COGS186: Assignment 1 Report (Genetic Algorithms and Perceptron)

Conditions:

- Population Size: 55
- Elite Size: 5
- Mutation Rate: 0.12
- Generations: 500

Experimental Data

Experiment #	Crossover Type	Fitness Type	Testing Accuracy
Crossover: ordered | Fitness: numcorrect			
1	ordered	numcorrect	0.8947368421052632
2	ordered	numcorrect	0.8947368421052632
3	ordered	numcorrect	0.8421052631578947
4	ordered	numcorrect	0.8947368421052632
5	ordered	numcorrect	0.8859649122807017
Crossover: ordered | Fitness: perceptron_fitness			
1	ordered	perceptron_fitness	0.8947368421052632
2	ordered	perceptron_fitness	0.868421052631579
3	ordered	perceptron_fitness	0.9035087719298246
4	ordered	perceptron_fitness	0.8947368421052632
5	ordered	perceptron_fitness	0.9035087719298246
Crossover: your_own_crossover | Fitness : numcorrect			
1	your_own_crossover	numcorrect	0.9385964912280702
2	your_own_crossover	numcorrect	0.9035087719298246
3	your_own_crossover	numcorrect	0.8771929824561403
4	your_own_crossover	numcorrect	0.8771929824561403
5	your_own_crossover	numcorrect	0.8859649122807017
Crossover: your_own_crossover | Fitness : perceptron_fitness			
1	your_own_crossover	perceptron_fitness	0.8771929824561403
2	your_own_crossover	perceptron_fitness	0.9035087719298246
3	your_own_crossover	perceptron_fitness	0.8070175438596491
4	your_own_crossover	perceptron_fitness	0.8421052631578947
5	your_own_crossover	perceptron_fitness	0.8947368421052632
Crossover: your_own_crossover | Fitness : numcorrect			
1	your_own_crossover2	numcorrect	0.9210526315789473
2	your_own_crossover2	numcorrect	0.9210526315789473
3	your_own_crossover2	numcorrect	0.8947368421052632
4	your_own_crossover2	numcorrect	0.9122807017543859
5	your_own_crossover2	numcorrect	0.8947368421052632
Crossover: your_own_crossover2 | Fitness : perceptron_fitness			
1	your_own_crossover2	perceptron_fitness	0.9473684210526315
2	your_own_crossover2	perceptron_fitness	0.868421052631579
3	your_own_crossover2	perceptron_fitness	0.8859649122807017
4	your_own_crossover2	perceptron_fitness	0.9122807017543859
5	your_own_crossover2	perceptron_fitness	0.9035087719298246

Perceptron with gradient descent Testing Accuracy: 0.8859649122807017

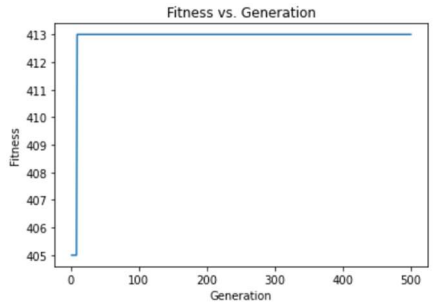
Average Testing Accuracies

Ranking	Method	Average Testing Accuracy
1	GA: your_own_crossover2/numcorrect	0.908771929824561
2	GA: your_own_crossover2/perceptron_fitness	0.903508771929824
3	GA: your_own_crossover/numcorrect	0.896491228070175
4	GA: ordered/perceptron_fitness	0.892982456140351
5	Perceptron w/ Gradient Descent	0.885964912280701
6	GA: ordered/numcorrect	0.882456140350877
7	GA: your_own_crossover/perceptron_fitness	0.864912280701754

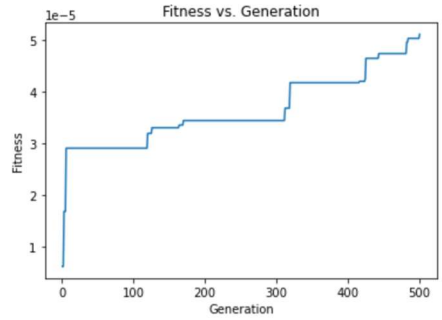
Fitness vs. Generation Curves

The fitness vs. generation curves for the different combinations for the genetic algorithm will utilize the experiment with the greatest testing accuracy. If there are multiple instances with the same testing accuracy, the first one's output will be utilized. The order of curves will follow the ranking order of the average testing accuracies (there is no curve for the Perceptron with gradient descent).

