Homework 3:

Find the new population and discuss the effect for only changing:

1. Crossover rate = CR = 0.7, 0.8, 0.9, 1
2. Mutate rate = MR = 0.04, 0.06, 0.08
3. Elite = E =0

**Answer**:

To find the new population and see the effect for changing crossover rate, mutation rate and elitism each of the population was generated based on identical base population with fitness value computed by the same fitness function:

bit\_length = 8;

range = [0; 100];

base\_popu = GA\_initpopu(10, bit\_length, 1);

crossover\_rate = [0; 0.7; 0.8; 0.9; 1];

mutate\_rate = [0; 0.04; 0.06; 0.08];

elite = [0; 1];

[fitness, popu\_real, popu] = GA\_fitpopu(base\_popu, bit\_length, range, 'GA\_fitfun3x');

disp(['Base population']);

disp(popu);

disp(['Base population real']);

disp(popu\_real);

disp(['Base population fitness']);

disp(transpose(fitness));

for cr\_index=2:length(crossover\_rate)

[fitness, popu\_real, popu] = GA\_fitpopu(base\_popu, bit\_length, range, 'GA\_fitfun3x');

[fitness, popu\_real, popu] = GA\_fitpopu(GA\_newpopu(popu, fitness, bit\_length, ...

crossover\_rate(cr\_index), mutate\_rate(1), elite(1)), bit\_length, range, 'GA\_fitfun3x');

disp(['CR = ',num2str(crossover\_rate(cr\_index))]);

disp(popu);

disp(popu\_real);

disp(transpose(fitness));

end

for mr\_index=2:length(mutate\_rate)

[fitness, popu\_real, popu] = GA\_fitpopu(base\_popu, bit\_length, range, 'GA\_fitfun3x');

[fitness, popu\_real, popu] = GA\_fitpopu(GA\_newpopu(popu, fitness, bit\_length, ...

crossover\_rate(1), mutate\_rate(mr\_index), elite(1)), bit\_length, range, 'GA\_fitfun3x');

disp(['MR = ',num2str(mutate\_rate(mr\_index))]);

disp(popu);

disp(popu\_real);

disp(transpose(fitness));

end

for e\_index=1:length(elite)

[fitness, popu\_real, popu] = GA\_fitpopu(base\_popu, bit\_length, range, 'GA\_fitfun3x');

[fitness, popu\_real, popu] = GA\_fitpopu(GA\_newpopu(popu, fitness, bit\_length, ...

crossover\_rate(2), mutate\_rate(1), elite(e\_index)), bit\_length, range, 'GA\_fitfun3x');

disp(['E = ',num2str(elite(e\_index))]);

disp(popu);

disp(popu\_real);

disp(transpose(fitness));

end

**Output:**

For readability output was organized into the tables and the effects of changing parameters are discussed below the tables.

Crossover rate

|  |  |  |  |
| --- | --- | --- | --- |
| Crossover rate | Population | Population Real | Fitness |
| Base population | 1 1 1 0 1 1 1 1  1 1 0 0 1 0 1 1  1 0 1 1 0 0 1 1  1 0 1 1 0 0 0 1  1 0 1 0 1 0 1 0  0 1 1 1 1 1 1 0  0 1 1 1 1 1 0 0  0 1 1 1 0 1 1 0  0 0 1 0 1 0 1 0  0 0 0 1 1 1 1 1 | 93.7255  79.6078  70.1961  69.4118  66.6667  49.4118  48.6275  46.2745  16.4706  12.1569 | 8.2333  5.0451  3.4589  3.3443  2.9630  1.2064  1.1499  0.9909  0.0447  0.0180 |
| 0.7 | **1 1 1 0 1 1 1 1**  **1 1 1 0 1 1 1 1**  **1 1 1 0 1 1 1 1**  1 1 0 0 1 0 1 0  **1 0 1 1 0 0 1 1**  **1 0 1 1 0 0 1 1**  1 0 1 1 0 0 0 1  1 0 1 1 0 0 0 1  1 0 1 1 0 0 0 1  1 0 1 0 1 0 1 1 | **93.7255**  **93.7255**  **93.7255**  79.2157  **70.1961**  **70.1961**  69.4118  69.4118  69.4118  67.0588 | **8.2333**  **8.2333**  **8.2333**  4.9709  **3.4589**  **3.4589**  3.3443  3.3443  3.3443  3.0156 |
| 0.8 | 1 1 1 0 1 1 1 0  1 1 1 0 1 0 0 1  **1 1 0 0 1 0 1 1**  **1 1 0 0 1 0 1 1**  **1 1 0 0 1 0 1 1**  1 0 1 1 0 1 1 1  **1 0 1 1 0 0 1 1**  1 0 1 1 0 0 0 0  1 0 1 0 1 0 1 1  0 1 1 1 1 1 1 1 | 93.3333  91.3725  **79.6078**  **79.6078**  **79.6078**  71.7647  **70.1961**  69.0196  67.0588  49.8039 | 8.1304  7.6286  **5.0451**  **5.0451**  **5.0451**  3.6960  **3.4589**  3.2879  3.0156  1.2354 |
| 0.9 | 1 1 1 1 0 1 1 0  1 1 1 0 1 1 0 1  1 1 1 0 1 1 0 1  **1 0 1 1 0 0 1 1**  **1 0 1 1 0 0 1 1**  1 0 1 1 0 0 1 0  1 0 1 1 0 0 0 1  **1 0 1 0 1 0 1 0**  1 0 1 0 1 0 0 1  0 0 1 1 0 0 1 1 | 96.4706  92.9412  92.9412  **70.1961**  **70.1961**  69.8039  69.4118  **66.6667**  66.2745  20.0000 | 8.9781  8.0283  8.0283  **3.4589**  **3.4589**  3.4013  3.3443  **2.9630**  2.9110  0.0800 |
| 1 | 1 1 1 1 0 0 0 1  1 1 1 0 1 1 0 1  1 1 1 0 1 0 0 1  1 1 1 0 0 1 1 0  1 0 1 1 1 0 1 0  1 0 1 1 0 1 1 1  1 0 1 1 0 0 1 1  1 0 1 0 1 1 1 1  1 0 1 0 1 0 0 1  1 0 1 0 0 0 1 1  0 1 1 1 1 1 1 1 | 94.5098  92.9412  91.3725  90.1961  72.9412  71.7647  70.1961  68.6275  66.2745  63.9216  49.8039 | 8.4417  8.0283  7.6286  7.3378  3.8808  3.6960  3.4589  3.2322  2.9110  2.6118  1.2354 |

