANK_FITNESS_SELECTION" ] = False;
127     bpy.types.Scene.GA_PERFORM_CROSSOVER_AND_MUTATION_SEQUENTIALLY = BoolProperty(
128         name
129             = "Perform Crossover and Mutation Sequentially",
130             description = "Perform crossover and mutation sequentially."
131     );
132     bpy.context.scene[ "GA_PERFORM_CROSSOVER_AND_MUTATION_SEQUENTIALLY" ] = False;
133     bpy.types.Scene.GA_USE_SELF_ADAPTATION = BoolProperty(
134         name
135             = "Use Self-adaptation",
136             description = "Adapt the crossover and mutation probabilities."
137     );
138     bpy.context.scene[ "GA_USE_SELF_ADAPTATION" ] = False;
139     bpy.types.Scene.BBAUTOTUNE_OPEN_GA_MONITOR_BROWSER_WINDOW = BoolProperty(
140         name
141             = "Open GA Monitor Browser Window",
142             description = "Open a browser window to the GA monitor."
143

```

```

147     );
149     bpy.context.scene[ "BBAUTOTUNE_OPEN_GA_MONITOR_BROWSER_WINDOW" ] = False;
150
151     bpy.types.Scene.BBAUTOTUNE_DEBUG = BoolProperty(
152         name      = "Debug",
153         description = "Log debug information."
154     );
155     bpy.context.scene[ "BBAUTOTUNE_DEBUG" ] = False;
156
157     initialize_bbautotune_parameter_properties( );
158
159     /**
160      * The start button operator on the BBAutoTune UI panel.
161      * Starts BBAutoTune with the values from the UI panel properties.
162     */
163
164     bpy.context.scene[ "BBAUTOTUNE_UI_START_BUTTON_OPERATOR" ] = bbautotune_start;
165
166     class BBAUTOTUNE_UI_START_BUTTON_OPERATOR( bpy.types.Operator ):
167
168         bl_idname = "bbautotune.start";
169         bl_label   = "Start"
170
171         def execute( self, context ):
172
173             bbautotune.start(
174                 bpy.context.scene.GA_POPULATION_SIZE,
175                 bpy.context.scene.GA_MAX_GENERATIONS,
176                 bpy.context.scene.GA_NUMBER_OF_ELITE,
177                 bpy.context.scene.GA_CROSSOVER_PROBABILITY,
178                 bpy.context.scene.GA_MUTATION_PROBABILITY,
179                 bpy.context.scene.GA_MAX_TORQUE,
180                 bpy.context.scene.GA_USE_RANK_FITNESS_SELECTION,
181                 bpy.context.scene.GA_PERFORM_CROSSOVER_AND_MUTATION_SEQUENTIALLY,
182                 bpy.context.scene.GA_USE_SELF_ADAPTATION,
183                 bpy.context.scene.BBAUTOTUNE_OPEN_GA_MONITOR_BROWSER_WINDOW,
184                 bpy.context.scene.BBAUTOTUNE_DEBUG
185             );
186
187             # Clean up on premature exit.
188             atexit.register( bbautotune.stop );
189
190             return { 'FINISHED' };
191
192         /**
193          * The BBAutoTune UI panel and its layout in Blender.
194        */
195
196         bpy.context.scene.BBAUTOTUNE_DEBUG = False;
197
198         bpy.context.scene.BBAUTOTUNE_OPEN_GA_MONITOR_BROWSER_WINDOW = False;
199
200         bpy.context.scene.BBAUTOTUNE_DEBUG = True;
201
202         class GA_UI_PANEL( bpy.types.Panel ):
203
204             bl_label      = "BBAutoTune Parameters";
205             bl_space_type = "PROPERTIES";
206             bl_region_type = "WINDOW";
207             bl_context    = "render";
208
209             def draw( self, context ):
210
211                 self.layout.prop( context.scene, "GA_POPULATION_SIZE" );
212                 self.layout.prop( context.scene, "GA_MAX_GENERATIONS" );
213                 self.layout.prop( context.scene, "GA_NUMBER_OF_ELITE" );
214                 self.layout.prop( context.scene, "GA_CROSSOVER_PROBABILITY" );
215                 self.layout.prop( context.scene, "GA_MUTATION_PROBABILITY" );
216                 self.layout.prop( context.scene, "GA_MAX_TORQUE" );
217                 self.layout.prop( context.scene, "GA_USE_RANK_FITNESS_SELECTION" );
218                 self.layout.prop( context.scene, "GA_PERFORM_CROSSOVER_AND_MUTATION_SEQUENTIALLY" );
219                 self.layout.prop( context.scene, "GA_USE_SELF_ADAPTATION" );
220                 self.layout.prop( context.scene, "BBAUTOTUNE_OPEN_GA_MONITOR_BROWSER_WINDOW" );
221                 self.layout.prop( context.scene, "BBAUTOTUNE_DEBUG" );
222
223                 self.layout.operator( "bbautotune.start" );
224
225         /**
226          * A single genome.
227        */
228
229         bpy.context.scene.BBAUTOTUNE_DEBUG = True;
230
231         class Genome( ):
232
233             new_id = itertools.count().__next__;
234
235             def __init__( self, genes = None, fitness = None ):
236
237                 self.id = Genome.new_id();
238
239                 if ( not genes == None ):
240
241                     self.genes = list( genes );
242
243                 else:
244
245                     self.genes = [ ];
246
247                 self.fitness = fitness or 0.0;

```

```

249     # Used to calculate either the crossover progress or mutation progress.
250     # If this genome is created via crossover, use the weighted average
251     # based on the cross over point.
252     # So if the crossover point is say 9 and the genome length is 10,
253     # then the weighted average pf = (p1.f*.9) + (p2.f*.1).
254     # In other words the offspring received 90% of its genes from parent one
255     # and it received 10% of its genes from parent two so its parent fitness is
256     # 90% of parent one's fitness and 10% of parent two's fitness.
257
258     self.parent_fitness = 0.0;
259
260     # Created by means if this genome was generated either by randomness, crossover,
261     # mutation, both crossover and mutation, or elitism.
262     # Initially it is created from nothing so set it to -1.
263     # 0 = randomness, 1 = crossover, 2 = mutation, 3 = crossover & mutation, 4 = elitism
264
265     # This encoding is to facilitate crossover's and mutation's progress at producing fitter
266     # offspring than the offspring's parents.
267
268     self.created_by = 0;
269
270     def set_genes( self, genes = None ):
271
272         if ( not genes == None ):
273
274             self.genes = list( genes );
275
276         else:
277
278             self.genes = [ ];
279
280     def get_genes( self ):
281
282         return list( self.genes );
283
284     def get_genes_as_string( self ):
285
286         return ":".join( map( str, self.genes ) );
287
288     def set_fitness( self, fitness = None ):
289
290         self.fitness = fitness or 0.0;
291
292     def get_fitness( self ):
293
294         return self.fitness;
295
296     def set_parent_fitness( self, parent_fitness = None ):
297
298         self.parent_fitness = parent_fitness or 0.0;
299
300     def get_parent_fitness( self ):
301
302         return self.parent_fitness;
303
304     def set_created_by( self, created_by = None ):
305
306         self.created_by = created_by or 0;
307
308     def get_created_by( self ):
309
310         return self.created_by;
311
312     def __repr__( self ):
313
314         return repr( ( self.id, self.created_by, self.fitness, self.parent_fitness, self.genes ) );
315
316     """
317     The main genetic algorithm object.
318     """
319
320     class Genetic_Algorithm():
321
322         def __init__(self,
323
324             self,
325             population_size = None,
326             max_generations = None,
327             number_of_elite = None,
328             crossover_probability = None,
329             mutation_probability = None,
330             use_rank_fitness_selection = None,
331             perform_crossover_and_mutation_sequentially = None,
332             use_self_adaptation = None
333
334         ):
335
336         """
337         """
338
339         Begin parameters.
340         """
341
342
343         # Size of population.
344
345         self.population_size = population_size or 0;
346
347         # Number of generations to run until termination of the algorithm.
348
349

```

```

351     self.max_generations = max_generations or 0;
353     # Set the number of elite that go on to the next generation.
355     self.number_of_elite = number_of_elite or 0;
357     # Probability of genome's crossing over bits.
358     # 0.7 is pretty good.
359     self.crossover_probability      = crossover_probability or 0.0;
360     self.crossover_probability_minimum = 0.001;
361     self.crossover_probability_adjustment = 0.01;
362     self.crossover_operator_progress_average = 0.0;
363     self.observed_crossover_rate = 0.0;
364     self.total_number_of_crossovers = 0;
365     self.total_number_of_crossover_attempts = 0;
366
367     # Probability that a genomes bits will mutate.
368     # Try figures around 0.05 to 0.3-ish.
369
370     self.mutation_probability      = mutation_probability or 0.0;
371     self.mutation_probability_minimum = 0.001;
372     self.mutation_probability_adjustment = 0.01;
373     self.mutation_operator_progress_average = 0.0;
374     self.observed_mutation_rate = 0.0;
375     self.total_number_of_mutations = 0;
376     self.total_number_of_mutation_attempts = 0;
377
378     # Use rank fitness selection?
379     self.use_rank_fitness_selection = use_rank_fitness_selection or False;
380
381     # Perform crossover and mutation sequentially or separately?
382     self.perform_crossover_and_mutation_sequentially = perform_crossover_and_mutation_sequentially or
383     False;
384
385     # Use self-adaptation?
386     self.use_self_adaptation = use_self_adaptation or False;
387
388     ...
389
390     End parameters.
391
392     ...
393
394     # Log file if debugging.
395     self.log_file_name = "";
396
397     # The amount of genes per genome.
398     self.number_of_genes_per_genome = 18;
399
400     # This holds the entire population of genomes.
401     self.population = [ ];
402
403     # Total fitness of population.
404     self.total_fitness = 0.0;
405
406     # Average fitness.
407     self.average_fitness = 0.0;
408
409     # Highest fitness.
410     self.highest_fitness = 0.0;
411
412     # Lowest fitness.
413     self.lowest_fitness = 0.0;
414
415     # Keeps track of the best genome.
416     self.fittest_genome_index = -1;
417
418     # Keep track of the worst genome.
419     self.weakest_genome_index = -1;
420
421     # Generation number.
422     self.generation_number = 0;
423
424     # Current population makeup of randoms, crossovers, mutants, crossover mutants, and elites.
425     self.population_makeup = "";
426
427     def set_population_size( self, size = None ):
428         self.population_size = size or 0;
429
430     def get_population_size( self ):
431         return self.population_size;
432
433     def set_max_generations( self, maximum = None ):
434         self.max_generations = maximum or 0;

```

```

451     def get_max_generations( self ):
453         return self.max_generations;
455     def set_crossover_probability( self, probability = None ):
457         self.crossover_probability = probability or 0;
459     def get_crossover_probability( self ):
461         return self.crossover_probability;
463     def set_mutation_probability( self, probability = None ):
465         self.mutation_probability = probability or 0;
467     def get_mutation_probability( self ):
469         return self.mutation_probability;
471     def set_number_of_genes_per_genome( self, number_of = None ):
473         self.number_of_genes_per_genome = number_of or 0;
475     def get_number_of_genes_per_genome( self ):
477         return self.number_of_genes_per_genome;
479     def set_use_rank_fitness_selection( self, boolean = None ):
481         self.use_rank_fitness_selection = boolean or 0;
483     def get_use_rank_fitness_selection( self ):
485         return self.use_rank_fitness_selection;
487     def set_perform_crossover_and_mutation_sequentially( self, boolean = None ):
489         self.perform_crossover_and_mutation_sequentially = boolean or 0;
491     def get_perform_crossover_and_mutation_sequentially( self ):
493         return self.perform_crossover_and_mutation_sequentially;
495     def set_use_self_adaptation( self, use_self_adaptation = None ):
497         self.use_self_adaptation = use_self_adaptation or False;
499     def get_use_self_adaptation( self ):
501         return self.use_self_adaptation;
503     def set_number_of_elite( self, number_of = None ):
505         self.number_of_elite = number_of or 0;
507         if ( self.number_of_elite > self.population_size ):
509             self.number_of_elite = self.population_size;
511     def get_number_of_elite( self ):
513         return self.number_of_elite;
515     def set_log_file_name( self, log_file_name ):
517         self.log_file_name = log_file_name;
519     def get_log_file_name( self ):
521         return self.log_file_name;
523     def log( self, log_string ):
525         if ( self.log_file_name != "" ):
527             log_file = open( self.log_file_name, "a+" );
529             log_file.write( log_string + "\n" );
531             log_file.close( );
533     def set_total_fitness( self, total_fitness = None ):
535         self.total_fitness = total_fitness or 0;
537     def get_total_fitness( self ):
539         return self.total_fitness;
541     def set_average_fitness( self, average_fitness = None ):
543         self.average_fitness = average_fitness or 0;
545     def get_average_fitness( self ):
547         return self.average_fitness;
549     def set_highest_fitness( self, highest_fitness = None ):
551         self.highest_fitness = highest_fitness or 0;

```