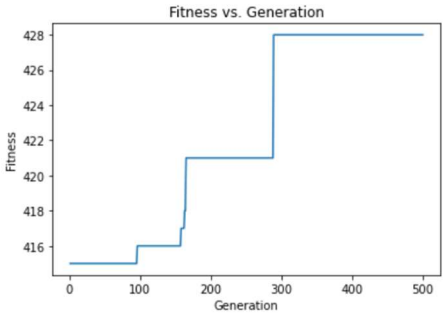
GA: your_own_crossover2/numcorrect



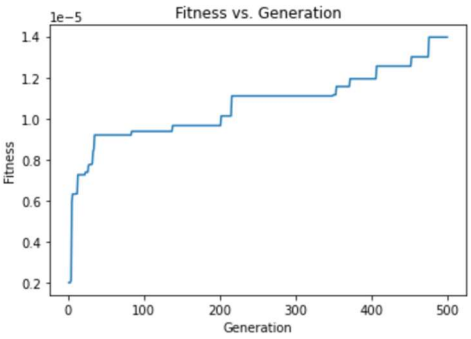
GA: your_own_crossover2/perceptron_fitness



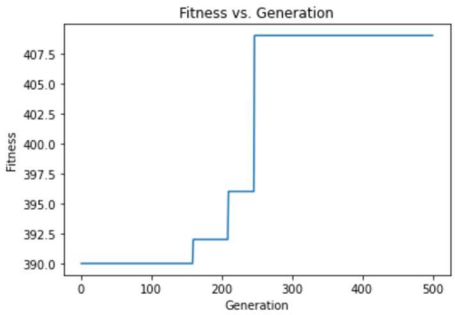
GA: your_own_crossover/numcorrect



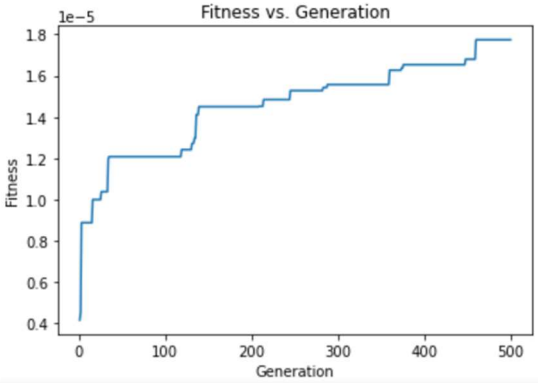
GA: ordered/perceptron_fitness



GA: ordered/numcorrect



GA: your_own_crossover/perceptron_fitness



Function Descriptions:

Mutation Function

This function takes a given Plane and based on the mutation rate given, it will determine whether to mutate the weight value. If mutation is selected to occur, the location of this is selected at random and within the given range of (-maxweight, maxweight) which in this case, maxweight=100.0, a random value ("noise") is added to the Plane. It will then return the Plane with the new, mutated weight value and original bias value.

Crossover Function 1 (your_own_crossover): Uniform Crossover

The first crossover function utilizes the concept of a uniform crossover, in which each gene is chosen from either parent plane with equal probability. Thus, for each position there is a 0.5 probability of the gene in the selected position being the value/gene from parent plane 1 or parent plane 2.

Crossover Function 2 (your_own_crossover2): One-Point Crossover

The second crossover function does a one-point crossover, in which a point is selected at random on parent plane 1. Everything up to this point location will be the values from parent plane 1; everything to the right of this point will be genes/values from parent plane 2. The point is completely random.