7CCSMDBIM Nature-Inspired Learning Algorithms

Assignment 2

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s_1	s_2	s_3	s_4	s_5	s_6	s_7
2	0	1	1	3	3	7

Table 1: First 7 digits of student ID

Question 1

Selection within the Genetic Algorithm is the process of selecting "parents" from a population of individuals to perform crossover in order to create new individuals within the population, the "children". Tournament Selection is a selection strategy. In K-Way tournament selection, we select at random K individuals from the population. From the K selected individuals chosen for the tournament we select the "fittest" individual using a fitness function. During Tournament Selection, multiple "tournaments" are carried out.

The Tournament Selection method has *selection pressure* which is a probabilistic measure of the likelihood a candidate is chosen for a tournament. The selection pressure is adjusted via the tournament size parameter. The larger the tournament size, the lower the probability weaker individuals have of being selected as there is a higher probability that a weaker individual will be competing against a stronger individual in the tournament.

Figure 1, shows an example of Tournament Selection where K, the size of the tournament is 3. From the population of size 10, 3 individuals, F, A and C are chosen at random. F, A and C now constitute the tournament. The fitness functions of the members of the tournament are compared and the member with the highest fitness function is selected for crossover. Individual F which has the highest fitness function of value 8 is therefore chosen.
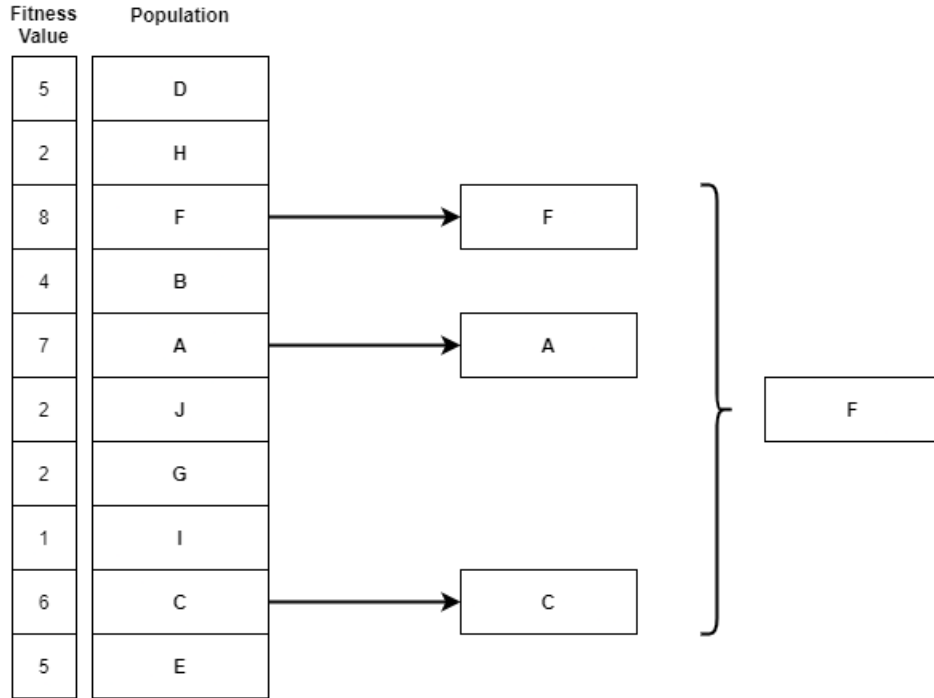
Figure 1: K=3 Tournament Selection example

Question 2

a.

In order to obtain a probability table we first define our cost function. The cost function is defined as $f(x, y) = xy$.

The initial population is then decoded. Each chromosome is split into a pair of 4 bits where each 4 bit element of the pair is decoded. In order to decode the x and y values we use the equation below.

$$Decoding \ x(n) = x_{lo} + decimal(Chromosome(n)) * \left(\frac{x_{hi} - x_{lo}}{2^m - 1}\right)$$

As each decision variable is represented by a 4-bit binary string $m = 4$. The h_i and l_o values are shown in the Table 2.

	lo	hi
x	10	13
y	-5	2

Table 2: hi and lo values

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Table 3 below outlines the decoded x and y values of the initial population.