```

553     def get_highest_fitness( self ):
555         return self.highest_fitness;
557     def set_lowest_fitness( self, lowest_fitness = None ):
559         self.lowest_fitness = lowest_fitness or 0;
561     def get_lowest_fitness( self ):
563         return self.lowest_fitness;
565     def set_fittest_genome_index( self, fittest_genome_index = None ):
567         self.fittest_genome_index = fittest_genome_index or -1;
569     def get_fittest_genome_index( self ):
571         return self.fittest_genome_index;
573     def set_weakest_genome_index( self, weakest_genome_index = None ):
575         self.weakest_genome_index = weakest_genome_index or -1;
577     def get_weakest_genome_index( self ):
579         return self.weakest_genome_index;
581     def set_generation_number( self, generation_number = None ):
583         self.generation_number = generation_number or 0;
585     def get_generation_number( self ):
587         return self.generation_number;
589     def get_population_makeup( self ):
591         self.compute_population_makeup( );
593         return self.population_makeup;
595     def get_genome( self, index ):
597         assert index < self.population_size and index >= 0, "Genome index out of bounds.";
599         return copy.deepcopy( self.population[ index ] );
601     def get_genome_fitness( self, index ):
603         assert index < self.population_size and index >= 0, "Genome index out of bounds.";
605         return self.population[ index ].fitness;
607     def set_genome_fitness( self, index, fitness ):
609         assert index < self.population_size and index >= 0, "Genome index out of bounds.";
611         self.population[ index ].set_fitness( fitness );
613     def get_genome_genes_as_string( self, index ):
615         assert index < self.population_size and index >= 0, "Genome index out of bounds.";
617         return self.population[ index ].get_genes_as_string();
619     def get_population_genes_as_string( self ):
621         if ( self.population_size == 0 ):
623             return "";
625         else:
627             gene_string = self.population[ 0 ].get_genes_as_string();
629             for i in range( self.population_size ):
631                 gene_string += "," + self.population[ i ].get_genes_as_string();
633             return gene_string;
635     def create_randomized_population( self ):
637         self.log( "Generating random population." );
639         self.population = [ ];
641         # Initialize population with genomes consisting of random
643         # genes and all fitness's set to zero.
645         for i in range( self.population_size ):
647             self.population.append( Genome( ) );
649             self.log( "Genome: " + str( i ) );
651             for j in range( self.number_of_genes_per_genome ):
653                 random_gene = random.uniform( 0.0, 1.0 );

```

```

655         self.log( "Random gene: " + str( j ) );
657         self.log( str( random_gene ) );
659         self.population[ i ].genes.append( random_gene );
661         self.set_generation_number( 0 );
663         self.update_population_metrics( );
665     def replace_population_genes( self, replacement_population_genes ):
667         # Assumes replacement_population_genes is one big array.
668         # Splices the big array based on the number of genes per genome.
669         # Big array: [ 1,2,3,4,5,6,7,8,9,10 ]
670         # Number of genes per genome: 2
671         # Population: [ [ 1, 2 ] G0
672         #                 [ 3, 4 ] G1
673         #                 [ 5, 6 ] ...
674         #                 [ 7, 8 ] ...
675         #                 [ 9, 10 ] GN-1
676         #                         ]
677
678         assert len( replacement_population_genes ) != 0, "Replacement gene size is zero.";
679         assert len( replacement_population_genes ) == self.population_size * self.number_of_genes_per_genome,
680             "Too few or too many replacement genes."
681
682         k = 0;
683
684         for i in range( self.population_size ):
685             self.population[ i ].genes = [ ];
686
687             for j in range( self.number_of_genes_per_genome ):
688
689                 self.population[ i ].genes.append( replacement_population_genes[ k ] );
690
691                 k += 1;
692
693     def selection_operator( self, number_of_indexes ):
694
695         self.log( "Entering selection operator." );
696
697         self.log( str( number_of_indexes ) + " genomes requested." );
698
699         # Assumes the population has been evaluated.
700
701         # Assumes the population is sorted in descending order according to fitness.
702
703         if ( not self.use_rank_fitness_selection ):
704
705             tournament_size = number_of_indexes + 1;
706
707             assert tournament_size <= self.population_size and tournament_size >= 0, "Tournament size too large/small.";
708
709             genome_indexes_selected = [ ];
710
711             self.log( "Selecting random players." );
712
713             for i in range( number_of_indexes ):
714
715                 tournament_players = [ ];
716
717                 for j in range( tournament_size ):
718
719                     random_int = random.randint( 0, self.population_size - 1 );
720
721                     tournament_players.append( [ random_int, self.population[ random_int ].get_fitness( ) ] );
722
723                     self.log( "Random players selected." );
724
725                     self.log( str( tournament_players ) );
726
727                     # Remember, lower fitness values are a higher fitness.
728                     # Sorts list in ascending orderer.
729                     # tournament_players = [ [genome_index,genome_fitness], ... ]
730                     # [ 0 ][ 0 ] = get the index with the lowest fitness value (thus the highest fitness ).
731
732                     player_ranking = sorted( tournament_players, key = lambda x: x[ 1 ] );
733
734                     self.log( "Player ranking." );
735
736                     self.log( str( player_ranking ) );
737
738                     winner = player_ranking[ 0 ][ 0 ];
739
740                     self.log( "Winner." );
741
742                     self.log( str( winner ) );
743
744                     genome_indexes_selected.append( winner );
745
746                     self.log( "Selected genomes with tournament selection." );
747
748                     self.log( str( genome_indexes_selected ) );
749
750                     return genome_indexes_selected;
751
752             genome_indexes_selected;
753
754         else:

```

```

755     self.log( "Sorted?" );
757     self.log( str( self.population[ 0 ].get_fitness() ) + " " + str( self.population[ -1 ].get_fitness(
759     ) ) );
761     # Assume the genomes are sorted in non-increasing order of fitness.
763     # Give the worst genome a rank fitness of 1.
764     # Give the second worst genome a rank fitness of 2.
765     # ...
766     # Give the best genome a rank fitness of the population size.
767     genome_indexes_selected = [ ];
768
769     # Genomes:          1, 2, 3, 4
770     # Genomes fitnesses: 4, 2, 3, 1 (Lowest is highest. )
771     # Rank fitnesses:   1, 2, 3, 4 (Highest is highest.)
772     # Partial sums:    1, 3, 6, 10
773     # Random number U(0,10): 7
774     # Genome 4 is selected.
775     # Since all random numbers are uniform,
776     # Genome 1 has a probability of being selected: (1-0)*(1/10) = 10%
777     # Genome 2 has a probability of being selected: (3-1)*(1/10) = 20%
778     # Genome 3 has a probability of being selected: (6-3)*(1/10) = 30%
779     # Genome 4 has a probability of being selected: (10-6)*(1/10) = 40%
780     # Total of any being selected:                = 100%
781
782     #
783     # 0.10 -----
784     # | | | | |
785     # | | | |
786     # 0---1---2---3---4---5---6---7---8---9---10
787     #      G1      G2      G3      G4
788
789     # Individual rank fitnesses.
790
791     rank_fitnesses = [ ];
792
793     for i in range( self.population_size ):
794         rank_fitnesses.append( i + 1 );
795
796     total_rank_fitness = sum( rank_fitnesses );
797
798     self.log( "Total rank fitness." );
799     self.log( str( total_rank_fitness ) );
800
801     # Partial sum. P[i] = sum( P[1:i] ) where i is in range [1,n].
802
803     partial_sums = list( itertools.accumulate( rank_fitnesses ) );
804
805     self.log( "Partial sums." );
806
807     self.log( str( partial_sums ) );
808
809     while ( len( genome_indexes_selected ) < number_of_indexes ):
810
811         random_number = random.randint( 0, total_rank_fitness );
812
813         self.log( "Random number: " + str( random_number ) );
814
815         for i in range( self.population_size ):
816
817             if ( partial_sums[ i ] >= random_number ):
818
819                 self.log( "Partial sum: " + str( partial_sums[ i ] ) );
820
821                 self.log( "Genome index selected: " + str( i ) );
822
823                 genome_indexes_selected.append( i );
824
825             break;
826
827         if ( len( genome_indexes_selected ) == number_of_indexes ):
828
829             break;
830
831         self.log( "Selected genomes with rank selection." );
832
833         self.log( str( genome_indexes_selected ) );
834
835         return genome_indexes_selected;
836
837     def elitism_operator( self, new_population ):
838
839         self.log( "Attempting to add elite genomes." );
840
841         if ( self.number_of_elite > self.population_size ):
842
843             self.number_of_elite = self.population_size;
844
845             # Assumes the population is sorted in ascending order of fitness.
846
847             # A = [ 0, 1, 2, 3, 4, 5, 6, 7, 8, 9 ]
848             # |A| = 10
849             # i = 2 check.
850             # i = 1 decrement.
851             # A[ ( 10 - 1 = 9 ) - i ] = 8 ]
852             # i = 1 check.
853             # i = 0 decrement.
854
855

```

```

857     # A[ ( ( 10 - 1 = 9 ) - i ) = 9 ]
858     # i = 0 check.
859     # Stop.
860
861     i = self.number_of_elite;
862
863     while ( i ):
864
865         i -= 1;
866
867         genome_temp = copy.deepcopy( self.population[ ( self.population_size - 1 ) - i ] );
868
869         self.log( "Adding elite genome. Its fitness: " + str( genome_temp.get_fitness() ) );
870
871         genome_temp.fitness      = 0.0;
872         genome_temp.parent_fitness = 0.0;
873         genome_temp.created_by    = 4;
874
875         new_population.append( genome_temp );
876
877         if ( len( new_population ) == self.population_size ):
878
879             break;
880
881     def crossover_operator( self, parent_one_index, parent_two_index ):
882
883         # One point crossover operator.
884
885         # Only returns one crossed offspring.
886
887         # Do we crossover?
888
889         self.log( "Attempting crossover." );
890
891         if ( random.uniform( 0.0, 1.0 ) <= self.crossover_probability ):
892
893             # If the parents are the same genome then this is not a true crossover.
894
895             if ( parent_one_index == parent_two_index ):
896
897                 self.log( "Parents are the same. Crossover failed." );
898
899                 return 0;
900
901             self.log( "Parent indexes." );
902
903             self.log( str( parent_one_index ) + " " + str( parent_two_index ) );
904
905             # Create a blank offspring.
906
907             offspring = Genome( );
908
909             offspring.genes      = [ ];
910             offspring.fitness    = 0.0;
911             offspring.parent_fitness = 0.0;
912             offspring.created_by = 0;
913
914             # Determine a crossover point.
915
916             # Let the uniform sample be in the range of [1,n-1].
917             # If the crossover point was zero than no true crossover takes place.
918             # as all of one parent's genes get copied into the offspring.
919             # If the cp = n-1 then at least you get n-1 from one parent and 1
920             # from another parent.
921
922             crossover_point = random.randint( 1, ( self.number_of_genes_per_genome - 1 ) );
923
924             self.log( "Crossover point." );
925
926             self.log( str( crossover_point ) );
927
928             # Cross the parent's genes into the offspring's genes.
929
930             for i in range( crossover_point ):
931
932                 offspring.genes.append( copy.deepcopy( self.population[ parent_one_index ].genes[ i ] ) );
933
934             for i in range( crossover_point, self.number_of_genes_per_genome ):
935
936                 offspring.genes.append( copy.deepcopy( self.population[ parent_two_index ].genes[ i ] ) );
937
938             # Determine if a crossover actually took place.
939             # The offspring should not match the parent one's genes and
940             # it should not match parent two's genes as the offspring
941             # should be a combination of the two.
942
943             if ( ( offspring.genes != self.population[ parent_one_index ].genes ) and
944                 ( offspring.genes != self.population[ parent_two_index ].genes ) ):
945
946                 # Weighted average fitness of the parents based on crossover point
947                 # determining percentage of genes received from parent one and parent two.
948                 # Let the number of genes per genome be 41 and let the crossover point be 1.
949                 # Offspring gets [0,1] = 1 gene from parent one and [1,41] = 40 genes from parent two.
950                 # PF = PF1 * (1/41) + PF2 * ((41-1)/41).
951
952                 parent_one_contribution = ( self.population[ parent_one_index ].fitness * ( (
953                     crossover_point ) / ( self.number_of_genes_per_genome ) ) );
954                 parent_two_contribution = ( self.population[ parent_two_index ].fitness * ( ( self.
955                     number_of_genes_per_genome - crossover_point ) / ( self.number_of_genes_per_genome ) ) );
956
957                 offspring.parent_fitness = parent_one_contribution + parent_two_contribution;

```