Bolded chromosomes are chromosomes that remained unchanged after finding new population.

The bigger the crossover rate is the less chromosome remain unchanged. For the crossover rate = 1 all the chromosomes were generated by combining chromosomes from the base population (by combining 3 bits of the first parent and 5 bits of the second parent.

Applying crossover to all population will produce more random results.

The conclusion is that too low crossover rate will not help the algorithm to get out of local extrema but it does not mean that bigger crossover rate guarantees better results.

Mutation rate

|  |  |  |  |
| --- | --- | --- | --- |
| Mutation rate | Population | Population Real | Fitness |
| Base population | 1 1 1 0 1 1 1 1  1 1 0 0 1 0 1 1  1 0 1 1 0 0 1 1  1 0 1 1 0 0 0 1  1 0 1 0 1 0 1 0  0 1 1 1 1 1 1 0  0 1 1 1 1 1 0 0  0 1 1 1 0 1 1 0  0 0 1 0 1 0 1 0  0 0 0 1 1 1 1 1 | 93.7255  79.6078  70.1961  69.4118  66.6667  49.4118  48.6275  46.2745  16.4706  12.1569 | 8.2333  5.0451  3.4589  3.3443  2.9630  1.2064  1.1499  0.9909  0.0447  0.0180 |
| 0.04 | 1 1 1 *1*  1 1 *0 0*  1 1 *1*  0 1 0 1 1  **1 1 0 0 1 0 1 1**  **1 0 1 1 0 0 1 1**  **1 0 1 1 0 0 0 1**  **1 0 1 0 1 0 1 0**  **0 1 1 1 1 1 1 0**  **0 1 1 1 0 1 1 0**  **0 0 1 0 1 0 1 0**  0 0 0 1 1 *0* 1 1 | 98.8235  92.1569  **79.6078**  **70.1961**  **69.4118**  **66.6667**  **49.4118**  **46.2745**  **16.4706**  10.5882 | 9.6512  7.8268  **5.0451**  **3.4589**  **3.3443**  **2.9630**  **1.2064**  **0.9909**  **0.0447**  0.0119 |
| 0.06 | **1 1 1 0 1 1 1 1**  **1 1 0 0 1 0 1 1**  **1 0 1 1 0 0 1 1**  **1 0 1 1 0 0 0 1**  **1 0 1 0 1 0 1 0**  **0 1 1 1 1 1 1 0**  **0 1 1 1 1 1 0 0**  **0 1 1 1 0 1 1 0**  **0 0 1 0 1 0 1 0**  **0 0 0 1 1 1 1 1** | **93.7255**  **79.6078**  **70.1961**  **69.4118**  **66.6667**  **49.4118**  **48.6275**  **46.2745**  **16.4706**  **12.1569** | **8.2333**  **5.0451**  **3.4589**  **3.3443**  **2.9630**  **1.2064**  **1.1499**  **0.9909**  **0.0447**  **0.0180** |
| 0.08 | 1 1 1 1 1 0 0 1  1 0 1 1 0 0 1 0  1 0 1 0 1 1 1 1  **1 0 1 0 1 0 1 0**  1 0 1 0 0 0 0 0  1 0 0 1 1 0 1 1  **0 1 1 1 1 1 0 0**  **0 1 1 1 0 1 1 0**  0 0 1 1 1 1 1 0  0 0 1 0 0 0 1 1 | 97.6471  69.8039  68.6275  **66.6667**  62.7451  60.7843  **48.6275**  **46.2745**  24.3137  13.7255 | 9.3106  3.4013  3.2322  **2.9630**  2.4702  2.2458  **1.1499**  **0.9909**  0.1437  0.0259 |

Bolded chromosomes are chromosomes that remained unchanged after finding new population.