Example decoding:
Chromosome = 1000 1100 , $m = 1$

$$Decoding \ x(n) = x_{lo} + decimal(Chromosome(n)) * \left(\frac{x_{hi}-x_{lo}}{2^m-1}\right)$$

$$Decoded \ (x) = 10 + 8 * \left(\frac{13-10}{16-1}\right)$$

$$Decoded \ (x) = 10 + 8 * \left(\frac{3}{15}\right) = 11.6$$

$$Decoding \ y(n) = y_{lo} + decimal(Chromosome(n)) * \left(\frac{y_{hi}-y_{lo}}{2^m-1}\right)$$

$$Decoded \ (y) = -5 + 12 * \left(\frac{2-(-5)}{16-1}\right)$$

$$Decoded \ (y) = -5 + 12 * \left(\frac{7}{15}\right) = 0.6$$

Chromosome	Decoded Population (x, y)
10001100	11.6, 0.6
01101011	11.2, 0.1333
01111010	11.4, -0.3333
01010100	11.0, -3.1333

Table 3: Decoded initial population

Once the x and y values have been decoded, we calculate cost using the pre-defined cost function $f(x, y) = xy$. Table 4 displays the costs for each pair of x and y.

Example cost calculation:
$x = 11.6$, $y = 0.6$

$$f(x, y) = xy$$

$$f(11.6, 0.6) = 11.6 * 0.6 = 6.96$$

Chromosome	Decoded Population (x, y)	c_n
10001100	11.6, 0.6	6.96
01101011	11.2, 0.1333	1.493
01111010	11.4, -0.3333	-3.7996
01010100	11.0, -3.1333	-34.4663

Table 4: Cost calculation for initial population

With the calculated costs of each individual of the population having been calculated we rank the population by ascending order of their costs. Table 5 shows the ranked population.

Chromosome	Decoded Population (x, y)	c_n
01010100	11.0, -3.1333	-34.4663
01111010	11.4, -0.3333	-3.7996
01101011	11.2, 0.1333	1.493
10001100	11.6, 0.6	6.96

Table 5: Ranked population by cost

Once the costs have been calculated and the population ranked in ascending order we then calculate the normalised costs for each member of the population. The normalised costs are calculated using the equation, $C_n = c_n - 2 * |c_{Npop}|$ where c_{Npop} is now the worst cost (highest value), these normalised costs are shown in Table 6.

Example cost normalisation:
$c_n = -34.4663$

$$C_n = c_n - 2 * |c_{Npop}|$$

$$C_n = -34.4663 - 2 * 6.96 = \text{-48.3863}$$

Chromosome	Decoded Population (x, y)	c_n	C_n
01010100	11.0, -3.1333	-34.4663	-48.3863
01111010	11.4, -0.3333	-3.7996	-17.7196
01101011	11.2, 0.1333	1.493	-12.427
10001100	11.6, 0.6	6.96	-6.96

Table 6: Normalised costs for the population

The probability, P_n and cumulative probability is then calculated. The probability is calculated using the equation below, which divides each individual's cost by the sum of all the costs of the population. The findings of which are outlined in Table 7.

$$P_n = \left| \frac{C_n}{\sum_{m=1}^{Npop} Cm} \right|$$

Example probability calculation:

$C_n = -48.3863$

$$P_n = \frac{-48.3863}{-85.4929} = 0.566$$

Chromosome	Decoded Population (x, y)	c_n	C_n	P_n	$\sum_{i=1}^{n} P_n$
01010100	11.0, -3.1333	-34.4663	-48.3863	0.566	0.566
01111010	11.4, -0.3333	-3.7996	-17.7196	0.2073	0.7733
01101011	11.2, 0.1333	1.493	-12.427	0.1454	0.9187
10001100	11.6, 0.6	6.96	-6.96	0.0814	1.0

Table 7: Probability and cumulative probability of the population

b.

Given a random sequence of numbers {0.7,0.2,0.8,0.9,0.2,0.1} where the left most number is generated first, two chromosomes were selected as parents to undergo crossover. The ordered cumulative probability of the chromosomes are drawn on a equally spaced number line, each parent having their respective bounds.