```

957         self.log( "Parent fitnesses." );
959         self.log( str( self.population[ parent_one_index ].fitness ) );
961         self.log( str( self.population[ parent_two_index ].fitness ) );
963         self.log( "Parent fitness contributions." );
965         self.log( str( parent_one_contribution ) );
967         self.log( str( parent_two_contribution ) );
969         offspring.created_by = 1;
971         self.log( "Returning crossed offspring." );
972         return offspring;
973     else:
974
975         self.log( "Did not actually perform crossover. Offspring genes match parents." );
976         return 0;
977     else:
978
979         self.log( "Greater than crossover probability." );
980         return 0;
981     else:
982
983         self.log( "Attempting mutation." );
984         return 0;
985     def mutation_operator( self, parent_index ):
986
987         # Mutates parent genome's genes on a whole genome basis based on the mutation probability.
988
989         # Gaussian distribution mutation.
990
991         # Do we mutate?
992
993         self.log( "Attempting mutation." );
994
995         if ( random.uniform( 0.0, 1.0 ) <= self.mutation_probability ):
996
997             # Create a blank offspring and fill its genes with the parent's genes.
998
1000            offspring = Genome();
1001            offspring.genes = [ ];
1002            offspring.genes = copy.deepcopy( self.population[ parent_index ].genes );
1003            offspring.fitness = 0.0;
1004            offspring.parent_fitness = 0.0;
1005            offspring.created_by = 0;
1006
1007            # Begin to mutate.
1008
1009            mutated = False;
1010
1011            for i in range( self.number_of_genes_per_genome ):
1012
1013                # Mutate this gene by sampling a value from a normal distribution
1014                # where the mean is the current gene value and the standard deviation
1015                # is the mutation step equal to the mutation probability in the range [0,1].
1016                # A low mutation probability will give a mutated gene value closer to the original gene
1017                # value (the mean) (most of the time) as the standard deviation is small and therefore the
1018                # mutation step is small.
1019                # A high mutation probability will give a mutated gene value farther from the original gene
1020                # value (the mean) as the standard deviation is large and therefore the mutation step is large.
1021
1022                # Note that gv = gv + *N(0,1) is the same as gv = N(gv, ).
1023
1024                # Clamp the gene to range [-1,1].
1025
1026                temp_gene_value = copy.deepcopy( offspring.genes[ i ] );
1027
1028                offspring.genes[ i ] = random.gauss( offspring.genes[ i ], self.mutation_probability );
1029                offspring.genes[ i ] = get_clamped_value( offspring.genes[ i ], 0.0, 1.0 );
1030
1031                self.log( "Mutation value before/after." );
1032
1033                self.log( str( temp_gene_value ) + " " + str( offspring.genes[ i ] ) );
1034
1035                # Test if it was truly mutated.
1036
1037                if ( temp_gene_value != offspring.genes[ i ] ):
1038
1039                    mutated = True;
1040
1041                if ( mutated ): # If truly mutated.
1042
1043                    offspring.parent_fitness = self.population[ parent_index ].fitness;
1044
1045                    offspring.created_by = 2;
1046
1047                    self.log( "Returning mutated offspring." );
1048
1049                    return offspring;
1050
1051                else:
1052
1053                    self.log( "Mutation did not actually take place." );
1054
1055                    return 0;
1056
1057            else:

```

```

1057     self.log( "Greater than mutation probability." );
1059     return 0;
1061
1062 def crossover_then_mutate_operator( self, parent_one_index, parent_two_index ):
1063     # Crossover and mutation done sequentially as in more traditional genetic algorithms.
1064
1065     # First attempts crossover and then attempts mutation.
1066
1067     self.log( "Attempting crossover and then mutation." );
1068
1069     offspring_one = copy.deepcopy( self.population[ parent_one_index ] );
1070     offspring_two = copy.deepcopy( self.population[ parent_one_index ] );
1071
1072     offspring_one.fitness = 0.0;
1073     offspring_two.fitness = 0.0;
1074
1075     offspring_one.parent_fitness = 0.0;
1076     offspring_two.parent_fitness = 0.0;
1077
1078     offspring_one.created_by = 0;
1079     offspring_two.created_by = 0;
1080
1081     self.log( "Attempting crossover first." );
1082
1083     # Attempt crossover.
1084
1085     crossover_point = random.randint( 0, ( self.number_of_genes_per_genome - 1 ) );
1086
1087     self.log( "Crossover point." );
1088
1089     self.log( str( crossover_point ) );
1090
1091     if ( ( random.uniform( 0.0, 1.0 ) <= self.crossover_probability ) and ( parent_one_index != parent_two_index ) and ( crossover_point != 0 ) ):
1092
1093         # Cross the parent's genes in the offspring.
1094
1095         offspring_one.genes = [ ];
1096         offspring_two.genes = [ ];
1097
1098         for i in range( crossover_point ):
1099
1100             offspring_one.genes.append( copy.deepcopy( self.population[ parent_one_index ].genes[ i ] ) );
1101             offspring_two.genes.append( copy.deepcopy( self.population[ parent_two_index ].genes[ i ] ) );
1102
1103         for i in range( crossover_point, self.number_of_genes_per_genome ):
1104
1105             offspring_one.genes.append( copy.deepcopy( self.population[ parent_two_index ].genes[ i ] ) );
1106             offspring_two.genes.append( copy.deepcopy( self.population[ parent_one_index ].genes[ i ] ) );
1107
1108             parent_one_contribution = ( self.population[ parent_one_index ].fitness * ( (
1109                 crossover_point ) / ( self.number_of_genes_per_genome ) ) );
1110             parent_two_contribution = ( self.population[ parent_two_index ].fitness * ( ( self.
1111                 number_of_genes_per_genome - crossover_point ) / ( self.number_of_genes_per_genome ) ) );
1112
1113             offspring_one.parent_fitness = parent_one_contribution + parent_two_contribution;
1114             offspring_one.created_by = offspring_one.created_by + 1;
1115
1116             parent_two_contribution = ( self.population[ parent_two_index ].fitness * ( (
1117                 crossover_point ) / ( self.number_of_genes_per_genome ) ) );
1118             parent_one_contribution = ( self.population[ parent_one_index ].fitness * ( ( self.
1119                 number_of_genes_per_genome - crossover_point ) / ( self.number_of_genes_per_genome ) ) );
1120
1121             offspring_two.parent_fitness = parent_two_contribution + parent_one_contribution;
1122             offspring_two.created_by = offspring_two.created_by + 1;
1123
1124             self.log( "Crossover complete." );
1125
1126             self.log( str( offspring_one.created_by ) + " " + str( offspring_two.created_by ) );
1127
1128     else:
1129
1130         self.log( "Crossover failed." );
1131
1132     # Crossover may or may not have happened but now try mutation.
1133
1134     self.log( "Attempting mutation second." );
1135
1136     # Attempt to mutate offspring one.
1137
1138     self.log( "Attempting to mutate the first offspring." );
1139
1140     mutated_one = False;
1141
1142     for i in range( self.number_of_genes_per_genome ):
1143
1144         self.log( "Attempting to mutate gene: " + str( i ) );
1145
1146         # Mutate this gene by sampling a value from a normal distribution where the mean
1147         # is the current gene value and the standard deviation is mutation step equal to the
1148         # mutation probability in the range [0,1]. A low mutation probability will give a mutated gene
1149         # value close to the original gene value (the mean) (most of the time) as the standard
1150         # deviation is small and therefore the mutation step is small. A high mutation probability
1151         # will give, or it can more easily, mutate a gene value farther from the original gene value
1152         # (the mean) as the standard deviation is large and therefore the mutation step is large.
1153
1154         # Note that gv = gv +   * N( 0, 1 ) is the same as gv = N( gv,   );
1155
1156         # Clamp the gene to range [0,1].

```

```

1155     if ( random.uniform( 0.0, 1.0 ) <= self.mutation_probability ): # Mutate this gene?
1156         temp_gene_value_one = copy.deepcopy( offspring_one.genes[ i ] );
1157
1158         offspring_one.genes[ i ] = random.gauss( offspring_one.genes[ i ], self.mutation_probability );
1159         # offspring_one.genes[ i ] = gaussian_distribution( offspring_one.genes[ i ], 0.5 );
1160         # offspring_one.genes[ i ] = offspring_one.genes[ i ] + ( get_random_float( -1.0, 1.0 ) * .3 );
1161
1162         offspring_one.genes[ i ] = get_clamped_value( offspring_one.genes[ i ], 0.0, 1.0 );
1163
1164         self.log( "Mutation value before/after." );
1165
1166         self.log( str( temp_gene_value_one ) + " " + str( offspring_one.genes[ i ] ) );
1167
1168         # Test if it was truly mutated.
1169
1170         if ( temp_gene_value_one != offspring_one.genes[ i ] ):
1171             mutated_one = True;
1172
1173         else:
1174             self.log( "Greater than mutation probability." );
1175
1176         # Attempt to mutate offspring two.
1177
1178         self.log( "Attempting to mutate the second offspring." );
1179
1180         mutated_two = False;
1181
1182         for i in range( self.number_of_genes_per_genome ):
1183             self.log( "Attempting to mutate gene: " + str( i ) );
1184
1185             # Mutate this gene by sampling a value from a normal distribution where the mean
1186             # is the current gene value and the standard deviation is mutation step equal to the
1187             # mutation probability in the range [0,1]. A low mutation probability will give a mutated gene
1188             # value close to the original gene value (the mean) (most of the time) as the standard
1189             # deviation is small and therefore the mutation step is small. A high mutation probability
1190             # will give (or it can more easily) mutate a gene value farther from the original gene value
1191             # (the mean) as the standard deviation is large and therefore the mutation step is large.
1192
1193             # Note that gv = gv +   * N( 0, 1 ) is the same as gv = N( gv,   );
1194
1195             # Clamp the gene to range [0,1].
1196
1197             if ( random.uniform( 0.0, 1.0 ) <= self.mutation_probability ): # Mutate this gene?
1198                 temp_gene_value_two = copy.deepcopy( offspring_two.genes[ i ] );
1199
1200                 offspring_two.genes[ i ] = random.gauss( offspring_two.genes[ i ], self.mutation_probability );
1201                 # offspring_two.genes[ i ] = gaussian_distribution( offspring_two.genes[ i ], 0.5 );
1202                 # offspring_two.genes[ i ] = offspring_two.genes[ i ] + ( get_random_float( -1.0, 1.0 ) * .3 );
1203
1204                 offspring_two.genes[ i ] = get_clamped_value( offspring_two.genes[ i ], 0.0, 1.0 );
1205
1206                 self.log( "Mutation value before/after." );
1207
1208                 self.log( str( temp_gene_value_two ) + " " + str( offspring_one.genes[ i ] ) );
1209
1210                 # Test if it was truly mutated.
1211
1212                 if ( temp_gene_value_two != offspring_two.genes[ i ] ):
1213                     mutated_two = True;
1214
1215                 else:
1216                     self.log( "Greater than mutation probability." );
1217
1218             if ( mutated_one ): # If truly mutated.
1219
1220                 # Mutation = 2, crossover = 1, crossover + mutation = 3.
1221
1222                 offspring_one.created_by = offspring_one.created_by + 2;
1223
1224                 # If this offspring was only mutated, that is, it was not crossed then it gets its parent fitness.
1225                 # If it was crossed before being mutated then offspring_one.created_by would equal 3.
1226
1227                 if ( offspring_one.created_by == 2 ):
1228                     self.log( "Offspring one only mutated." );
1229
1230                     offspring_one.parent_fitness = copy.deepcopy( self.population[ parent_one_index ].fitness );
1231
1232             if ( mutated_two ): # If truly mutated.
1233
1234                 offspring_two.created_by = offspring_two.created_by + 2;
1235
1236                 # If this offspring was only mutated, that is, it was not crossed then it gets its parent fitness.
1237                 # If it was crossed before being mutated then offspring_two.created_by would equal 3.
1238
1239                 if ( offspring_two.created_by == 2 ):
1240                     self.log( "Offspring two only mutated." );
1241
1242                     offspring_two.parent_fitness = copy.deepcopy( self.population[ parent_two_index ].fitness );
1243
1244             # No parents->offspring not crossed and/or not mutated enter into the new population.
1245             # Each offspring going into the new population must either be crossed, mutated, or both.
1246
1247             # No parents->offspring not crossed and/or not mutated enter into the new population.
1248             # Each offspring going into the new population must either be crossed, mutated, or both.
1249
1250             # No parents->offspring not crossed and/or not mutated enter into the new population.
1251             # Each offspring going into the new population must either be crossed, mutated, or both.
1252
1253             # No parents->offspring not crossed and/or not mutated enter into the new population.
1254             # Each offspring going into the new population must either be crossed, mutated, or both.
1255

```

