

# CSSE220 Final Report

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## 0.1 Introduction

Evolution—specifically Baldwinian adaptation—is the foundational concept for this study. It operates on the assumption that some individuals are more “fit” to survive and reproduce than others, leading their genes to be preserved, as they are passed on to more offspring than those of less fit organisms. Mutations that occur during reproduction provide opportunities for even better organisms to be introduced into the population. The “Baldwin effect” suggests that the evolutionary fitness of a population can be improved not only through mutations in the permanent genotype of organisms but also through learning that is passed on in some way to offspring. This investigation tested both classic evolution and Baldwinian evolution by generating artificial populations of “chromosomes” and simulating the populations’ progress over time based on an algorithm that prioritizes chromosomes with a higher “fitness” as being more likely to survive. The genetic algorithm represents real-world patterns with an artificial representation. For example, chromosomes and genes were represented with arrays of integers, and instead of measuring fitness with real-world traits like height or strength, it was measured with characteristics of the array like total value or symmetry. Each chromosome was assigned a “fitness score” based on some calculation of the integers it contained, and this score determined the probability that the chromosome would be copied to the next generation.

## 0.2 Basic Experiments

### 0.2.1 Experiment 1: Generations Taken to Evolve a Solution with Mutation Only

Using the settings outlined in Fig. 1, the simulator was run until at least one individual in the population reached the maximum fitness score of 100. The number of generations taken to do so was recorded. This was repeated ten times.

It was hypothesized that the fitness of the population as a whole—including the worst and average fitness scores—would increase somewhat steadily over time, decreasing only occasionally and by relatively small amounts, until at least one chromosome reached the maximum fitness score of 100. The maximum score was expected to be reached after about 200 generations.

The results of Experiment 1 are summarized in Fig. 2. Output from the simulator for the shortest trial, a typical trial, and the longest trial are shown in Fig. 3, Fig. 4, and Fig. 5, respectively.

Generally, the fitness of the population as a whole experienced a net increase over time. There were occasional decreases in the average and worst fitness scores of the population. The best score never decreased because elitism was non-zero. Diversity decreased significantly over time: although the number of completely unique individuals did not decrease by a large amount, it is clear from the drop in hamming distance that the genotypes of individuals were becoming

Parameter	Value
<i>genome length:</i>	100
<i>population size:</i>	100
<i>selection:</i>	truncation selection
<i>elitism</i>	1%
<i>mutation rate:</i>	1%
<i>crossover method:</i>	false
<i>max generations:</i>	500

Figure 1: Simulator Settings for Experiment 1

increasingly more similar to each other over time, even if they were not perfectly identical.

In ten trials, it took an average of 215.2 generations and a median of 207.5 generations to evolve a solution. The standard deviation of the results was 48.0 generations. The typical number of generations taken to evolve a solution is reasonably close to the expected value; the amount of variation between trials as indicated by the standard deviation of results is larger than expected. Experiment 1 provides evidence that, with only mutation, the number of generations taken for a population with the settings outlined in Fig. 1 to evolve a solution varies significantly but is roughly 200 generations.

### 0.2.2 Experiment 2: Generations Taken to Evolve a Solution with Mutation and Single-Point Crossover

The simulator was set to the values outlined in Fig. 6. As in Experiment 1, the simulator was run until at least one individual in the population reached the maximum fitness score of 100. The number of generations taken to do so was recorded. This was repeated ten times.

It was hypothesized that the results of this experiment would be similar to the results of Experiment 1, except that the typical number of generations to evolve a solution would be lesser. This was because the introduction of crossover mutation was expected to provide more opportunity for chromosome fitness to change and possibly increase, while the continued implementation of elitism would prevent this additional mutation from destroying the fitness of the best chromosomes. As in Experiment 1, it was expected that the fitness of the

Trial	Number of generations to evolve a solution
1	179
2	178
3	329
4	247
5	227
6	193
7	189
8	164
9	222
10	224

Figure 2: Summary of Results of Experiment 1

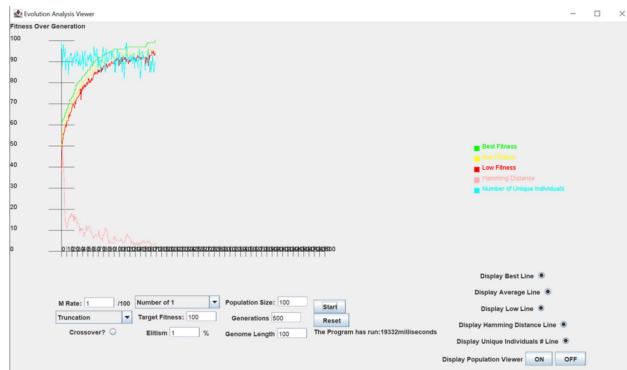


Figure 3: Trial 2 Required 178 Generations to Evolve Solution (Experiment 1)

population as a whole would increase somewhat steadily with minor decreases in average and worst fitness over time. It was also expected that diversity would fall significantly over time.

