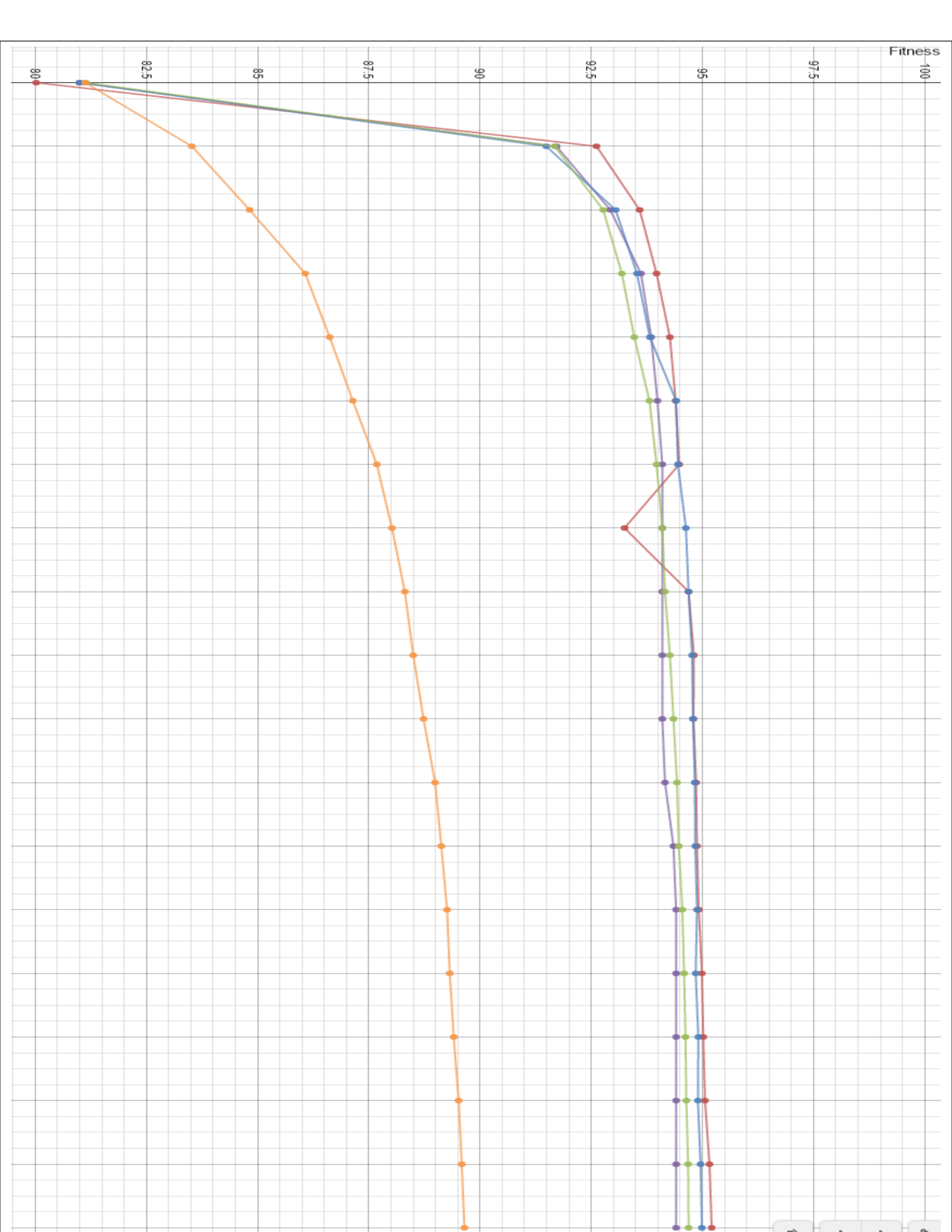# Graph Two

Different Ratios of Crossover and Hill Climbing

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(Note the X axis is shifted vertically so the data is more viewable, also the X axis is the time in minutes passed where each data point represents a jump in 10 minutes)

NOTE: Each data point represents a jump in 10 minutes on the x axis.