```

1257     if ( ( offspring_one.created_by == 0 ) or ( offspring_two.created_by == 0 ) ):
1258         self.log( "No crossover and/or mutation occurred." );
1259         return 0;
1260     elif ( ( offspring_one.genes == self.population[ parent_one_index ].genes ) or ( offspring_two.genes
1261           == self.population[ parent_two_index ].genes ) ):
1262         self.log( "Offspring genes not different from parents." );
1263         return 0;
1264     else:
1265         self.log( "Returning offspring." );
1266     return { "one": offspring_one, "two": offspring_two };
1267
1268 def reset_population_metrics( self ):
1269
1270     self.total_fitness      = 0.0;
1271     self.highest_fitness    = 0.0;
1272     self.lowest_fitness     = 0.0;
1273     self.average_fitness   = 0.0;
1274     self.fittest_genome_index = -1;
1275     self.weakest_genome_index = -1;
1276
1277 def update_population_metrics( self ):
1278
1279     # 0.0 is the highest fitness
1280     # 1.7976931348623157e+308 is lowest fitness.
1281
1282     self.reset_population_metrics( );
1283
1284     highest_so_far = self.population[ 0 ].fitness;
1285     lowest_so_far = self.population[ 0 ].fitness;
1286
1287     self.fittest_genome_index = 0;
1288     self.weakest_genome_index = 0;
1289
1290     self.total_fitness      = self.population[ 0 ].fitness;
1291     self.highest_fitness    = self.population[ 0 ].fitness;
1292     self.lowest_fitness     = self.population[ 0 ].fitness;
1293
1294     for i in range( self.population_size ):
1295
1296         # Update fittest if necessary.
1297
1298         if ( highest_so_far > self.population[ i ].fitness ):
1299             highest_so_far = self.population[ i ].fitness;
1300             self.fittest_genome_index = i;
1301             self.highest_fitness = highest_so_far;
1302
1303         # Update worst if necessary.
1304
1305         if ( lowest_so_far < self.population[ i ].fitness ):
1306             lowest_so_far = self.population[ i ].fitness;
1307             self.weakest_genome_index = i;
1308             self.lowest_fitness = lowest_so_far;
1309
1310             self.total_fitness += self.population[ i ].fitness;
1311
1312             # Next genome.
1313
1314             self.average_fitness = self.total_fitness / float( self.population_size );
1315
1316             self.log( "Population metrics. T H L A Fi Wi." );
1317
1318             self.log( str( self.total_fitness ) );
1319             self.log( str( self.highest_fitness ) );
1320             self.log( str( self.lowest_fitness ) );
1321             self.log( str( self.average_fitness ) );
1322             self.log( str( self.fittest_genome_index ) );
1323             self.log( str( self.weakest_genome_index ) );
1324
1325     def compute_population_makeup( self ):
1326
1327         randoms      = 0;
1328         crossovers   = 0;
1329         mutants      = 0;
1330         crossover_mutants = 0;
1331         elites       = 0;
1332
1333         for i in range( self.population_size ):
1334
1335             if ( self.population[ i ].created_by == 0 ):
1336                 randoms = randoms + 1;
1337
1338             elif ( self.population[ i ].created_by == 1 ):
1339                 crossovers = crossovers + 1;
1340
1341             elif ( self.population[ i ].created_by == 2 ):
1342
1343

```

```

1357         mutants = mutants + 1;
1359     elif ( self.population[ i ].created_by == 3 ):
1361         crossover_mutants = crossover_mutants + 1;
1363     elif ( self.population[ i ].created_by == 4 ):
1365         elites = elites + 1;
1367     self.population_makeup = str( randoms ) + " " + str( crossovers ) + " " + str( mutants ) + " " + str(
1368         crossover_mutants ) + " " + str( elites );
1369     self.log( "Population makeup. R C M CM E." );
1371     self.log( self.population_makeup );
1373 def adapt_crossover_and_mutation_probabilities( self ):
1375     # Calculate the crossover and mutation operators' progress where
1376     # their progress is based on how well they produced offspring that
1377     # had a better fitness than their parent.
1379     self.log( "Adapting crossover and mutation probabilities." );
1381     crossover_operator_progress_sum = 0.0;
1382     number_of_crossovers = 0;
1383     mutation_operator_progress_sum = 0.0;
1384     number_of_mutations = 0;
1387     # Sum all of the progresses.
1389     # Since the GA is looking to minimize the fitness function, progress is when the offspring has a lower
1390     # fitness score
1391     # than its parent.
1392     for i in range( self.population_size ):
1393         if ( self.population[ i ].created_by == 1 ): # Created by crossover.
1395             crossover_operator_progress_sum += ( self.population[ i ].parent_fitness - self.population[ i ].fitness );
1397             number_of_crossovers += 1;
1399         elif ( self.population[ i ].created_by == 2 ): # Created by mutation.
1400             mutation_operator_progress_sum += ( self.population[ i ].parent_fitness - self.population[ i ].fitness );
1402             number_of_mutations += 1;
1405     # Now calculate the average crossover and mutation progress for the population.
1407     self.crossover_operator_progress_average = 0.0;
1408     self.mutation_operator_progress_average = 0.0;
1411     if ( number_of_crossovers != 0 ):
1413         self.crossover_operator_progress_average = ( crossover_operator_progress_sum ) / float(
1414             number_of_crossovers );
1415     if ( number_of_mutations != 0 ):
1417         self.mutation_operator_progress_average = ( mutation_operator_progress_sum ) / float(
1418             number_of_mutations );
1419     # Adjust crossover and mutation rate adjustments.
1421     self.log( "Adjusting crossover and mutation rate adjustments." );
1423     if ( self.lowest_fitness > self.highest_fitness ):
1425         self.log( "L > H" );
1427         self.crossover_probability_adjustment = 0.01 * ( ( self.lowest_fitness - self.average_fitness ) / (
1428             self.lowest_fitness - self.highest_fitness ) );
1429         self.mutation_probability_adjustment = 0.01 * ( ( self.lowest_fitness - self.average_fitness ) / (
1430             self.lowest_fitness - self.highest_fitness ) );
1431         self.log( str( self.crossover_probability_adjustment ) + " " + str( self.
1432             mutation_probability_adjustment ) );
1433     elif ( self.lowest_fitness == self.average_fitness ):
1435         self.log( "L == A" );
1437         self.crossover_probability_adjustment = 0.01;
1439         self.mutation_probability_adjustment = 0.01;
1441         self.log( "Crossover progress average." );
1443         self.log( str( self.crossover_operator_progress_average ) );
1445         self.log( "Mutation progress average." );
1447         self.log( str( self.mutation_operator_progress_average ) );
1449     # Adjust crossover and mutation rates.

```

```

1451     if ( self.crossover_operator_progress_average > self.mutation_operator_progress_average ):
1453         self.log( "Adjusting crossover/mutation probabilities. CPA > MPA." );
1455         self.crossover_probability = self.crossover_probability + self.crossover_probability_adjustment;
1457         self.mutation_probability = self.mutation_probability - self.mutation_probability_adjustment;
1459     elif ( self.crossover_operator_progress_average < self.mutation_operator_progress_average ):
1461         self.log( "Adjusting crossover/mutation probabilities. CPA < MPA." );
1463         self.crossover_probability = self.crossover_probability - self.crossover_probability_adjustment;
1465         self.mutation_probability = self.mutation_probability + self.mutation_probability_adjustment;
1467     elif ( self.crossover_operator_progress_average == self.mutation_operator_progress_average ):
1469         self.log( "Not adjusting crossover/mutation probabilities. CPA == MPA." );
1471     # Do not adjust.
1473     pass;
1475     self.crossover_probability = get_clamped_value( self.crossover_probability, self.
1476         crossover_probability_minimum, 1.0 - self.mutation_probability_minimum );
1477     self.mutation_probability = get_clamped_value( self.mutation_probability, self.
1478         mutation_probability_minimum, 1.0 - self.crossover_probability_minimum );
1479 def sort_population( self, descending = None ):
1481     self.log( "Sorting population. Descending: " + str( descending ) );
1483     if ( descending == None or descending == False ):
1485         self.population = sorted( self.population, key = lambda genome: genome.fitness, reverse = False );
1487     elif ( descending == True ):
1489         self.population = sorted( self.population, key = lambda genome: genome.fitness, reverse = True );
1491     self.log( "Sorted." );
1493     self.log( str( self.population[ 0 ].fitness ) + " " + str( self.population[ -1 ].fitness ) );
1495 def generate_new_generation( self ):
1497     self.log( "Creating a new generation." );
1499     # Sort the population based on fitness in ascending order.
1500     # 0.0 is the highest fitness and infinity is the lowest fitness.
1501     # So sort in non-increasing order.
1503     self.log( "Sorting population." );
1505     self.sort_population( descending = True );
1507     # Update population metrics.
1509     self.log( "Updating population metrics." );
1511     self.update_population_metrics( );
1513     # Adapt crossover and mutation probabilities if using self-adaptation.
1515     if ( self.use_self_adaptation == True ):
1517         self.log( "Adapting crossover/mutation probabilities." );
1519         self.adapt_crossover_and_mutation_probabilities( );
1521     # Calculate current population makeup.
1523     self.log( "Computing population makeup." );
1525     self.compute_population_makeup( );
1527     # Create a temporary population to store newly created generation.
1529     self.log( "Creating empty new population." );
1531     new_population = [ ];
1533     # Allow the top N elite to pass into the next generation.
1535     self.log( "Performing elitism." );
1537     self.elitism_operator( new_population );
1539     # Perform crossover and mutation separately?
1541     if ( not self.perform_crossover_and_mutation_sequentially ):
1543         self.log( "Performing crossover and mutation separately." );
1545         self.log( "Entering the loop." );
1547     # Now we enter the GA loop.
1549     # Repeat until a new population is generated.

```

```

1551     while ( len( new_population ) < self.population_size ):
1553         # Perform crossover and mutation separately.
1555         # Try to generate an offspring via crossover first.
1557         self.total_number_of_crossover_attempts += 1;
1559         # Select two genome indexes.
1561         parents = self.selection_operator( 2 );
1563         crossover_offspring = self.crossover_operator( parents[ 0 ], parents[ 1 ] );
1565         if ( crossover_offspring != 0 ):
1567             self.log( "Adding crossover offspring." );
1569             new_population.append( crossover_offspring );
1571             self.total_number_of_crossovers += 1;
1573             # There is the possibility of adding up to two
1574             # offspring per while loop.
1575             # Don't create more than the population size.
1577             if ( len( new_population ) == self.population_size ):
1579                 break;
1581             # Try to generate an offspring via mutation second.
1583             self.total_number_of_mutation_attempts += 1;
1585             # Select one genome index.
1587             parent = self.selection_operator( 1 );
1589             mutation_offspring = self.mutation_operator( parent[ 0 ] );
1591             if ( mutation_offspring != 0 ):
1593                 self.log( "Adding mutation offspring." );
1595                 new_population.append( mutation_offspring );
1597                 self.total_number_of_mutations += 1;
1599             assert len( new_population ) == self.population_size, "New population size does not equal population
size setting.";
1601             # Finished so assign new pop to the current population.
1603             self.population = [ ];
1604             self.population = copy.deepcopy( new_population );
1605             new_population = [ ];
1607     else: # Perform crossover and mutation in sequence.
1609         self.log( "Performing crossover and mutation in sequence." );
1611         self.log( "Entering the loop." );
1613         # Now we enter the GA loop.
1615         # Repeat until a new population is generated.
1617         while ( len( new_population ) < self.population_size ):
1619             # Attempt crossover and then mutation in sequence.
1621             parents = self.selection_operator( 2 );
1623             self.log( "Parents selected." );
1625             self.log( str( parents ) );
1627             offspring = self.crossover_then_mutate_operator( parents[ 0 ], parents[ 1 ] );
1629             if ( offspring != 0 ):
1631                 self.log( "Adding first offspring." );
1633                 # First offspring.
1635                 if ( offspring[ "one" ].created_by == 1 ):
1637                     self.log( "Adding crossover offspring." );
1639                     self.total_number_of_crossovers += 1;
1640                     self.total_number_of_crossover_attempts += 1;
1641                     self.total_number_of_mutation_attempts += 1;
1643                     new_population.append( offspring[ "one" ] );
1645                     elif ( offspring[ "one" ].created_by == 2 ):
1647                         self.log( "Adding mutation offspring." );
1649                         self.total_number_of_mutations += 1;
1650                         self.total_number_of_crossover_attempts += 1;

```