The results of Experiment 2 are summarized in Fig. 7. Output from the simulator for the shortest trial, a typical trial, and the longest trial are illustrated in Fig. 8, Fig. 9, and Fig. 10, respectively.

The general trends of Experiment 2 were similar to the general trends noted in Experiment 1. This experiment affirmed that the fitness of the population tends to increase over time, with occasional small decreases in fitness. Again, a drop in hamming distance combined with an oscillating number of unique individuals indicates that genotypes within a population become more similar—though not necessarily more identical—over time.

In ten trials, it took an average of 201.6 generations and a median of 183.5 generations to evolve a solution using the parameter values specified in Fig. 6. These results had a standard deviation of 38.8 generations. The confidence interval for the mean number of generations taken to evolve a solution with single-point crossover is  $201.6 \pm 27.7$  generations. Thus, although the mean

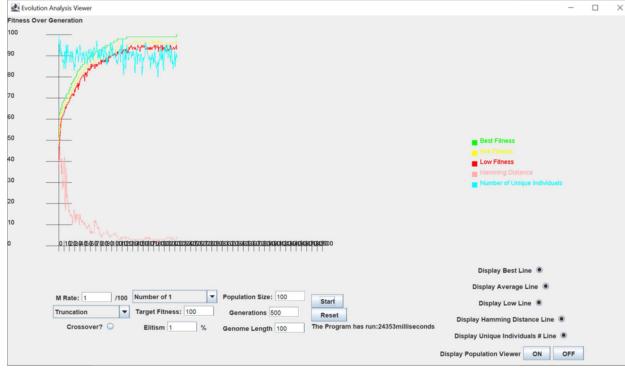


Figure 4: Trial 10 Required 224 Generations to Evolve Solution (Experiment 1)

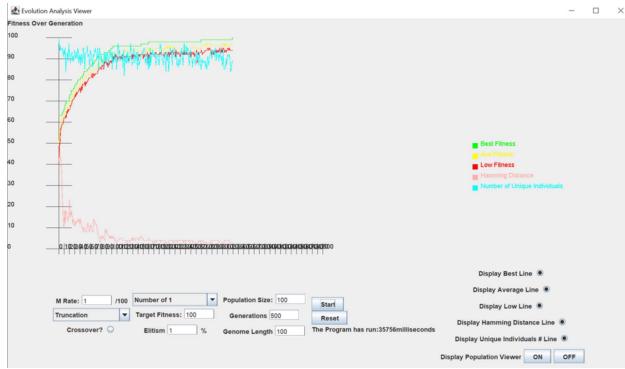


Figure 5: Trial 3 Required 329 Generations to Evolve Solution (Experiment 1)

number of generations taken to evolve a solution using single-point crossover was less than the mean number of generations taken to evolve a solution with mutation only, there is not yet sufficient evidence to support the hypothesis that single-point crossover accelerates evolution of a solution since the mean values of each experiment fall within each other's confidence intervals.

### 0.2.3 Experiment 3: Effect of Mutation Rate on Generations Taken to Evolve a Solution

In order to observe the effect of mutation rate on the rate of evolution, the simulator was set to the values listed in Fig. 11. The mutation rate was set to one percent, and the simulation was run three times until at least one individual in the population reached a target fitness score of 85. The number of generations taken to do so was recorded. This process was then repeated for mutation rates of two, three, and four percent.

It was hypothesized that the number of generations taken to evolve a solution

Parameter	Value
<i>genome length:</i>	100
<i>population size:</i>	100
<i>selection:</i>	truncation selection
<i>elitism</i>	1%
<i>mutation rate:</i>	1%
<i>crossover method:</i>	true
<i>max generations:</i>	500

Figure 6: Simulator Settings for Experiment 2

would first increase with mutation rate because there would be more chances to create better chromosomes in a shorter period of time. Then, it was hypothesized that high mutation rates would eventually become a hindrance because they would change the population too substantially and thereby prevent it from maintaining high fitness.

Experiment 3 revealed a positive correlation between mutation rate and number of generations taken to evolve a solution. These results are summarized in Fig. 12, and a linear regression on the data can be observed in Fig. 13. This was somewhat inconsistent with the hypothesis: it was expected that increased mutation rate would be somewhat helpful at first and then become a hindrance, but it seems that, with zero percent elitism, a one percent mutation rate may be ideal.