The random numbers are assigned on the number line where their value is less than the cumulative probability for the next parent but greater than that of the parent before. Figure 2 shows the described number line with plotted random numbers.
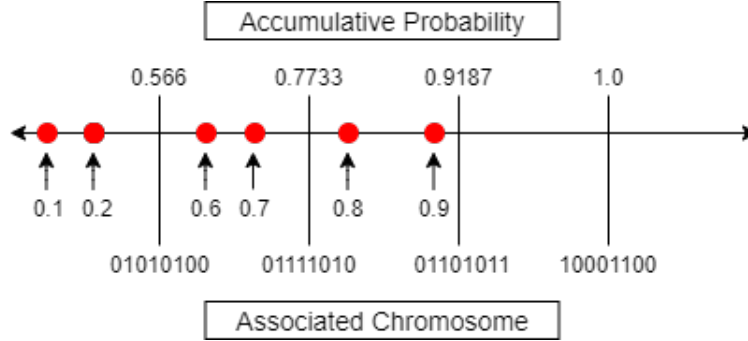

Figure 2: Number line and plotted random numbers

The chromosomes 01010100 and 01111010 are selected as parents to undergo crossover. Allocating the random numbers to the bounds of the chromosomes sequentially beginning at the left most number the bound for chromosome 01111010 was the first to have two of the random numbers to be associated with its bound and the chromosome 01010100 has three random numbers within it's bounds compared to 01101011 which has two.

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c.

Double-point crossover was applied to the parents 01010100 and 01111010. The first crossover point is after the 3rd bit and the second crossover point is before the 7th bit of the chromosome. Table 8 outlines the parent's crossover points and the resulting offspring from double-point crossover.

Chromosome 1	010 | 101 | 00
Chromosome 2	011 | 110 | 10
Offspring 1	010 | 110 | 00
Offspring 2	011 | 101 | 10

Table 8: Offspring of double-point crossover

After the double-point crossover has been applied, two offspring are produced. The resulting offspring are Offspring 1: (01011000) and Offspring 2: (01110110).

d.

We can calculate how many bits in the population will be mutated using the equation $\#mutation = \mu N_{pop} N_{bits}$. We calculate the number of bits which will be mutated below.

$\mu = 0.1$, $N_{pop} = 4$, $N_{bits} = 8$

$$\#mutation = \mu N_{pop} N_{bits}$$

$$\#mutation = 0.1 * 4 * 8 = 3.2 \approx 3$$

Question 3

a.

For the function $f(x, y) = (x - y)^2$ which is constrained by $x \geq 10y$.

- The function formulated as a minimisation function:

$$\min_{x,y} f(x, y) = -(x - y)^2 \text{ subject to x - 10y} \geq 0$$

- The penalised cost function for the minimisation function:

$f(x, y) = -(x - y)^2 + \lambda_1 c_1$

$$c_1 = \begin{cases} |x - 10y| & \text{if } x - 10y < 0 \\ 0 & \text{otherwise} \end{cases}$$

$$\lambda_1 = 10$$

b.

Considering $5 \le x \le 5 + (s_1 + s_2 + s_3)$ and $-10 \le y \le 10 + (s_4 + s_5)(s_6 + s_7)$ we are able to calculate the hi and lo values for each variable and as a consequence calculate the number of bits. Below we show the calculations to achieve the number of bits for each variable.

Calculating the number of bits for x:
$s_1 = 2, \ s_2 = 0, \ s_3 = 1$

$$5 \le x \le 5 + (s_1 + s_2 + s_3)$$

$$5 \le x \le 5 + (2 + 0 + 1)$$

$$5 \le x \le 8$$

$hi = 8, lo = 5, d = 1$

$$\#\text{Bits}(x) = \left\lceil \frac{log\left(\frac{(x_{hi} - x_{lo})}{(10^{-d})} + 1\right)}{log(2)} \right\rceil$$

$$\#\text{Bits}(x) = \left\lceil \frac{log\left(\frac{(8-5)}{(10^{-1})} + 1\right)}{log(2)} \right\rceil$$

$$\#\text{Bits}(x) = 4.95 \approx 5$$

Calculating the number of bits for y:
$s_4 = 1, \ s_5 = 3, \ s_6 = 3, \ s_7 = 7$

$$-10 \le y \le 10 + (s_4 + s_5)(s_6 + s_7)$$

$$-10 \le y \le 10 + (1 + 3)(3 + 7)$$

$$-10 \le y \le 50$$

$hi = 50, lo = -10, d = 1$

$$\#\text{Bits}(y) = \left\lceil \frac{log\left(\frac{(x_{hi} - x_{lo})}{(10^{-d})} + 1\right)}{log(2)} \right\rceil$$

$$\#\text{Bits}(y) = \left\lceil \frac{log\left(\frac{(50 - (-10))}{(10^{-2})} + 1\right)}{log(2)} \right\rceil$$

$$\#\text{Bits}(y) = 12.55 \approx 13$$

Given the above calculations, the variable x would have 5 total bits and y would have 13 total bits. The chromosomes can be represented in the form $[x, y]$ as x and y are both decision variables and therefore have a direct effect on the cost defined in part a of the question. The size of the chromosome would be calculated by adding the total bits of x and y, the total number of bits for the chromosome being 18.