```

1651         self.total_number_of_mutation_attempts += 1;
1653     new_population.append( offspring[ "one" ] );
1655     elif ( offspring[ "one" ].created_by == 3 ):
1657         self.log( "Adding crossed over and mutated offspring." );
1659         self.total_number_of_crossovers += 1;
1661         self.total_number_of_mutations += 1;
1662         self.total_number_of_crossover_attempts += 1;
1663         self.total_number_of_mutation_attempts += 1;
1665     new_population.append( offspring[ "one" ] );
1666     # Old population size should match this new population size.
1667     if ( len( new_population ) == self.population_size ):
1669         break;
1671     self.log( "Adding second offspring." );
1673     # Second offspring.
1675     if ( offspring[ "two" ].created_by == 1 ):
1677         self.log( "Adding crossover offspring." );
1679         self.total_number_of_crossovers += 1;
1681         self.total_number_of_crossover_attempts += 1;
1682         self.total_number_of_mutation_attempts += 1;
1683     new_population.append( offspring[ "two" ] );
1685     elif ( offspring[ "two" ].created_by == 2 ):
1687         self.log( "Adding mutation offspring." );
1689         self.total_number_of_mutations += 1;
1691         self.total_number_of_crossover_attempts += 1;
1692         self.total_number_of_mutation_attempts += 1;
1693     new_population.append( offspring[ "two" ] );
1695     elif ( offspring[ "two" ].created_by == 3 ):
1697         self.log( "Adding crossed over and mutated offspring." );
1699         self.total_number_of_crossovers += 1;
1701         self.total_number_of_mutations += 1;
1702         self.total_number_of_crossover_attempts += 1;
1703         self.total_number_of_mutation_attempts += 1;
1705     new_population.append( offspring[ "two" ] );
1707     assert len( new_population ) == self.population_size, "New population size does not equal population size setting.";
1709     # Finished so assign new pop to the current population.
1711     self.population = [ ];
1712     self.population = copy.deepcopy( new_population );
1713     new_population = [ ];
1715     # Calculate the observed rates.
1717     self.observed_crossover_rate = self.total_number_of_crossovers / self.
1718     total_number_of_crossover_attempts;
1719     self.observed_mutation_rate = self.total_number_of_mutations / self.
1720     total_number_of_mutation_attempts;
1721     self.log( "Observed cross/mut rates." );
1722     self.log( str( self.observed_crossover_rate ) + " " + str( self.observed_mutation_rate ) );
1723     # Advance generation counter.
1725     self.generation_number += 1;
1727     '',
1729     The BBAutoTune object.
1731   '',
1733   class BBAutoTune( ):
1735     def __init__( self, ga, dbm ):
1737       # The genetic algorithm and the database manager.
1739       self.ga = ga;
1741       self.dbm = dbm;
1743       # Run ID.
1745       self.run_id = None;
1747       # The current genome being evaluated.
1749       self.current_genome = 0;

```

```

1751     # Log debug statements.
1753     self.debug = False
1755     self.log_file_name = "";
1757     # Open a browser window to the GA monitor.
1759     self.open_ga_monitor_browser_window = False;
1761     # Load in real robot data.
1763     real_forward_x_primes = pickle.load( open( get_scripts_location() + "data/real_robot_motion/forward/
1764         x_p_values.pkl", "rb" ) );
1765     real_forward_y_primes = pickle.load( open( get_scripts_location() + "data/real_robot_motion/forward/
1766         y_p_values.pkl", "rb" ) );
1767     real_forward_t_primes = pickle.load( open( get_scripts_location() + "data/real_robot_motion/forward/
1768         t_p_values.pkl", "rb" ) );
1769     real_forward_motion = [ ];
1770     for i in range( len( real_forward_x_primes ) ):
1771         x = real_forward_x_primes[ i ];
1772         y = real_forward_y_primes[ i ];
1773         t = real_forward_t_primes[ i ];
1774         real_forward_motion.append(
1775             [ x, y, t ]
1776         );
1777     real_forward_motion = numpy.array( real_forward_motion );
1778     # Calculate the robust covariance matrix and the robust mean (location).
1779     self.mcd_fitted = sklearn.covariance.MinCovDet( assume_centered = False, support_fraction = 0.5 * (
1780         len( real_forward_motion ) + 3.0 + 1.0 ) ).fit( real_forward_motion );
1781     self.rcm = self.mcd_fitted.covariance_;
1782     self.rcm_inv = numpy.linalg.inv( self.rcm );
1783     self.rm = self.mcd_fitted.location_;
1784     # The threshold for Chi-square with 3 degrees of freedom (x,y,t) and an alpha value of 0.005.
1785     self.genome_fitness_threshold = math.sqrt( scipy.stats.chi2.isf( 1.0 - 0.995, 3 ) );
1786     self.genome_fitness_threshold = math.sqrt( scipy.stats.chi2.isf( 1.0 - 0.995, 3 ) );
1787     def start(
1788         self,
1789         population_size,
1790         max_generations,
1791         number_of_elite,
1792         crossover_probability,
1793         mutation_probability,
1794         max_torque,
1795         use_rank_fitness_selection,
1796         perform_crossover_and_mutation_sequentially,
1797         use_self_adaptation,
1798         open_ga_monitor_browser_window,
1799         debug
1800     ):
1801         self.run_id = int( round( time.time() * 1000 ) );
1802         self.debug = debug or False;
1803         if ( self.debug == True ):
1804             logs_location = get_scripts_location() + "logs/";
1805             self.log_file_name = logs_location + "log_" + str( self.run_id ) + ".dat";
1806             self.ga.set_log_file_name( self.log_file_name );
1807             bpy.data.objects[ "robot_monitor" ].game.properties[ "log_file_name" ].value = self.log_file_name;
1808             self.log( "Run ID." );
1809             self.log( str( self.run_id ) );
1810             # Pass the file name and directory where the robot
1811             # monitor will record the robot's initial and final state.
1812             self.log( "Setting the robot monitor's shared data file name." );
1813             bpy.data.objects[ "robot_monitor" ].game.properties[ "shared_data_file_name" ].value =
1814                 get_scripts_location() + "shared_data/genome_I_F.dat";
1815             self.log( "Connecting to the database." );
1816             self.dbm.connect_to_database();
1817             self.log( "Starting the GA manager." );
1818             self.open_ga_monitor_browser_window = open_ga_monitor_browser_window;

```

```

1847     self.start_ga_monitor( );
1849     self.log( "Setting the GA parameters. PS MG NE CP MP URFS PCMS USA." );
1851     self.log( str( population_size ) );
1853     self.log( str( max_generations ) );
1855     self.log( str( number_of_elite ) );
1857     self.log( str( crossover_probability ) );
1859     self.log( str( mutation_probability ) );
1861     self.log( str( use_rank_fitness_selection ) );
1863     self.log( str( perform_crossover_and_mutation_sequentially ) );
1865     self.log( str( use_self_adaptation ) );
1867     self.log( "Max torque." );
1869     self.max_torque = max_torque;
1871     self.ga.set_population_size( population_size );
1873     self.ga.set_max_generations( max_generations );
1875     self.ga.set_number_of_elite( number_of_elite );
1877     self.ga.set_crossover_probability( crossover_probability );
1879     self.ga.set_mutation_probability( mutation_probability );
1881     self.ga.set_use_rank_fitness_selection( use_rank_fitness_selection );
1883     self.ga.set_perform_crossover_and_mutation_sequentially( perform_crossover_and_mutation_sequentially );
1885     self.ga.set_use_self_adaptation( use_self_adaptation );
1887     self.log( "Creating a random GA population." );
1889     self.ga.create_randomized_population( );
1891     self.log( "Setting the current genome to 0." );
1893     self.current_genome = 0;
1895     self.log( "Entering loop." );
1897     while ( self.ga.get_generation_number( ) < self.ga.get_max_generations( ) ):
1899         self.log( "Current genome." );
1901         self.log( str( self.ga.get_genome( self.current_genome ) ) );
1903         # Populate physics engine parameters.
1905         self.log( "Populating the physics engine parameters." );
1907         self.populate_physics_engine_parameters( self.ga.get_genome( self.current_genome ).get_genes( ) );
1909         # Run game engine.
1911         self.log( "Starting the game engine." );
1913         self.start_game_engine( );
1915         # Calculate current genome fitness.
1917         # Read in I=(x_pos,y_pos,z_pos,x_ori,y_ori,z_ori,s_time) and F=(x_pos,y_pos,z_pos,x_ori,y_ori,z_ori,
1919         # e_time)
1921         # which was recorded by the robot monitor while the game engine was running.
1923         self.log( "Game engine stopped." );
1925         self.log( "Getting genome (I)initial and (F)inal state." );
1927         self.log( "x_pos , y_pos , z_pos , x_ori , y_ori , z_ori , s/e_time" );
1929         shared_data_file = open( get_scripts_location( ) + "shared_data/genome_I_F.dat", "r" );
1931         I = shared_data_file.readline( ).rstrip( );
1933         I = I.split( "," );
1935         I[ 0 ] = float( I[ 0 ] ); # x position.
1937         I[ 1 ] = float( I[ 1 ] ); # y position.
1939         I[ 2 ] = float( I[ 2 ] ); # z position.
1941         I[ 3 ] = float( I[ 3 ] ); # x orientation.
1943         I[ 4 ] = float( I[ 4 ] ); # y orientation.
1945         I[ 5 ] = float( I[ 5 ] ); # z orientation.
1947         I[ 6 ] = float( I[ 6 ] ); # Start time.
1949         F = shared_data_file.readline( ).rstrip( );
1951         F = F.split( "," );
1953         F[ 0 ] = float( F[ 0 ] ); # x' position.
1955         F[ 1 ] = float( F[ 1 ] ); # y' position.
1957         F[ 2 ] = float( F[ 2 ] ); # z' position.
1959         F[ 3 ] = float( F[ 3 ] ); # x' orientation.
1961         F[ 4 ] = float( F[ 4 ] ); # y' orientation.
1963         F[ 5 ] = float( F[ 5 ] ); # z' orientation.
1965         F[ 6 ] = float( F[ 6 ] ); # End time.
1967         shared_data_file.close( );
1969         os.remove( get_scripts_location( ) + "shared_data/genome_I_F.dat" );
1971         # Record simulated robot motion and its resulting fitness.
1973         simulated_robot_motion_file = open( get_scripts_location( ) + "data/
1975         simulated_robot_motion_with_fitness/forward/" + "srmfwf_" + str( self.run_id ) + ".dat", "a" );
1977         write_string = str( I[ 0 ] ) + ",";
1979         write_string += str( I[ 1 ] ) + ",";
1981         write_string += str( I[ 2 ] ) + ",";

```