Notice how the best fitness line in Fig. 14 often climbs a bit and then suddenly loses too much fitness to reach the target fitness score, failing to reach the target fitness of 85 after 500 generations. Based this and other graphs generated in Experiment 3, it was concluded that increasing the mutation rate causes genotypes with high fitness to be lost too often for the population to make satisfactory progress toward a solution.

#### 0.2.4 Experiment 4: Analysis of Relationship Between Mutation Rate and Elitism

Based on the results of Experiment 3, this Experiment was carried out to determine the effects of elitism on populations with differing mutation rates. The simulator was set to the values listed in Fig. 15. Take note that elitism was set

Trial	Number of generations to evolve a solution
1	261
2	183
3	186
4	184
5	183
6	167
7	225
8	276
9	183
10	168

Figure 7: Summary of Results of Experiment 2

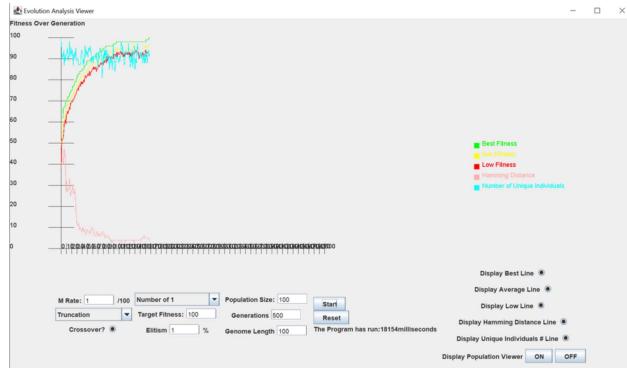


Figure 8: Trial 6 Required 167 Generations to Evolve a Solution (Experiment 2)

to one percent, as opposed to zero percent in Experiment 3. The mutation rate was set to one percent, and the simulation was run three times until at least one individual in the population reached a target fitness score of 85. The number of generations taken to do so was recorded. This process was then repeated for mutation rates of two, three, and four percent.

It was hypothesized that the introduction of elitism in this experiment would make high mutation rates an advantage rather than a disadvantage. This was expected because, in Experiment 3, high mutation rates were a hindrance because high fitness was mutated too much to be preserved. However, in this experiment, elitism would preserve the best chromosomes while allowing high mutation rates to increase chances of randomly creating more favorable genotypes from less favorable organisms.

Experiment 4 revealed a less positive correlation between mutation rate and number of generations taken to evolve a solution. These results are summarized in Fig. 16, and a linear regression on the data can be observed in Fig. 17. This is consistent with the hypothesis in that elitism significantly reduced the problem

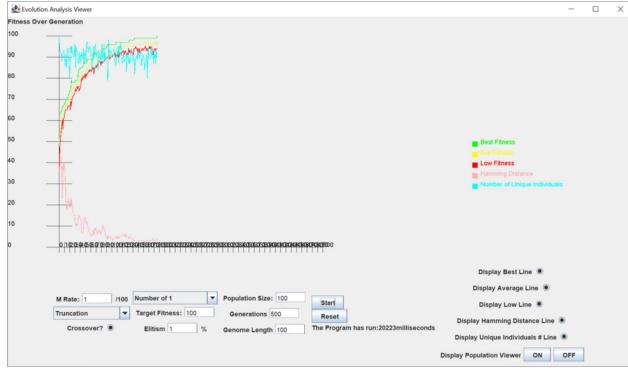


Figure 9: Trial 3 Required 186 Trials to Evolve a Solution (Experiment 2)

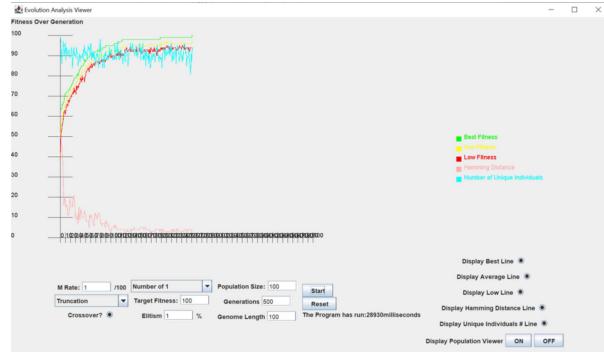


Figure 10: Trial 1 Required 261 Generations to Evolve a Solution (Experiment 2)

of high mutation rates slowing the rate of evolution. However, the hypothesis that one percent elitism could make high mutation rates an advantage was not supported.