Key:

Table of Pure Hill Climbing Points:

x_2	y_2
0	80.99
1	91.72
2	92.93
3	93.62
4	93.85
5	93.99
6	94.10
7	94.10
8	94.10
9	94.10
10	94.10
11	94.16
12	94.35
13	94.41
14	94.41
15	94.41
16	94.41
17	94.41
18	94.41

Table of Pure Crossover Points:

x_3		y_3
0		81.12
1		83.52
2		84.82
3		86.07
4		86.62
5		87.14
6		87.68
7		88.02
8		88.31
9		88.50
10		88.73
11		88.99
12		89.13
13		89.26
14		89.32
15		89.41
16		89.52
17		89.59
18		89.65

Table of Crossover after every 1500 generations:

x	y_1
0	80.02
1	92.62
2	93.59
3	93.97
4	94.27
5	94.40
6	94.48
7	93.25
8	94.69
9	94.81
10	94.80
11	94.86
12	94.88
13	94.92
14	94.99
15	95.02
16	95.06
17	95.16
18	95.21

Table of Cross over after every 3000 generations:

x_4	y_4
0	81.00
1	91.49
2	93.05
3	93.53
4	93.82
5	94.41
6	94.45
7	94.63
8	94.69
9	94.77
10	94.79
11	94.83
12	94.84
13	94.88
14	94.85
15	94.91
16	94.90
17	94.96
18	94.99

Table of Crossover after every 5000 generations:

x_5	y_5
0	81.14
1	91.68
2	92.77
3	93.19
4	93.47
5	93.81
6	93.97
7	94.10
8	94.16
9	94.27
10	94.35
11	94.43
12	94.47
13	94.55
14	94.59
15	94.62
16	94.64
17	94.68
18	94.69

(Note the cross over performed after N number of generations is a total of 205)

Examples of some progression photos to gauge the meaning of the fitness levels:

Current Best Fitness: 91.72187223276407

Current Best Fitness: 94.41743265378939

Description of what the graph is showing/conclusion:

Following our testing we have found that the best combination of crossover to hill climbing for our tests was doing cross over for 205 generations every 1500 hill climbing generations. Also note if you look at the red line in the graph there is a dip at one part of the graph this is a result of some of the methodology we put in place (Described below in the answers to the questions).

Questions:

What mutations were used in the hill climbing?

The mutations that were used in our hill climbing include single mutations of either the alpha, red, blue, or green value or a single mutation in one of the x/y values in one of the vertices of the triangle. We were thinking about implementing mutations of translation and order shifting but we thought sticking with just the basic required mutations made the creation of the adaptive hill climbing more intuitive and simplistic.

What was adaptive about the adaptive hill climbing and what heuristics were used in the adaptation?

Firstly the algorithm is given a genome which will be used for hill climbing. With the given genome mutate a random gene to a random value within range of the respective gene (stochastic element). Following the mutation determine whether that mutation was an improvement in the genomes fitness. **If the mutation results in an improvement obtain the direction of the random mutation and begin to adaptively mutate in that direction in incremental step sizes starting at one doing the same type of mutation (probability changes from equal distribution to solely the beneficial mutation). If the mutation of the adaptive step size results in an improved fitness increment the step size while staying below its defined max, and perform a mutation with the new step size. Continue to perform mutations in the same direction on the same gene in the same triangle in incremental step sizes (caps out at defined max) until one of the mutations results in no improvement in the genomes fitness.** Once this occurs find a new random gene mutation resulting in improvement and begin to adaptively mutate in the new direction with the new triangle and gene in an incremental fashion (step size starts at one again). This process repeats continuously during the hill climbing.