```

1947     write_string += str( I[ 3 ] ) + ",";
1948     write_string += str( I[ 4 ] ) + ",";
1949     write_string += str( I[ 5 ] ) + ",";
1950
1951     write_string += str( F[ 0 ] ) + ",";
1952     write_string += str( F[ 1 ] ) + ",";
1953     write_string += str( F[ 2 ] ) + ",";
1954     write_string += str( F[ 3 ] ) + ",";
1955     write_string += str( F[ 4 ] ) + ",";
1956     write_string += str( F[ 5 ] ) + ",";
1957
1958     simulated_robot_motion_file.write( write_string );
1959
1960     simulated_robot_motion_file.close( );
1961
1962     self.log( str( I ) );
1963
1964     self.log( str( F ) );
1965
1966     self.log( "Calculating genome fitness." );
1967
1968     current_genome_fitness = self.calculate_genome_fitness( I, F );
1969
1970     self.log( "Genome fitness." );
1971
1972     self.log( str( current_genome_fitness ) );
1973
1974     self.ga.set_genome_fitness( self.current_genome, current_genome_fitness );
1975
1976     # Add the fitness to the last line of the simulated robot motion recorded.
1977
1978     simulated_robot_motion_file = open( get_scripts_location( ) + "data/
1979                                         simulated_robot_motion_with_fitness/forward/" + "srmfwf_" + str( self.run_id ) + ".dat", "a" );
1980
1981     simulated_robot_motion_file.write( str( current_genome_fitness ) + "\n" );
1982
1983     simulated_robot_motion_file.close( );
1984
1985     # Record the genome's phenotype (the physics parameters) and its corresponding fitness.
1986
1987     physics_parameters_with_fitness_file = open( get_scripts_location( ) + "data/
1988                                         physics_parameters_with_fitness/" + "ppwf_" + str( self.run_id ) + ".dat", "a" );
1989
1990     physics_parameters_with_fitness_file.write( "fitness," + str( current_genome_fitness ) + "\n\n" );
1991
1992     physics_parameters_with_fitness_file.close( );
1993
1994     # Increase current genome + 1.
1995
1996     self.current_genome += 1;
1997
1998     self.log( str( self.current_genome ) );
1999
2000     # If current genome is equal to the population size.
2001
2002     if ( self.current_genome == self.ga.get_population_size( ) ):
2003
2004         self.log( "Evaluated all genomes in population." );
2005
2006         # Separate recorded simulated robot motion by generation.
2007
2008         simulated_robot_motion_file = open( get_scripts_location( ) + "data/
2009                                         simulated_robot_motion_with_fitness/forward/" + "srmfwf_" + str( self.run_id ) + ".dat", "a" );
2010
2011         simulated_robot_motion_file.write( "\n" );
2012
2013         simulated_robot_motion_file.close( );
2014
2015         self.log( "Current generation number: " + str( self.ga.get_generation_number( ) ) );
2016
2017         # Update the population metrics.
2018
2019         self.log( "Updating population metrics." );
2020
2021         self.ga.update_population_metrics();
2022
2023         # Store the population metrics in the database.
2024
2025         self.log( "Storing population metrics in the database." );
2026
2027         a = str( self.ga.get_generation_number( ) );
2028         b = str( self.ga.get_highest_fitness( ) );
2029         c = str( self.ga.get_average_fitness( ) );
2030         d = str( self.ga.get_lowest_fitness( ) );
2031         e = str( self.ga.get_crossover_probability( ) );
2032         f = str( self.ga.get_mutation_probability( ) );
2033
2034         mysql_string = "INSERT INTO `population_metrics` ( `generation_number`, `highest_fitness`, `average_fitness`, `lowest_fitness`, `crossover_probability`, `mutation_probability` ) ";
2035         mysql_string += "VALUES( " + a + ", " + b + ", " + c + ", " + d + ", " + e + ", " + f + " );";
2036
2037         self.dbm.execute( mysql_string );
2038
2039         self.log( mysql_string );
2040
2041         # Generate a new population.
2042
2043         self.log( "Generating a new generation." );
2044
2045         self.ga.generate_new_generation();

```

```

2045     # Set current genome to 0.
2047     self.log( "Setting the current genome to 0." );
2049     self.current_genome = 0;
2051     self.log( "Exited loop." );
2053     self.log( "Stopping." );
2055     self.stop( );
2057     def stop( self ):
2059         if ( self.run_id != None ):
2061             self.dbm.close_database_connection( );
2063             self.stop_ga_monitor( );
2065             self.run_id = None;
2067     def start_ga_monitor( self ):
2069         scripts_location = get_scripts_location( );
2071         if ( self.open_ga_monitor_browser_window == True ):
2073             self.cgi_http_server = subprocess.Popen( [ scripts_location + "cgi_http_server.py", "-w" ] );
2075         else:
2077             self.cgi_http_server = subprocess.Popen( scripts_location + "cgi_http_server.py" );
2079     def stop_ga_monitor( self ):
2081         self.cgi_http_server.kill( );
2083     def start_game_engine( self ):
2085         bpy.ops.view3d.game_start( );
2087     def log( self, log_string ):
2089         if ( self.log_file_name != "" ):
2091             log_file = open( self.log_file_name, "a+" );
2093             log_file.write( log_string + "\n" );
2095             log_file.close( );
2097     def calculate_mahalanobis_distance( self, point ):
2099         self.log( "Point." );
2101         self.log( str( point ) );
2103         md = scipy.spatial.distance.mahalanobis( point, self.rm, self.rcm_inv );
2105         md2 = md * md;
2107         return md, md2;
2109     def calculate_genome_fitness( self, initial, final ):
2111         # Blender returns NaN for large positions/orientations for x, y, and z.
2112         # If this is the case, set the fitness to some large value.
2113         # initial/final structure:
2114         #   x_pos    0
2115         #   y_pos    1
2116         #   z_pos    2
2117         #   x_rot    3
2118         #   y_rot    4
2119         #   z_rot    5
2120         # s/e_tim   6
2121
2122         fitness = 9999999999.0;
2123
2124         for i in range( len( final ) ):
2125             if ( numpy.isnan( final[ i ] ) ):
2126                 return fitness;
2127
2128         # Only 3 dof was recorded for the real robot.
2129         # So assemble for the simulated robot its x' position, y' position, and z' orientation.
2130
2131         final_trimmed = [ final[ 0 ], final[ 1 ], final[ 5 ] ];
2132
2133         md, md2 = self.calculate_mahalanobis_distance( final_trimmed );
2134
2135         self.log( "Genome mahalanobis distance." );
2136         self.log( str( md ) );
2137
2138         # Penalties?
2139         self.log( "Penalties." );
2140
2141
2142
2143
2144
2145

```

```

2147     # Time > 1 seconds.
2148     elapsed_time = abs( ( final[ 6 ] - initial[ 6 ] ) / 1000.0 ) - 1.0 );
2149     self.log( "Elapsed time > 1 seconds: " + str( elapsed_time ) );
2151     # Rotation in x.
2153     rotation_x = abs( final[ 3 ] - initial[ 3 ] );
2155     self.log( "X rotation: " + str( rotation_x ) );
2157     # Rotation in y.
2159     rotation_y = abs( final[ 4 ] - initial[ 4 ] );
2161     self.log( "Y rotation: " + str( rotation_y ) );
2163     # Translation in z.
2165     translation_z = abs( final[ 2 ] - initial[ 2 ] );
2167     self.log( "Z translation: " + str( translation_z ) );
2169     fitness = md + elapsed_time + rotation_x + rotation_y + translation_z;
2171     return fitness;
2173
2175 def populate_physics_engine_parameters( self, genome_genes ):
2176     self.log( "Genome genes." );
2177     self.log( str( genome_genes ) );
2179     assert len( genome_genes ) == self.ga.get_number_of_genes_per_genome( ), "Cannot populate physics
        engine parameters.";
2181     # Blender API call examples:
2182     #
2183     # bpy.data.objects["Cylinder"].game.actuators["Motion"].torque = [0,401,0];
2184     # bpy.data.objects["Cylinder"].game.sensors["Always"].use_tap = False;
2185     # bpy.ops.logic.actuator_add( type="MOTION", name="motion1", object="Cylinder");
2186     # bpy.data.objects["Cylinder"].game.controllers[ "Python" ].link( sensor=None, actuator=bpy.data.
        objects["Cylinder"].game.actuators["motion1"] );
2187     # bpy.data.objects["Cylinder"].game.mass = 10000.0;
2188     # bpy.data.scenes["Scene"].game_settings.physics_gravity;
2189
2190     # Blender's largest number called "inf".
2191     # To find, set an appropriate field to a very large
2192     # number and then click on the field and copy the number.
2193     # When clicking the field, the "inf" will turn numeric.
2194
2195     INF = 340282346638528859811704183484516925440.0;
2196
2197     BOOLEANS = [ False, True ];
2198
2199     # Assumes the correct scene, wheel object, sensor, controller, and actuator names.
2200     # These names were set by hand in the .blend file. If they are changed, Blender
        # will throw an exception.
2201
2202     scene      = "bbautotune";
2203     front_wheel_l = "robot_1_wheel_front_L";
2204     front_wheel_r = "robot_1_wheel_front_R";
2205     back_wheel_l = "robot_1_wheel_back_L";
2206     back_wheel_r = "robot_1_wheel_back_R";
2207     wheel_material = "wheel";
2208     actuator      = "torque_z";
2209
2210     #### WORLD
2211
2212     # Gravity.
2213
2214     #gravity = get_clamped_value( ( genome_genes[ 0 ] * 10000.0 ), 0.0, 10000.0 );
2215     gravity = get_clamped_value( ( genome_genes[ 0 ] * 15.0 ), 0.0, 100.0 );
2216     self.log( "Setting gravity." );
2217     self.log( str( gravity ) );
2218
2219     bpy.data.scenes[ scene ].game_settings.physics_gravity = gravity;
2220
2221     # Sub-steps.
2222
2223     # You can input 1 up to 50. However, if only sliding the values, the value only goes from 1 to 5.
2224     # Not sure if this is a bug in the Blender code.
2225
2226     sub_steps = get_clamped_value( math.floor( ( genome_genes[ 1 ] * ( 5 - 1 ) ) + 1 ), 1, 5 );
2227
2228     self.log( "Setting sub steps." );
2229     self.log( str( sub_steps ) );
2230
2231     bpy.data.scenes[ scene ].game_settings.physics_step_sub = sub_steps;
2232
2233     # FPS.
2234
2235     # Setting FPS within [1,30) makes the game engine run extremely slow so allow the GA to find a
        solution
        # within the range of 30 to 10000 FPS.
2236
2237     fps = get_clamped_value( math.floor( ( genome_genes[ 2 ] * ( 10000 - 30 ) ) + 30 ), 30, 10000 );
2238
```