Observe the graph in Fig. 18. Notice that, in comparison to Fig. 14, this graph evolves a solution in far fewer generations. The only difference between the graphs is the use of elitism in Fig. 18. From this, it was concluded that elitism can enable populations with high mutation rates to evolve quickly by preventing genotypes with high fitness scores from being lost.

### 0.3 Reproducing Results from a Classic Paper

In their research paper "How Learning Can Guide Evolution," [1] Geoffrey E. Hinton and Steven J. Nowlan assert that—though the adaptations an organism makes throughout its lifetime do not affect its genotype and, consequently, cannot be passed directly to its offspring—learning's effect on the progress of a

Parameter	Value
<i>genome length:</i>	100
<i>population size:</i>	100
<i>selection:</i>	rank selection
<i>elitism</i>	0%
<i>mutation rate:</i>	varied
<i>crossover method:</i>	false
<i>fitness method:</i>	number of 1's
<i>max generations:</i>	500
<i>target fitness:</i>	85

Figure 11: Simulator Settings for Experiment 3

population is evident in accelerated rates of evolution as compared to populations of non-learning organisms. This argument is founded upon the principles of Baldwinism. Hinton and Nowlan conducted their research using a genetic algorithm somewhat similar to the one developed here. Below are the details of an attempt to replicate Hinton and Nowlan’s experimental procedure and results with the genetic algorithm developed by group R-301.

Just as in Hinton and Nowlan’s experiment, chromosomes in these tests were assumed to have three types of alleles: one “correct” allele represented by the integer value “1”, one “incorrect” allele represented by the integer value “0,” and one undetermined allele represented by the integer value “2.” Additionally, a new “Baldwinian” fitness option was added to the simulator. For every chromosome, this method simulated 1000 days of life, during which the chromosome’s undetermined alleles were randomly assigned to a correct or incorrect value. If the chromosome ever achieved a phenotype made entirely of correct values, its fitness score increased significantly based on the number of “days” remaining in its life when it reached maximum fitness. In a new “Baldwinian” parent selection method, pairs of chromosomes were selected randomly with a probability proportional to their fitness score, and single-point crossover was applied to them to produce offspring.

Additional simulator settings used for testing can be found in Fig. 19. The simulation was run with these settings multiple times, and the numbers of cor-

Mutation Rate (%)	Elitism (%)	Generations Taken to Reach Fitness Score of 85
1	0	50
1	0	40
1	0	55
2	0	84
2	0	58
2	0	54
3	0	Over 500
3	0	368
3	0	Over 500
4	0	Over 500
4	0	Over 500
4	0	Over 500

Figure 12: Summary of Results of Experiment 3

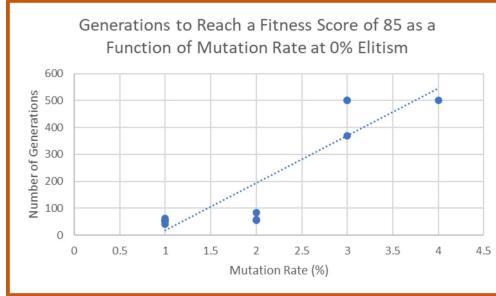


Figure 13: Linear Fit of Relationship Between Mutation Rate and Generations Taken to Evolve a Solution (Experiment 3)

rect, incorrect, and undetermined alleles remaining in the population were examined over time.

It was hypothesized that the results of this experiment would be similar to those of Hinton and Nowlan's study, which showed, over time, a decline in incorrect alleles, an increase in correct alleles, and a slight decrease in unknown alleles. The model for this hypothesis can be found in Fig. 20.

The results of the experiment conducted with team R-301's simulator mirrored that of Hinton and Nowlan's experiment quite closely. As can be seen in Fig. 21, the simulation results showed an eventual decline in incorrect alleles and a simultaneous increase in correct alleles in the population. The number of undecided alleles increased slightly and then decreased when the number of correct alleles reached its maximum, as in Hinton and Nowlan's study.

In numerous trials running for various numbers of generations, it was noted that the end behavior of the average numbers of correct, incorrect, and unknown alleles was asymptotic, with the graph looking approximately the same no mat-

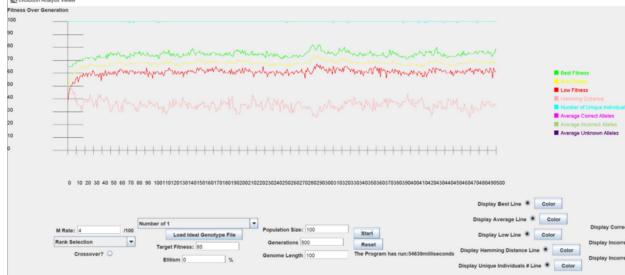


Figure 14: Simulator Results for a Mutation Rate of 4 Percent and Zero Percent Elitism (Experiment 3)

ter the number of generations. See an example of this in Fig. 22, a graph of the Baldwinian simulation for 100 trials as opposed to 50. It was also observed that the population appeared to stabilize much more quickly than in the non-learning simulations, stabilizing after only about 50 generations in every trial.