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Question 4

With the variables $x_1(t) = 2$, $x_2(t) = -1$, $\sigma_1(t) = 0.1$ and $\sigma_2(t) = 0.3$ at the tth generation, we can determine the population and strategy at the next generation when minimising the function $f(x_1, x_2) = x_1 - x_2$ using both $(1+1)$-ES and $(1,1)$-ES given the mutation process:

$$\text{Offspring: } x'_j(t) = x_j(t) + \sigma_j(t)N_j, j = 1, 2,$$

$$\text{Strategy parameter: } \sigma'_j(t) = 0.5\left(1 + \frac{s_1 + s_2}{s_1 + s_2 + s_3}\right)\sigma_j(t), j = 1, 2,$$

Next generation calculations:

$x_1(t) = 2$, $x_2(t) = -1$, $\sigma_1(t) = 0.1$ and $\sigma_2(t) = 0.3$

$$f(x_1, x_2) = x_1 - x_2$$
$$f(2, -1) = 2 - (-1) = 3$$

$$\sigma'_j(t) = 0.5\left(1 + \frac{s_1 + s_2}{s_1 + s_2 + s_3}\right)\sigma_j(t), j = 1, 2,$$
$$\sigma'_1(1) = 0.5\left(1 + \frac{2+0}{2+0+1}\right)0.1 = 0.0833$$
$$\sigma'_2(2) = 0.5\left(1 + \frac{2+0}{2+0+1}\right)0.3 = 0.25$$
$$\vec{\sigma'}(t) = [0.0833, 0.25]$$

$$N_j = j(3 - j)$$
$$N_1 = 1(3 - 1) = 2$$
$$N_2 = 2(3 - 2) = 2$$

$$x'_j(t) = x_j(t) + \sigma_j(t)N_j, j = 1, 2,$$
$$x'_1(1) = 2 + 0.1 * 2 = 2.2$$
$$x'_2(2) = -1 + 0.3 * 2 = \text{-0.4}$$
$$x'(t) = [2.2, -0.4]$$

$$f'(x_1, x_2) = x_1 - x_2$$
$$f'(2.2, -0.4) = 2.2 - (-0.4) = 2.6$$

The $(1+1)$-ES selection method chooses between parents and offspring, selecting the option which yields the lowest value from the function we are minimising as the population for the next generation. The $(1,1)$-ES method selects the offspring as the population for the next generation.

Using the (1+1)-ES selection method we can determine the population and strategy at the next generation using the following logic based on the previous calculations:

(1+1)-ES, population selection:

$$x(t+1) \begin{cases} x'(t), \text{ if } f(x'(t)) < f(x(t)) \\ \qquad x(t) \text{ otherwise} \end{cases}$$

$$2.6 < 3 \ \therefore \ x(t+1) = x'(t)$$

We would select the produced offspring as the next generation's population as the output from the function we are minimising for the offspring is less than the output produced by the parent values. The next generations population is therefore $x'(t) = [2.2, -0.4]$

(1+1)-ES, strategy parameter selection:

$$\vec{\sigma}(t+1) \begin{cases} \vec{\sigma'}(t), \text{ if } f(x'(t)) < f(x(t)) \\ \qquad \sigma(t) \text{ otherwise} \end{cases}$$

$$2.6 < 3 \ \therefore \ \vec{\sigma}(t+1) = \vec{\sigma'}(t)$$

We would therefore select $\vec{\sigma'}(t)$ as the next generation's strategy parameter. The next generations strategy parameter is $\vec{\sigma}(t) = [0.0833, 0.25]$.

(1,1)-ES, population selection:

The (1,1)-ES selection method chooses the best offspring to replace the parent as the population for the next generation. As there is only one offspring in this case the population for the next generations method is $x'(t) = [2.2, -0.4]$.

(1,1)-ES, strategy parameter selection:

The (1,1)-ES selection method chooses the strategy parameter of the best offspring for the next population. Therefore the next generations strategy parameter is $\vec{\sigma}(t) = [0.0833, 0.25]$.

Question 5

a.