```

2245     self.log( "Setting FPS." );
2247     self.log( str( fps ) );
2249     bpy.data.scenes[ scene ].game_settings.fps = fps;
2251     ### Object
2253     # Scale XYZ?
2255     ,
2257     scale = get_clamped_value( ( genome_genes[ 3 ] * INF ), 0.0, INF );
2259     bpy.data.objects[ front_wheel_l ].scale = [ scale, scale, scale ];
2261     bpy.data.objects[ front_wheel_r ].scale = [ scale, scale, scale ];
2263     bpy.data.objects[ back_wheel_l ].scale = [ scale, scale, scale ];
2265     bpy.data.objects[ back_wheel_r ].scale = [ scale, scale, scale ];
2266     ,
2267     ### MATERIAL
2269     # Use physics?
2271     # Round returns incorrect values but converting its return value to a string does return the right
     # value.
     # Convert only the numbers before the decimal '.' to an integer.
2273     ,
2275     index = int( str( round( genome_genes[ 4 ] ) ).split( "." )[ 0 ] );
2277     use_material_physics = BOOLEANS[ index ];
2279     self.log( "Setting use material physics." );
2281     self.log( str( use_material_physics ) );
2283     bpy.data.objects[ front_wheel_l ].material_slots[ 0 ].material.game_settings.physics =
     use_material_physics;
2285     bpy.data.objects[ front_wheel_r ].material_slots[ 0 ].material.game_settings.physics =
     use_material_physics;
     bpy.data.objects[ back_wheel_l ].material_slots[ 0 ].material.game_settings.physics =
     use_material_physics;
2287     bpy.data.objects[ back_wheel_r ].material_slots[ 0 ].material.game_settings.physics =
     use_material_physics;
2288     ,
2289     # Friction.
2291     material_friction = get_clamped_value( ( genome_genes[ 5 ] * 100.0 ), 0.0, 100.0 );
2293     self.log( "Setting material friction." );
2295     self.log( str( material_friction ) );
2297     bpy.data.objects[ front_wheel_l ].material_slots[ 0 ].material.physics.friction = material_friction;
     bpy.data.objects[ front_wheel_r ].material_slots[ 0 ].material.physics.friction = material_friction;
2301     bpy.data.objects[ back_wheel_l ].material_slots[ 0 ].material.physics.friction = material_friction;
     bpy.data.objects[ back_wheel_r ].material_slots[ 0 ].material.physics.friction = material_friction;
2303     # Elasticity.
2305     material_elasticity = get_clamped_value( ( genome_genes[ 6 ] ), 0.0, 1.0 );
2307     self.log( "Setting material elasticity." );
2309     self.log( str( material_elasticity ) );
2311     bpy.data.objects[ front_wheel_l ].material_slots[ 0 ].material.physics.elasticity =
     material_elasticity;
     bpy.data.objects[ front_wheel_r ].material_slots[ 0 ].material.physics.elasticity =
     material_elasticity;
     bpy.data.objects[ back_wheel_l ].material_slots[ 0 ].material.physics.elasticity =
     material_elasticity;
2315     bpy.data.objects[ back_wheel_r ].material_slots[ 0 ].material.physics.elasticity =
     material_elasticity;
2317     ### PHYSICS
2319     # Type?
2321     ,
2323     PHYSICS_TYPES = [ "NO_COLLISION", "STATIC", "DYNAMIC", "RIGID_BODY", "SOFT_BODY", "OCCLUDE", "SENSOR",
     "NAVMESH", "CHARACTER" ];
2325     physics_type = get_clamped_value( math.floor( genome_genes[ 7 ] * len( PHYSICS_TYPES ) ), 0, len(
     PHYSICS_TYPES ) - 1 );
2327     physics_type = PHYSICS_TYPES[ physics_type ];
2329     bpy.data.objects[ front_wheel_l ].game.physics_type = physics_type;
     bpy.data.objects[ front_wheel_r ].game.physics_type = physics_type;
2331     bpy.data.objects[ back_wheel_l ].game.physics_type = physics_type;
     bpy.data.objects[ back_wheel_r ].game.physics_type = physics_type;
2333     ,
2335

```

```

# Ghost?
2337     '',
2339
2340     index = int( str( round( genome_genes[ 8 ] ) ).split( "." )[ 0 ] );
2341
2342     use_ghost = BOOLEANS[ index ];
2343
2344     bpy.data.objects[ front_wheel_l ].game.use_ghost = use_ghost;
2345     bpy.data.objects[ front_wheel_r ].game.use_ghost = use_ghost;
2346     bpy.data.objects[ back_wheel_l ].game.use_ghost = use_ghost;
2347     bpy.data.objects[ back_wheel_r ].game.use_ghost = use_ghost;
2348
2349     ''
2350
2351 # Mass.
2352
2353     #mass = get_clamped_value( ( genome_genes[ 9 ] * ( 10000.0 - 0.01 ) ) + 0.010, 0.010, 10000.0 );
2354
2355     mass = get_clamped_value( ( genome_genes[ 9 ] * ( 15.0 - 0.010 ) ) + 0.010, 0.010, 15.0 );
2356
2357     self.log( "Setting mass." );
2358
2359     self.log( str( mass ) );
2360
2361     bpy.data.objects[ front_wheel_l ].game.mass = mass;
2362     bpy.data.objects[ front_wheel_r ].game.mass = mass;
2363     bpy.data.objects[ back_wheel_l ].game.mass = mass;
2364     bpy.data.objects[ back_wheel_r ].game.mass = mass;
2365
2366 # Form factor?
2367
2368     ''
2369
2370     form_factor = get_clamped_value( ( genome_genes[ 10 ] ), 0.0, 1.0 );
2371
2372     self.log( "Setting form factor." );
2373
2374     self.log( str( form_factor ) );
2375
2376     bpy.data.objects[ front_wheel_l ].game.form_factor = form_factor;
2377     bpy.data.objects[ front_wheel_r ].game.form_factor = form_factor;
2378     bpy.data.objects[ back_wheel_l ].game.form_factor = form_factor;
2379     bpy.data.objects[ back_wheel_r ].game.form_factor = form_factor;
2380
2381     ''
2382
2383 # Velocity maximum.
2384
2385     velocity_max = get_clamped_value( ( genome_genes[ 11 ] * 1000.0 ), 0.0, 1000.0 );
2386
2387     self.log( "Setting velocity max." );
2388
2389     self.log( str( velocity_max ) );
2390
2391     bpy.data.objects[ front_wheel_l ].game.velocity_max = velocity_max;
2392     bpy.data.objects[ front_wheel_r ].game.velocity_max = velocity_max;
2393     bpy.data.objects[ back_wheel_l ].game.velocity_max = velocity_max;
2394     bpy.data.objects[ back_wheel_r ].game.velocity_max = velocity_max;
2395
2396 # Damping translation.
2397
2398     damping = get_clamped_value( ( genome_genes[ 12 ] ), 0.0, 1.0 );
2399
2400     self.log( "Setting translation damping." );
2401
2402     self.log( str( damping ) );
2403
2404     bpy.data.objects[ front_wheel_l ].game.damping = damping;
2405     bpy.data.objects[ front_wheel_r ].game.damping = damping;
2406     bpy.data.objects[ back_wheel_l ].game.damping = damping;
2407     bpy.data.objects[ back_wheel_r ].game.damping = damping;
2408
2409 # Damping rotation.
2410
2411     rotation_damping = get_clamped_value( ( genome_genes[ 13 ] ), 0.0, 1.0 );
2412
2413     self.log( "Setting rotation damping." );
2414
2415     self.log( str( rotation_damping ) );
2416
2417     bpy.data.objects[ front_wheel_l ].game.rotation_damping = rotation_damping;
2418     bpy.data.objects[ front_wheel_r ].game.rotation_damping = rotation_damping;
2419     bpy.data.objects[ back_wheel_l ].game.rotation_damping = rotation_damping;
2420     bpy.data.objects[ back_wheel_r ].game.rotation_damping = rotation_damping;
2421
2422 # Use collision bounds?
2423
2424     ''
2425
2426     index = int( str( round( genome_genes[ 14 ] ) ).split( "." )[ 0 ] );
2427
2428     use_collision_bounds = BOOLEANS[ index ];
2429
2430     self.log( "Setting use collision bounds." );
2431
2432     self.log( str( use_collision_bounds ) );
2433
2434     bpy.data.objects[ front_wheel_l ].game.use_collision_bounds = use_collision_bounds;
2435     bpy.data.objects[ front_wheel_r ].game.use_collision_bounds = use_collision_bounds;
2436     bpy.data.objects[ back_wheel_l ].game.use_collision_bounds = use_collision_bounds;
2437     bpy.data.objects[ back_wheel_r ].game.use_collision_bounds = use_collision_bounds;

```

```

2439     ,
2440     # Collision margin?
2441     ,
2442     ,
2443     collision_margin = get_clamped_value( ( genome_genes[ 15 ] ), 0.0, 1.0 );
2444     self.log( "Setting collision margin." );
2445     self.log( str( collision_margin ) );
2446
2447     bpy.data.objects[ front_wheel_l ].game.collision_margin = collision_margin;
2448     bpy.data.objects[ front_wheel_r ].game.collision_margin = collision_margin;
2449     bpy.data.objects[ back_wheel_l ].game.collision_margin = collision_margin;
2450     bpy.data.objects[ back_wheel_r ].game.collision_margin = collision_margin;
2451     ,
2452     # Collision bound type.
2453     #COLLISION_BOUNDS_TYPES = [ "TRIANGLE_MESH", "CONVEX_HULL", "CONE", "CYLINDER", "SPHERE", "BOX", "CAPSULE" ];
2454     COLLISION_BOUNDS_TYPES = [ "TRIANGLE_MESH", "CONVEX_HULL", "CYLINDER", "SPHERE" ];
2455     collision_bounds_type = get_clamped_value( math.floor( genome_genes[ 16 ] * len(
2456         COLLISION_BOUNDS_TYPES ) ), 0, len( COLLISION_BOUNDS_TYPES ) - 1 );
2457     collision_bounds_type = COLLISION_BOUNDS_TYPES[ collision_bounds_type ];
2458     self.log( "Setting collision bounds type." );
2459     self.log( str( collision_bounds_type ) );
2460
2461     bpy.data.objects[ front_wheel_l ].game.collision_bounds_type = collision_bounds_type;
2462     bpy.data.objects[ front_wheel_r ].game.collision_bounds_type = collision_bounds_type;
2463     bpy.data.objects[ back_wheel_l ].game.collision_bounds_type = collision_bounds_type;
2464     bpy.data.objects[ back_wheel_r ].game.collision_bounds_type = collision_bounds_type;
2465
2466     ### LOGIC BRICKS
2467
2468     # Torque.
2469
2470     #torque_z = get_clamped_value( ( -INF + ( genome_genes[ 17 ] * ( INF + INF ) ) ), -INF, INF );
2471     torque_z = get_clamped_value( genome_genes[ 17 ] * self.max_torque, 0.0, self.max_torque );
2472     self.log( "Setting torque_z." );
2473     self.log( str( torque_z ) );
2474
2475     # In order to make the collision_bounds_type "CYLINDER" feasible, the wheel had to be rotated in model
2476     # space by -90deg around the x-axis. This allows the cylinder shape to coincide with the wheel shape.
2477     # Otherwise, if the wheel is unrotated, the cylinder bounds' flat sides reside at the rounded sides
2478     # of the wheel. Imagine standing a tire up, putting a tube over it and rolling the wheel.
2479     # Thus, in local space, applying torque to the wheels must be done around the z-axis since in local
2480     # space,
2481     # the z-axis points out of the wheel hub.
2482
2483     bpy.data.objects[ front_wheel_l ].game.actuators[ actuator ].use_local_torque = True;
2484     bpy.data.objects[ front_wheel_r ].game.actuators[ actuator ].use_local_torque = True;
2485     bpy.data.objects[ back_wheel_l ].game.actuators[ actuator ].use_local_torque = True;
2486     bpy.data.objects[ back_wheel_r ].game.actuators[ actuator ].use_local_torque = True;
2487
2488     bpy.data.objects[ front_wheel_l ].game.actuators[ actuator ].torque = [ 0, 0, torque_z ];
2489     bpy.data.objects[ front_wheel_r ].game.actuators[ actuator ].torque = [ 0, 0, torque_z ];
2490     bpy.data.objects[ back_wheel_l ].game.actuators[ actuator ].torque = [ 0, 0, torque_z ];
2491     bpy.data.objects[ back_wheel_r ].game.actuators[ actuator ].torque = [ 0, 0, torque_z ];
2492
2493     # Record the genome's phenotype (the physics parameters) and its eventual fitness.
2494
2495     physics_parameters_with_fitness_file = open( get_scripts_location( ) + "data/
2496         physics_parameters_with_fitness/" + "ppwf_" + str( self.run_id ) + ".dat", "a" );
2497
2498     physics_parameters_with_fitness_file.write( "gravity," + str( gravity ) + "\n" );
2499     physics_parameters_with_fitness_file.write( "sub_steps," + str( sub_steps ) + "\n" );
2500     physics_parameters_with_fitness_file.write( "fps," + str( fps ) + "\n" );
2501     #physics_parameters_with_fitness_file.write( "scale," + str( scale ) + "\n" );
2502     #physics_parameters_with_fitness_file.write( "use_material_physics," + str( use_material_physics ) +
2503     "\n" );
2504     physics_parameters_with_fitness_file.write( "material_friction," + str( material_friction ) + "\n" );
2505     physics_parameters_with_fitness_file.write( "material_elasticity," + str( material_elasticity ) + "\n" );
2506     #physics_parameters_with_fitness_file.write( "physics.type," + str( physics_type ) + "\n" );
2507     #physics_parameters_with_fitness_file.write( "use_ghost," + str( use_ghost ) + "\n" );
2508     physics_parameters_with_fitness_file.write( "mass," + str( mass ) + "\n" );
2509     #physics_parameters_with_fitness_file.write( "form_factor," + str( form_factor ) + "\n" );
2510     physics_parameters_with_fitness_file.write( "velocity_max," + str( velocity_max ) + "\n" );
2511     physics_parameters_with_fitness_file.write( "damping," + str( damping ) + "\n" );
2512     physics_parameters_with_fitness_file.write( "rotation_damping," + str( rotation_damping ) + "\n" );
2513     #physics_parameters_with_fitness_file.write( "use_collision_bounds," + str( use_collision_bounds ) +
2514     "\n" );
2515     #physics_parameters_with_fitness_file.write( "collision_margin," + str( collision_margin ) + "\n" );
2516     physics_parameters_with_fitness_file.write( "collision_bounds_type," + str( collision_bounds_type ) +
2517     "\n" );
2518     physics_parameters_with_fitness_file.write( "torque_z," + str( torque_z ) + "\n" );
2519
2520     physics_parameters_with_fitness_file.close( );
2521
2522     class Database_Manager( ):

```