Additionally, it was noted that the overall diversity of the population decreased significantly over time, just as it did in non-learning populations. This is evidenced by the plot of hamming distance over time in Fig. 23.

It was inferred that the reason for the observed behavior in both this experiment and in the study by Hinton and Nowlan was the prioritization of organisms that are genetically predisposed to developing desirable phenotypes. In this case, organisms with permanent incorrect alleles received much lower fitness scores than their counterparts with only correct and unknown alleles and were therefore removed from the population by natural selection. Organisms with no incorrect alleles and more correct alleles than unknown alleles were favored by evolutionary pressure and tended to survive. This explains the drop in incorrect alleles, the increase in correct alleles, and the slight decrease in unknown alleles after incorrect alleles had been removed. The fact that learning populations stabilized sooner than the tested non-learning populations provides some support for Nowlan and Hinton's assertion that learning can, in fact, guide evolution.

## 0.4 Further Experiments

### 0.4.1 Further Experiment 1: Target Binary Value Fitness Function

This experiment tested a new type of fitness function, which favored organisms whose genotype most closely matched a chosen binary value. The simulator was set to the values shown in Fig. 24, and the simulation was run until a solution was generated or the maximum number of generations was surpassed. This was repeated for a total of ten trials.

It was hypothesized that the number of generations to reach maximum fitness

Parameter	Value
<i>genome length:</i>	100
<i>population size:</i>	100
<i>selection:</i>	rank selection
<i>elitism</i>	0%
<i>mutation rate:</i>	varied
<i>crossover method:</i>	false
<i>fitness method:</i>	number of 1's
<i>max generations:</i>	500
<i>target fitness:</i>	85

Figure 15: Simulator Settings for Experiment 4

would be slightly greater for this fitness function than for the others since this function relies on both position and quantity of correct alleles, so mutation would be less likely to improve fitness.

The results of this experiment were somewhat surprising: in nearly every trial, the best fitness remained constant over time, and the average and worst fitness fluctuated but did not experience significant net increases or decreases. Diversity dropped initially and then assumed a somewhat stable value. A summary of these results can be found in Fig. 25, and a typical simulator output for the ten trials can be found in Fig. 26.

The populations tested in this experiment performed significantly worse than what had been hypothesized. From this experiment, it was concluded that evolution of organisms whose binary genotype value most closely matches a target value is quite difficult and potentially infeasible with the parameter values used in this experiment.

#### 0.4.2 Further Experiment 2: Symmetry Fitness Function

Symmetry is heavily favored by real-world evolution. This experiment aimed to reflect that by implementing a fitness function that favors organisms whose genotype is symmetrical, with pairs of alleles on each end of the chromosome being identical. The simulator was set to the values shown in Fig. 27, and the

Mutation Rate (%)	Elitism (%)	Generations Taken to Reach Fitness Score of 85
1	1	47
1	1	54
1	1	42
2	1	45
2	1	42
2	1	47
3	1	51
3	1	45
3	1	52
4	1	74
4	1	64
4	1	41

Figure 16: Summary of Results of Experiment 4

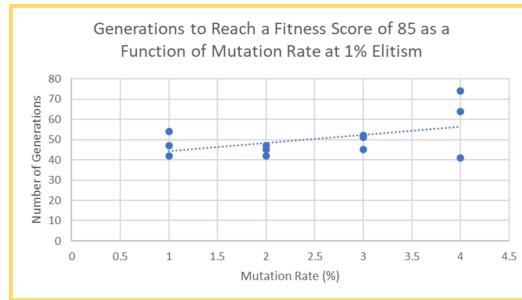


Figure 17: Linear Fit of Relationship Between Mutation Rate and Generations Taken to Evolve a Solution (Experiment 4)

simulation was run until a solution was generated or until the maximum number of generations was reached. The number of generations required to reach the maximum fitness was recorded. This was repeated for a total of ten trials.

It was hypothesized that a solution would be reached but that this would take significantly more time than with the basic fitness functions because, similarly to the binary value fitness function, this fitness function relied on both type and position of alleles rather than just position.

