Colin Conn

While creating an SGA for the Rosenbrock function, I decided to represent the genomes as a 12 bit string, with the first six bits of the string being the value for x and the last six bits being the value of y. I set the fitness of the function by dividing 100 by the result of the rosenbrock function plus one. I added one to the result of the function because my understanding of the function is its minimum result is 0. I wanted to divide the result by a constant so a higher fitness was denoted by a higher number. If I didn’t add the extra one, then there was a possibility of a dividing by zero error in the situation that the function was minimized. I’m not sure that my function works as intended, however, I have had several test runs of 10000 generations where the highest fitness in the last generation was a perfect 100. However, I also had situations where the champion fitness was higher than 100 by a tiny decimal, which should not have been possible. I also had trouble getting the percentage of identical genomes to work, so I couldn’t find out how close the population was to converging.