```

2533     def __init__( self, database_name ):
2535         self.database_name = database_name;
2537         variables_location = get_scripts_location( ) + "variables/";
2539         database_file = open( variables_location + "database.var", "r" );
2541         self.user_name = database_file.readline( ).rstrip( );
2543         self.password = database_file.readline( ).rstrip( );
2545         self.connection = None;
2547         self.cursor = None;
2549     def connect_to_database( self ):
2551         connection_config = {
2553             "user": self.user_name,
2554             "password": self.password,
2555             "database": self.database_name,
2556             'raise_on_warnings': True
2557         };
2559     try:
2561         self.connection = mysql.connector.connect( **connection_config );
2563         self.cursor = self.connection.cursor( );
2565     except Exception:
2567         print( "Database_Manager: could not open a connection to the database." );
2569     def close_database_connection( self ):
2571     try:
2573         self.connection.close( );
2575     except Exception:
2577         print( "Database_Manager: could not close the database." );
2579     def execute( self, mysql_string = None ):
2581     if mysql_string == None:
2583         pass;
2585     elif self.cursor == None:
2587         print( "Database_Manager: you must open a connection the database first." );
2589     else:
2591         self.cursor.execute( mysql_string );
2593         self.connection.commit( );
2595     # Seed the random module.
2597     random.seed( );
2599     # Create the BBAutoTune object.
2601     bbautotune = BBAutoTune( Genetic_Algorithm( ), Database_Manager( "bbautotune" ) );
2603     # Add the bbautotune object instance to Blender.
2605     bpy.bbautotune = bbautotune;
2607     # Switch to the game engine in Blender.
2609     bpy.context.scene.render.engine = "BLENDER_GAME";
2611     # Switch to the render pane.
2613     bpy.data.screens[ "Default" ].areas[ 1 ].spaces[ 0 ].context = "RENDER";
2615     # Setup the robot-monitor object's python controller.
2617     position_recorder_script_text = bpy.data.texts.load( get_scripts_location( ) + "robot_monitor.py" );
2619     bpy.data.objects[ "robot_monitor" ].game.controllers[ 0 ].text = position_recorder_script_text;
2621     # Register the UI panel properties, the UI panel layout, and the start button operator with blender.
2623     bpy.utils.register_module( __name__ );

```

B.3 BlenderSim

LISTING B.5: Robot_1_Controller.py

```

    ...
2   David Lettier (C) 2014.
4   http://www.lettier.com/
6   BlenderSim Version 2.0
8   This file controls the robot's movements.
10  ...
12  # Imports.
14  import mathutils, math, time, copy, datetime, os, pickle, random;
16  def robot_1_moving( ):
18      robot_1_base = bge.logic.getCurrentScene().objects[ "robot_1_base" ];
20      test = {
22          "xpos": robot_1_base.worldPosition.x * 100.0,
24          "ypos": robot_1_base.worldPosition.y * 100.0,
26          "zpos": robot_1_base.worldPosition.z * 100.0,
28          "xrot": robot_1_base.worldOrientation.to_euler( ).x,
        "yrot": robot_1_base.worldOrientation.to_euler( ).y,
        "zrot": robot_1_base.worldOrientation.to_euler( ).z
30      };
32      stopped = len( set( test.items( ) ) ^ set( bge.logic.globalDict[ "robot_1_state" ].items( ) ) );
34      if ( stopped == 0 ):
36          return False;
38      else:
40          x1 = bge.logic.globalDict[ "robot_1_simulated_poses" ][ -2 ][ 1 ];
42          y1 = bge.logic.globalDict[ "robot_1_simulated_poses" ][ -2 ][ 2 ];
44          z1 = bge.logic.globalDict[ "robot_1_simulated_poses" ][ -2 ][ 3 ];
46          x2 = test[ "xpos" ];
48          y2 = test[ "ypos" ];
50          z2 = test[ "zrot" ];
52          dx = abs( x1 - x2 );
54          dy = abs( y1 - y2 );
56          dz = abs( z1 - z2 );
58          if ( dx <= 0.02 and dy <= 0.02 and dz <= 0.00087 ):
59              return True;
60      def update_robot_1_state( ):
62          robot_1_base = bge.logic.getCurrentScene().objects[ "robot_1_base" ];
64          bge.logic.globalDict[ "robot_1_state" ] = {
66              "xpos": robot_1_base.worldPosition.x * 100.0,
68              "ypos": robot_1_base.worldPosition.y * 100.0,
70              "zpos": robot_1_base.worldPosition.z * 100.0,
72              "xrot": robot_1_base.worldOrientation.to_euler( ).x,
74              "yrot": robot_1_base.worldOrientation.to_euler( ).y,
76              "zrot": robot_1_base.worldOrientation.to_euler( ).z
78      };
79      def stop_robot_1( ):
80          bge.logic.robot_1_wheel_front_L.applyTorque( [ 0.0, 0.0, 0.0 ], True );
81          bge.logic.robot_1_wheel_front_R.applyTorque( [ 0.0, 0.0, 0.0 ], True );
82          bge.logic.robot_1_wheel_back_L.applyTorque( [ 0.0, 0.0, 0.0 ], True );
83          bge.logic.robot_1_wheel_back_R.applyTorque( [ 0.0, 0.0, 0.0 ], True );
84      def drop_robot_1_campose_marker( ):
85          robot_1_campose_marker = bge.logic.getCurrentScene().addObject( "robot_1_campose_marker", obj );
86          robot_1_campose_marker.worldPosition = obj.worldPosition;
87          robot_1_campose_marker.worldPosition.z = 23.0 / 100.0;
88      def drop_robot_1_waypoint_marker( waypoint ):
89          robot_1_waypoint_marker = bge.logic.getCurrentScene().addObject( "waypoint_marker", obj );
90          robot_1_waypoint_marker.worldPosition.x = waypoint[ 1 ] / 100.0;
91          robot_1_waypoint_marker.worldPosition.y = waypoint[ 0 ] / 100.0;
92          robot_1_waypoint_marker.worldPosition.z = 25.0 / 100.0;
93      def add_sim_pose( ):
94          bge.logic.globalDict[ "robot_1_simulated_poses" ].append(
95              [
96                  time.time( ) * 1000.0,
97                  obj.worldPosition[ 0 ] * 100.0,
98                  obj.worldPosition[ 1 ] * 100.0,
99                  obj.worldOrientation.to_euler( ).z
100             ]
101         )

```

```

104      ]
106  );
108 # Globals.
110 local = True;
112 world = False;
114 # Get the controller.
116 controller = bge.logic.getCurrentController();
118 # Get the game object that the controller is attached to.
120 obj = controller.owner;
122 # Initialize variables and flags.
124 if ( obj[ "init" ] == True ):
126   obj[ "init" ] = False;
128 # Robot 1's wheels.
130 bge.logic.robot_1_wheel_front_L = bge.logic.getCurrentScene().objects[ "robot_1_wheel_front_L" ];
131 bge.logic.robot_1_wheel_front_R = bge.logic.getCurrentScene().objects[ "robot_1_wheel_front_R" ];
132 bge.logic.robot_1_wheel_back_L = bge.logic.getCurrentScene().objects[ "robot_1_wheel_back_L" ];
133 bge.logic.robot_1_wheel_back_R = bge.logic.getCurrentScene().objects[ "robot_1_wheel_back_R" ];
134
135 bge.logic.robot_1_last_move_time = time.time() * 1000.0;
136 update_robot_1_state();
138 bge.logic.globalDict[ "robot_1_waypoints" ] = [
140   "stop"
142 ];
144 bge.logic.globalDict[ "robot_1_simulated_poses" ] = [ ];
146 add_sim_pose();
148 add_sim_pose();
150 if ( ( bge.logic.globalDict[ "robot_1_waypoints" ][ 0 ] != "stop" ) and ( not robot_1_moving() ) and ( ( time.time() * 1000.0 ) - bge.logic.robot_1_last_move_time >= 0.0 ) ):
152 # Get and drop the next waypoint in the arena.
154 waypoint = bge.logic.globalDict[ "robot_1_waypoints" ][ 0 ];
156 drop_robot_1_waypoint_marker( waypoint );
158 # Calculate the angle to turn in order to face the waypoint.
160 # Convert the waypoint to a 3D vector.
162 waypoint = mathutils.Vector( ( waypoint[ 1 ], waypoint[ 0 ], 1.0 ) );
164 # Translate the waypoint to the robot's local space.
166 mat_trans = mathutils.Matrix.Translation( ( -obj.worldPosition[ 0 ] * 100.0, -obj.worldPosition[ 1 ] * 100.0, -obj.worldPosition[ 2 ] * 100.0 ) );
168 waypoint_trans = mat_trans * waypoint;
170 waypoint_rot = mathutils.Matrix.Rotation( -obj.worldOrientation.to_euler()[ 2 ], 4, "Z" ) *
    waypoint_trans;
172 # Now that the waypoint world coordinate is transformed to the robot's local space,
173 # compute the angle between the robot's x-axis and the waypoint line going from the
174 # robot's origin to the waypoint.
176 rotateZ = math.atan2( waypoint_rot[ 1 ], waypoint_rot[ 0 ] );
178 # First turn and then move forward.
180 rotateZ = rotateZ * 180.0 / math.pi;
182 if ( abs( rotateZ ) < 1.0 ): # Turn error threshold.
184   a = 82.7271515601;
185   b = 23.12349975;
186   c = waypoint_rot[ 0 ];
187   f = ( a / b ) * c;
188
189   bge.logic.robot_1_wheel_front_L.applyTorque( [ 0.0, 0.0, f ], True );
190   bge.logic.robot_1_wheel_front_R.applyTorque( [ 0.0, 0.0, f ], True );
191   bge.logic.robot_1_wheel_back_L.applyTorque( [ 0.0, 0.0, f ], True );
192   bge.logic.robot_1_wheel_back_R.applyTorque( [ 0.0, 0.0, f ], True );
193
194 bge.logic.globalDict[ "robot_1_waypoints" ] = bge.logic.globalDict[ "robot_1_waypoints" ][ 1 : ];
196 elif ( rotateZ < 0.0 ):
198   a = 20.8;
199   b = 44.260811;
200   c = abs( rotateZ );
201   t = ( a / b ) * c;

```

```

202     bge.logic.robot_1_wheel_front_L.applyTorque( [ 0.0, 0.0,   t ], True );
204     bge.logic.robot_1_wheel_front_R.applyTorque( [ 0.0, 0.0, -t ], True );
206     bge.logic.robot_1_wheel_back_L.applyTorque( [ 0.0, 0.0,   t ], True );
208     bge.logic.robot_1_wheel_back_R.applyTorque( [ 0.0, 0.0, -t ], True );
210
211     elif ( rotateZ > 0.0 ):
212         a = 20.8;
213         b = 44.260811;
214         c = abs( rotateZ );
215         t = ( a / b ) * c;
216
217         bge.logic.robot_1_wheel_front_L.applyTorque( [ 0.0, 0.0, -t ], True );
218         bge.logic.robot_1_wheel_front_R.applyTorque( [ 0.0, 0.0,   t ], True );
219         bge.logic.robot_1_wheel_back_L.applyTorque( [ 0.0, 0.0, -t ], True );
220         bge.logic.robot_1_wheel_back_R.applyTorque( [ 0.0, 0.0,   t ], True );
221
222     bge.logic.robot_1_last_move_time = time.time( ) * 1000.0;
223
224     stop_robot_1( );
225
226     add_sim_pose( );
227
228     drop_robot_1_compose_marker( );
229
230     if ( not robot_1_moving( ) ):
231
232         pickle_file = open( "./pickled_data/robot_1_simulated_motion.pkl", "wb" );
233
234         pickle.dump( bge.logic.globalDict[ "robot_1_simulated_poses" ], pickle_file, protocol = 2, fix_imports =
235                     True );
236
237         pickle_file.close( );

```

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