The results of this experiment reflected Further Experiment 1 in that, in all trials, no solution was generated, as summarized in Fig. 28. As can be seen in Fig. 29, in nearly every trial, the best, average, and worst fitness changed frequently but made little net improvement or decline. It was also noted that, unlike in other experiments, diversity did not seem to decrease significantly over time.

It was concluded from this experiment that it may be difficult or infeasible for a population to evolve solutions to the symmetry fitness method.

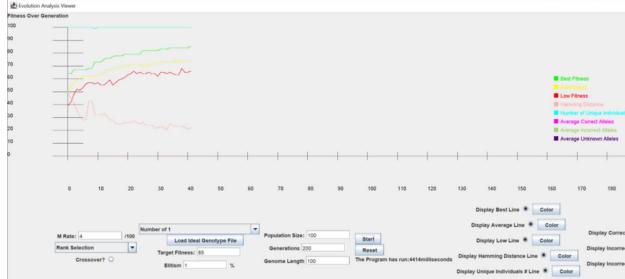


Figure 18: Simulator Results for a Mutation Rate of 4 Percent and One Percent Elitism (Experiment 4)

#### 0.4.3 Further Experiment 3: Timing Analysis

In order to understand the efficiency of the code running the simulator, a timing analysis was performed on the main function of the program. This function runs the simulator for some number of generations specified by the user. In order to test this, a small class was written to run the function for increasing numbers of generations  $n$  and record the amount of time taken to do so. The settings for this experiment were the default settings of the simulator, which can be found in Fig. 30.

It was hypothesized that the function being tested would run in  $O(n \text{ squared})$  time.

The results of this experiment are summarized in Fig. 31. From the graph, it was determined that the method for running for some number of generations runs in approximately  $O(n \text{ squared})$  time, which is consistent with the hypothesis.

It was concluded from the experiment that the experiment runs in a satisfactory amount of time, although it would be beneficial to do further optimization of the program to attempt to reduce its runtime.

## 0.5 Conclusion

The development of this simulator, in combination with the various tests run on it, have led to the conclusions discussed above. Most importantly, it was found that a computer program can simulate certain types of evolution quite well, with populations evolving solutions and losing diversity in the same way that they do in real life. It was also found that this type of simulation is better suited for certain types of fitness than for others, as some types of fitness appear impossible to solve in a reasonable amount of time with this simulation technique. Finally, with regards to the study that served as the foundation of this project, it was found that learning likely does play a significant role in accelerating evolution, as suggested by Hinton and Nolan.

Parameter	Value
<i>genome length:</i>	20
<i>population size:</i>	1000
<i>selection:</i>	Baldwinian selection
<i>elitism</i>	1%
<i>mutation rate:</i>	0%
<i>crossover method:</i>	false
<i>fitness method:</i>	Baldwinian
<i>max generations:</i>	varied

Figure 19: Simulator Settings for Reproduction of Hinton and Nowlan's Results

## 0.6 References

- [1] Geoffrey E. Hinton Steven J. Nowlan. *How Learning Can Guide Evolution.* Complex Systems. 1987.