Figure 3 depicts a 5 node graph where the edge information is in the format dij, $\tau ij(t)$ where dij is the edge distance and $\tau ij(t)$ is the pheromone concentration.
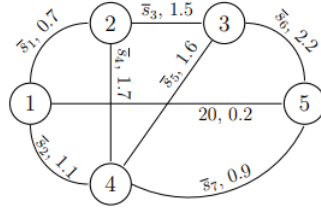

Figure 3: Five node graph

Given the above graph and assuming unidirectional edges we can determine the cost of two ants $x^1\{1, 2, 4, 5\}$ and $x^2\{1, 4, 2, 3, 5\}$. The calculations of which are outlined below.

Ant 1: $x^1(t) = \{1, 2, 4, 5\}$

$f(x^k(t)) = d_{12} + d_{24} + d_{45}$
$f(x^k(t)) = (s_1 + 1) + (s_4 + 1) + (s_7 + 1)$
$f(x^k(t)) = (3) + (2) + (8) = 13$

Ant 2: $x^2(t) = \{1, 4, 2, 3, 5\}$

$f(x^k(t)) = d_{14} + d_{42} + d_{23} + d_{35}$
$f(x^k(t)) = (s_2 + 1) + (s_4 + 1) + (s_3 + 1) + (s_6 + 1)$
$f(x^k(t)) = (1) + (2) + (2) + (4) = 9$

b.

Using the findings from the Q5.a we are able to determine the pheromone concentrations for $\tau_{24}(t + 1)$ and $\tau_{25}(t + 1)$ using the equations for pheromone evaporation and update which we outline below.

$$\text{Pheromone evaporation: } \tau_{ij}(t) \leftarrow 0.5\left(1 + \frac{s_1+s_2}{s_1+s_2+s_3}\right)\tau_{ij}(t)$$

$$\text{Pheromone update: } \tau_{ij}(t + 1) = \tau_{ij}(t) + \sum_{k=1}^{2} \Delta\tau_{ij}^k(t)$$

$$\Delta\tau_{ij}^k(t) = \begin{cases} \frac{1}{f(x^k(t))} & \text{if edge } (i, j) \text{ occurs in path } x^k(t) \\ 0 & \text{otherwise} \end{cases}$$

In order to calculate the pheromone concentration we first calculate $\tau_{ij}(t)$ after evaporation for all edges using the pheromone equation. Below we outline two tables, Table 9 with the $\tau_{ij}(t)$ values before evaporation and Table 10 with the $\tau_{ij}(t)$ after evaporation.

i,j	1	2	3	4	5
1	-	0.7	-	1.1	0.2
2	0.7	-	1.5	1.7	-
3	-	1.5	-	1.6	2.2
4	1.1	1.7	1.6	-	0.9
5	0.2	-	2.2	0.9	-

Table 9: $\tau_{ij}(t)$ for edges (i,j)

Below we show an example of the calculation for $\tau_{ij}(t)$ after evaporation has occurred.

Example pheromone evaporation calculation:
$\tau_{ij}(t) = 0.7$

$$\tau_{ij}(t) \leftarrow 0.5\left(1 + \frac{s_1+s_2}{s_1+s_2+s_3}\right)\tau_{ij}(t)$$

$$\tau_{ij}(t) \leftarrow 0.5\left(1 + \frac{2+0}{2+0+1}\right)0.7$$

$$\tau_{ij}(t) \leftarrow 0.5\left(1 + \frac{2}{3}\right)0.7 = 0.583$$

i,j	1	2	3	4	5
1	-	0.583	-	0.917	0.167
2	0.583	-	1.25	1.417	-
3	-	1.25	-	1.333	1.833
4	0.917	1.417	1.333	-	0.75
5	0.167	-	1.833	0.75	-

Table 10: $\tau_{ij}(t)$ after evaporation for edges (i,j)

Using Table 10 we are able to determine the pheromone concentrations for $\tau_{24}(t+1)$ and $\tau_{25}(t+1)$ the calculations of which are shown below.

$\tau_{24}(t+1) = 1.417 + \Delta\tau_{24}^1 + \Delta\tau_{24}^2$
$\tau_{24}(t+1) = 1.417 + \frac{1}{13} + 0 = 1.4939$

$\tau_{45}(t+1) = 0.75 + \Delta\tau_{45}^1 + \Delta\tau_{45}^2$
$\tau_{45}(t+1) = 0.75 + \frac{1}{13} + 0 = 0.8269$