The reason we added the stochastic element was because we noticed it helped find small paths that could be adaptively climbed that would have been harder to reach without using this element of randomness. The stochastic element does not alter the fact that the hill climbing is really adaptive, for all mutations that are kept resulted from a mutation of an incremental step size in some direction with a gene in a triangle. The reason we have a cap on the step size is eventually the step size gets so large that it can skip over a section of beneficial gene that may be surrounded by unbeneficial genes, which happens with the color ranges mostly. Also capping the

step size does not negatively affect performance or any other elements of the hill climbing process.

How often was each type of cross-over used?

We ended up doing an equal distribution of both double and single point cross over, each type of crossover has around a 50 percent probabilistic chance (via Java's random number generator) of being selected. The reason we ended up having around an equal distribution was because we found that using one or the other had minimalist impact and most of the time the impact was hard to gauge do to other factors during the programs process. We believe that in this case uniform cross over with a decent number of randomly selected cross over points might have been more beneficial because it would have introduced more gene splicing which with single or double point can only occur once or twice if the cross over point is within the genetic makeup of a single triangle. We think the increase in gene splicing would make the cross over more explorative and aid in keeping diversity.

Did your cross-over include mutation? If so, how?

Our cross over does include mutation, during cross over there is a **0.0025% chance a <u>gene</u> get mutated during cross over, for fives genes per cross over.** By mutation we mean the gene changes to a random value within its bounds. The reason we added mutation during cross over was to force diversity upon the tribes population. We could not come up with an efficient diversity check heuristic and our tribe is sorted from most to least fitness so through cross over prior to including this additional mutation the tribes population would get saturated in similar genes. But after adding this mutation added just the amount of diversity we needed in the population.

Relevant Tangent:

I think it is important to know what we wanted out of the cross over and it accomplishes what we want. For our implementation of crossover its purpose is to keep a tribal population that is similar to the genome being hill climbed with (the best genome), yet still have a reasonable amount of genetic differences. Through our cross over, both inner tribal and cross tribal (and with the gene mutation that occurs during cross over) our populations are able to achieve what purpose I just described. Then when the program gets stuck hill climbing on the best genome on the tribe for a while we force the hill climbing to happen on the next best member in the tribe. To force it to start hill climbing on the next best member in the tribe (index one since ordered by fitness) we have a random gene injection in genome we are hill climbing on and reinsert it in the tribe (pushing it back in the list) which in turn triggers the next best member to move to index zero and hill climbing starts again. This new genome being hill climbed on is very similar to the previous one usually with very small fitness differentials but it does have some genetic differences and those genetic differences usually provide enough to overcome the previous local optima.

How did your cross-over do selection? / How were genomes shared between tribes?

Once the cross over is triggered the threads are momentarily paused (pause is nanoseconds long and not noticeable). When the threads are paused each thread/tribe gathers genomes from the other tribes in an array list called globalPool. Each tribe will end up getting its own unique global pool and these are recreated every time the cross over is triggered pooling the latest genomes from the tribal populations. Each global pool consists of 5(NumThreads-1) +100 genomes, to increase probability of cross over occurring with the other tribes best genomes the global pool is filled with 5 copies of each of the other tribes best genome (except for the tribe who the pool is for). After that the rest of the genomes in each of the pools are obtained by first randomly selecting a tribe and then randomly selecting one of the genomes to add to the pool. After each tribe/thread has their global pool created the pools are set into the threads GA objects and then the threads are un paused and then cross over starts. Using the global pool given to each tribe the tribe performs cross over with each member of the global pool and a random member of their own tribe (cross tribal cross over). There currently is an equally weighted chance of single or double point cross over occurring. Immediately after the cross tribal cross over inner tribal cross over occurs where the tribe performs cross over 100 times (again with an equally weighted chance of either single point or double point cross over) with random members of the tribes population. As for the actual cross over itself, we added the chance of mutation occurring during cross over.

What caused switching between hill climbing and cross-over?

The switching is triggered after around 1500 generations (if currently adaptively mutating a gene it will wait till it stops with a non-beneficial mutation.)