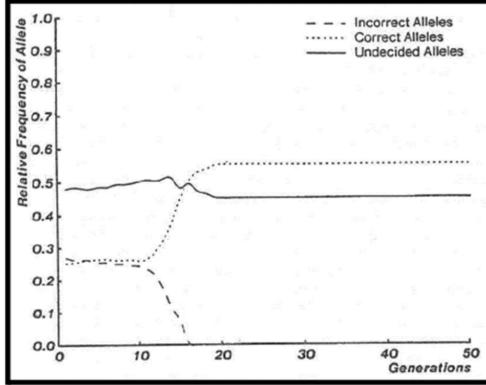


Figure 20: Hinton and Nowlan's Results

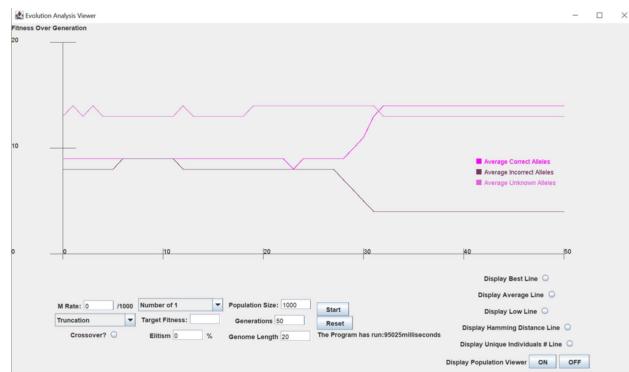


Figure 21: Typical Simulator Results From The Baldwin Experiment

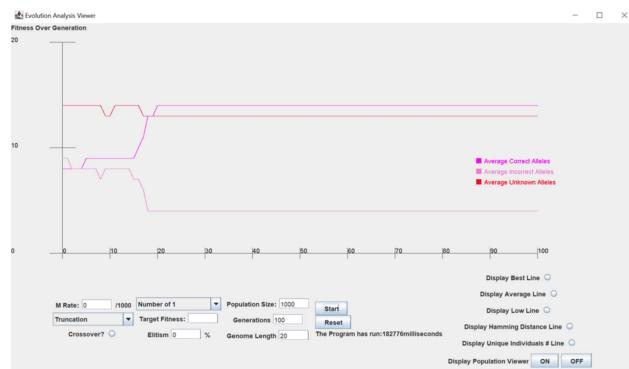


Figure 22: Simulator Results for 100 Generations of Baldwinian Evolution

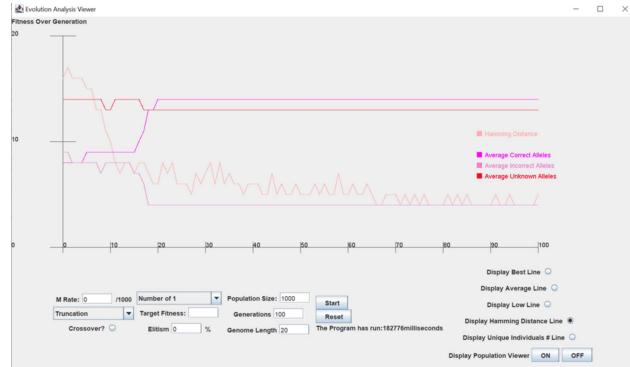


Figure 23: Hamming Distance Over Time in Balwinian Evolution Simulation

Parameter	Value
<i>genome length:</i>	20
<i>population size:</i>	100
<i>selection:</i>	truncation selection
<i>elitism</i>	1%
<i>mutation rate:</i>	1%
<i>crossover method:</i>	false
<i>fitness method:</i>	binary value
<i>max generations:</i>	500

Figure 24: Simulator Settings for Further Experiment 1

Trial	Number of generations to evolve a solution
1	over 500
2	over 500
3	over 500
4	over 500
5	over 500
6	over 500
7	over 500
8	over 500
9	over 500
10	over 500

Figure 25: Summary of Results of Further Experiment 1

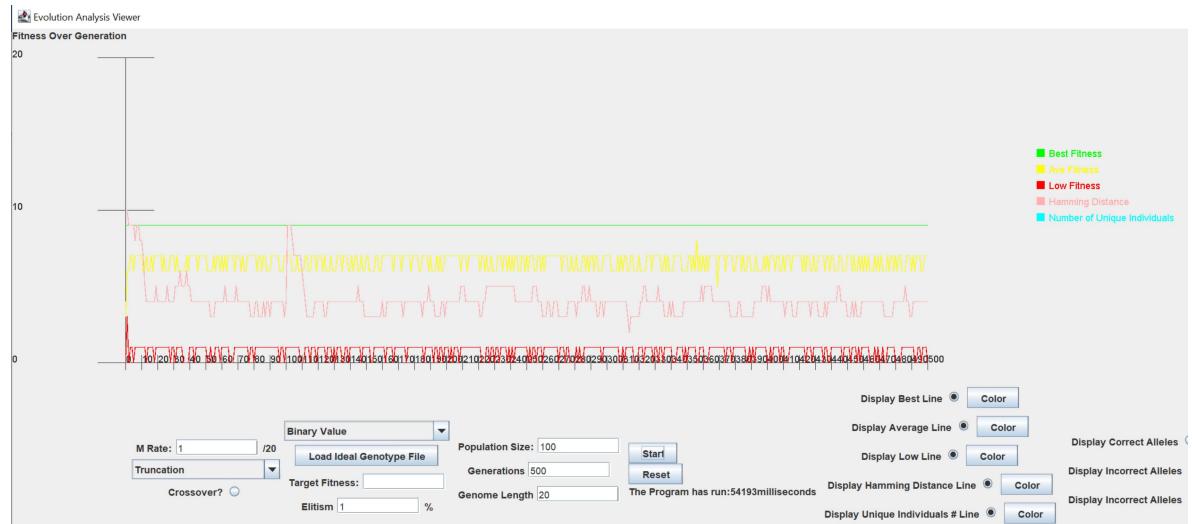


Figure 26: Typical Simulator Results for Further Experiment 1

Parameter	Value
<i>genome length:</i>	20
<i>population size:</i>	100
<i>selection:</i>	truncation selection
<i>elitism</i>	1%
<i>mutation rate:</i>	1%
<i>crossover method:</i>	false
<i>fitness method:</i>	symmetry
<i>max generations:</i>	500