By increasing mutation rate we increase the possibility that a single chromosome will be mutated. For 0.04 rate it was possible to find the bits that seem to have mutated (*underlined italic bits)* but the same wasn’t possible for 0.08 rate (too many bits have changed to identify that). It seems plausible, that 5 bits changed because 5/80 bits (0.05) is close to mutation rate 0.04. It also shows, that these chromosomes were produced by crossing-over the best two chromosomes.

The base population remained unchanged in case of 0.06 rate, meaning that either no mutation occurred or mutation cancelled mutation rate effect out, e.g.:

1 1 1 1 1 0 0 1 > mutate > 1 0 1 1 0 0 1 0

1 0 1 1 0 0 1 0 > mutate > 1 1 1 1 1 0 0 1

as the Hamming distance of these chromosomes is small.

Even if no mutation actually occurred, it does not mean that the results are invalid, because mutation rate 0.06 means that on average 6 in 100 bits will be changed. It would be seldom but possible that no mutation occurred and very rare but still possible that mutation of e.g. all the bits occurred.

It is another method to help GA get out of local extrema. Applying mutation produces random results so overly big mutation rate might make algorithm work randomly.

Elitism

|  |  |  |  |
| --- | --- | --- | --- |
| Elitism | Population | Population Real | Fitness |
| Base population | **1 1 1 0 1 1 1 1**  **1 1 0 0 1 0 1 1**  1 0 1 1 0 0 1 1  1 0 1 1 0 0 0 1  1 0 1 0 1 0 1 0  0 1 1 1 1 1 1 0  0 1 1 1 1 1 0 0  0 1 1 1 0 1 1 0  0 0 1 0 1 0 1 0  0 0 0 1 1 1 1 1 | **93.7255**  **79.6078**  70.1961  69.4118  66.6667  49.4118  48.6275  46.2745  16.4706  12.1569 | **8.2333**  **5.0451**  3.4589  3.3443  2.9630  1.2064  1.1499  0.9909  0.0447  0.0180 |
| FALSE | 1 1 1 1 1 1 1 0  **1 1 1 0 1 1 1 1**  **1 1 1 0 1 1 1 1**  1 1 1 0 1 0 1 0  **1 0 1 1 0 0 1 1**  **1 0 1 1 0 0 0 1**  1 0 1 0 1 1 1 1  0 1 1 0 1 1 1 1  0 0 1 0 1 0 1 0  0 0 0 1 1 1 1 1 | 99.6078  **93.7255**  **93.7255**  91.7647  **70.1961**  **69.4118**  68.6275  43.5294  16.4706  12.1569 | 9.8828  **8.2333**  **8.2333**  7.7273  **3.4589**  **3.3443**  3.2322  0.8248  0.0447  0.0180 |
| TRUE | **1 1 1 0 1 1 1 1**  **1 1 1 0 1 1 1 1**  **1 1 1 0 1 1 1 1**  1 1 1 0 1 0 1 1  1 1 1 0 1 0 1 1  1 1 0 0 1 1 1 1  1 1 0 0 1 1 1 0  **1 1 0 0 1 0 1 1**  1 0 1 1 0 1 1 1  0 1 1 1 1 0 1 1 | **93.7255**  **93.7255**  **93.7255**  92.1569  92.1569  81.1765  80.7843  **79.6078**  71.7647  48.2353 | **8.2333**  **8.2333**  **8.2333**  7.8268  7.8268  5.3492  5.2721  **5.0451**  3.6960  1.1223 |

Bolded chromosomes are chromosomes that remained unchanged after finding new population.

Underlined chromosomes are 1st or 2nd best chromosomes in the initial population.

Elitism prevents the best genes to disappear. In the case of GA\_newpopu.m two best chromosomes are preserved by elitism.

In the case of Elitism = FALSE the best gene is preserved only because it has higher chances to stay in roulette wheel selection. The second best gene was not preserved. Because the first chromosome is much better than other chromosomes in terms of fitness, it’s repeated twice and only two other genes are passed to new population.

In the case of Elitism = TRUE two best genes were preserved because of elitism. Because the first chromosome is significantly better than the second best chromosome, the first chromosome is repeated more times.

Elitism will prevent mutation or crossover to eliminate the best chromosomes.