

COMSM0302 - WEEK 10 SOLUTIONS

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1. EXERCISE 1 - MIXING MATRIX FOR POINT MUTATION

$$U = \begin{pmatrix} 1 - \mu & \frac{\mu}{2} & \frac{\mu}{2} & 0 \\ \frac{\mu}{2} & 1 - \mu & 0 & \frac{\mu}{2} \\ \frac{\mu}{2} & 0 & 1 - \mu & \frac{\mu}{2} \\ 0 & \frac{\mu}{2} & \frac{\mu}{2} & 1 - \mu \end{pmatrix}$$

2. EXERCISE 2 - FIXED POINTS OF MUTATION AND SELECTION GA

In conducting this analysis the calculated eigenvectors must first be normalised to be unit vectors, i.e. vectors whose entries sum to 1. The normalised fixed-points of the mutation and selection GA are

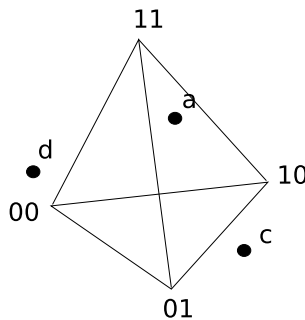
$$a = (0.0132 \quad 0.1207 \quad 0.1207 \quad 0.7455) \text{ (mean population fitness 2.7324)}$$

$$b = (0 \quad -k \quad k \quad 0) \text{ (mean population fitness 1.8)}$$

$$c = (0.1132 \quad 0.4974 \quad 0.4974 \quad -0.108) \text{ (mean population fitness 1.7788)}$$

$$d = (1.1181 \quad -0.0625 \quad -0.0625 \quad 0.0069) \text{ (mean population fitness 0.8888)}$$

We can sketch the unit simplex as follows, ignoring the fixed-point b as it cannot be normalised to a unit vector.



3. EXERCISE 3 - WALSH TRANSFORM OF GOLDBERG'S DECEPTIVE FUNCTION

The Walsh coefficients are as follows

w_0	3.5
w_1	0.25
w_2	0.25
w_3	1
w_4	0.75
w_5	1.5
w_6	1.5
w_7	-1.75

The schema fitness averages can be calculated from subsets of the Walsh coefficients directly. The Walsh coefficients used to calculate a particular schema fitness will be w_0 (the population fitness average), and those for which the binary representation of their subscript contains at least one ‘1’ at a position that is specified (i.e. non-wildcard) by that schema, but only has ‘0’s at the unspecified positions in the schema. E.g. the Walsh coefficient w_2 is involved in the calculation of the fitness of schema *01 because the binary representation of 3, 010 has a ‘1’ corresponding to a specified position in the schema (the second position). We can formalise this by representing a schema using ‘0’s to represent wildcards and ‘1’s to represent specified positions, and saying a Walsh coefficient is involved in the schema fitness calculation iff

$$(j \wedge s) > 0,$$

and

$$(j \wedge \neg s) = 0,$$

where j is the binary representation of the Walsh coefficient index, s is the schema representation just introduced, \wedge is bitwise-AND and \neg is bitwise-NOT.

Having identified the Walsh coefficients involved in the fitness calculations, we just need to determine the signs they should have. We need to choose these signs such that the Walsh coefficients are always added for those chromosomes that are members of the schema. By doing this, the additions and subtractions of Walsh coefficients that are not schema-members will exactly cancel. The addition of Walsh coefficients will then look like this:

$$w_0 + w_i\psi_i(x) + w_j\psi_j(x) + \dots + w_n\psi_n(x),$$

where x is a chromosome that is a member of the schema we are calculating the fitness of. In other words, if the j -th Walsh function is positive for a member of the schema we add the j -th Walsh coefficient, otherwise we subtract it.

This relationship can be illustrated by calculating the fitness average for the schema *01. Applying the inequality above we find the Walsh coefficients involved in the calculation are w_0 , w_1 , w_2 and w_3 . Examining the corresponding Walsh functions for a member of the schema, say 101 we find the sum should be

$$w_0 - w_1 + w_2 - w_3.$$

By examining what happens in this sum we can see that the schema fitness average is arrived at by starting with the mean population fitness (w_0), then progressively adding more copies of the chromosomes that are members of the schema, while cancelling out those that are not. The Walsh coefficients are defined as

$$w_j = \frac{1}{2^\ell} \sum_{x=0}^{2^\ell-1} f(x)\psi_j(x).$$

For our example, expanding out the sum in the above expression into its constituent terms for each of our w_j we get

$$\begin{aligned} & \left(\frac{1}{8}f(000) + \frac{1}{8}f(001) + \frac{1}{8}f(010) + \frac{1}{8}f(011) + \frac{1}{8}f(100) + \frac{1}{8}f(101) + \frac{1}{8}f(110) + \frac{1}{8}f(111) \right) - \\ & \left(\frac{1}{8}f(000) - \frac{1}{8}f(001) + \frac{1}{8}f(010) - \frac{1}{8}f(011) + \frac{1}{8}f(100) - \frac{1}{8}f(101) + \frac{1}{8}f(110) - \frac{1}{8}f(111) \right) + \\ & \left(\frac{1}{8}f(000) + \frac{1}{8}f(001) - \frac{1}{8}f(010) - \frac{1}{8}f(011) + \frac{1}{8}f(100) + \frac{1}{8}f(101) - \frac{1}{8}f(110) - \frac{1}{8}f(111) \right) - \\ & \left(\frac{1}{8}f(000) - \frac{1}{8}f(001) - \frac{1}{8}f(010) + \frac{1}{8}f(011) + \frac{1}{8}f(100) - \frac{1}{8}f(101) - \frac{1}{8}f(110) + \frac{1}{8}f(111) \right) \end{aligned}$$

which simplifies to

$$\frac{1}{2}f(001) + \frac{1}{2}f(101),$$

i.e. the mean fitness of the two chromosomes that are members of the schema.

4. EXERCISE 4 - FITNESS LANDSCAPES

Assuming the CX operator described in the lecture notes, the basin of attraction of the global attractor 11111 is the entire search space. This answer could be arrived at without writing a computer program!