COMSM0302 - WEEK 1 SOLUTIONS

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1. Solution 2 - Effects of mutation under standard and Gray binary encoding

Under standard binary encoding, the expected deviation in the integer encoded for under a single point mutation is 3.75 with variance 7.3. Under Gray binary reflected coding, the expected deviation is the same at 3.75 but with variance of 14.16 (all figures given to 2 d.p.)

The following pseudocode describes a program for generating the answers above.

```
for standard binary and Gray binary reflected codings do
    initialise empty set of deviations devset;
    for all possible binary strings of length 4 do
        for all positions in string do
            i1 ← integer current string encodes under current coding;
            bit-flip current position;
            i2 ← integer current string encodes under current coding;
            bit-flip current position;
            devset ← |i1 − i2|;
        end
    end
    calculate mean of devset;
    calculate variance of devset;
end
```

2. Solution 3 - Sparseness of permutation encoding

The number of permutations of ℓ items is given by $\ell!$, while the number of possible base ℓ strings of length ℓ is given by ℓ^ℓ. Hence the proportion of chromosomes encoding valid solutions is

$$\frac{\ell!}{\ell^\ell}.$$

This shows that for a 5 item permutation encoding only 3.84% of chromosomes encode valid solutions.

3. Solution 4 - Positional bias of crossover operators

1X: The only way in which the two alleles may end up on different chromosomes is if the crossover point is selected to lie between them. As the crossover point is uniformly selected from $\ell - 1$ possible points, and $l + 1$ of those lie between the two alleles, the probablity that the alleles *are* separated is $\frac{l+1}{\ell-1}$. Hence the probability that the alleles end up on the same offspring chromosome is

$$1 - \frac{l+1}{\ell - 1}.$$

2X: There are two situations in which the alleles will end up on the same offspring chromosome. Either both of the crossover points are selected to fall between the two alleles, with probability $\frac{l+1}{\ell-1}\frac{l}{\ell-2}$, or neither of the crossover points are selected to fall between the two alleles, with probability $(1-\frac{l+1}{\ell-1})(1-\frac{l+1}{\ell-2})$. Adding these probabilities together and simplifying yields

$$1-\frac{(l+1)(2\ell-2l-4)}{(\ell-1)(\ell-2)}.$$

UX: There are two situations in which both alleles end up on the same offspring chromosome. Either they are both selected for inclusion in one of the offspring chromsomes, with probability p^2, or they are both selected for inclusion in the other offspring chromosome, with probability $(1-p)^2$. Hence the overall probability of the alleles ending up on the same offspring chromosome is

$$p^2+(1-p)^2.$$