Figure 27: Simulator Settings for Further Experiment 2

Trial	Number of generations to evolve a solution
1	over 500
2	over 500
3	over 500
4	over 500
5	over 500
6	over 500
7	over 500
8	over 500
9	over 500
10	over 500

Figure 28: Summary of Results of Further Experiment 2

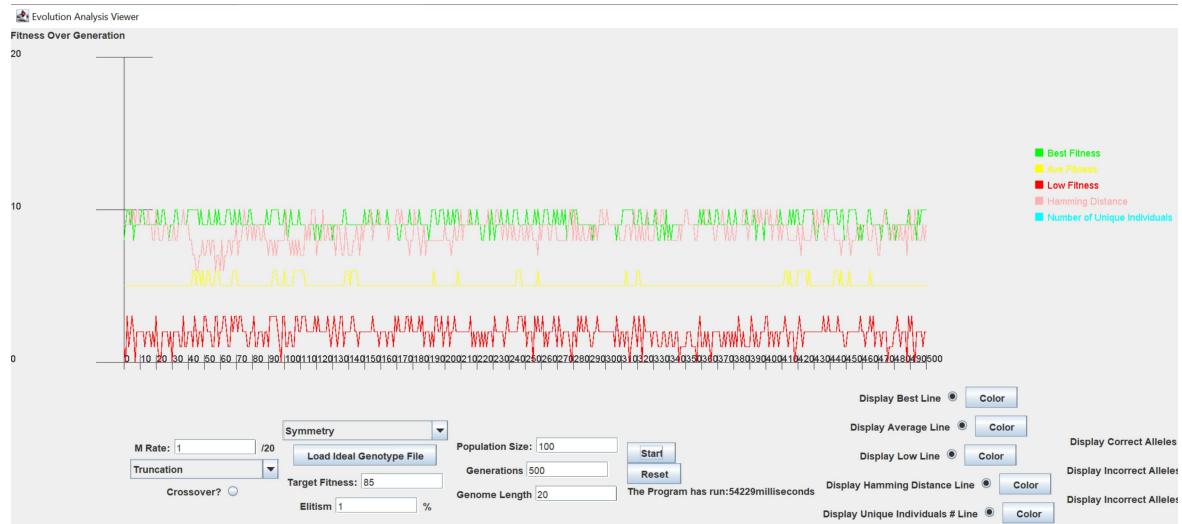


Figure 29: Typical Simulator Results for Further Experiment 2

Parameter	Value
<i>genome length:</i>	100
<i>population size:</i>	100
<i>selection:</i>	truncation selection
<i>elitism</i>	1%
<i>mutation rate:</i>	1%
<i>crossover method:</i>	false
<i>fitness method:</i>	number of 1's
<i>max generations:</i>	varied

Figure 30: Simulator Settings for Further Experiment 3

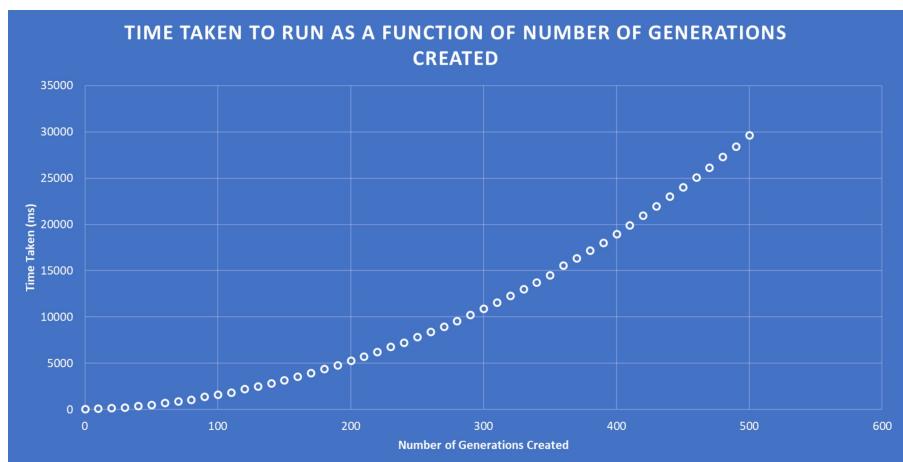


Figure 31: Simulator Settings for Further Experiment 3