

Exercise Sheet 5

Exercise 17 Genetic Operators

- a) Consider the two chromosomes

$$[3, 9, 1, 6, 8, 8, 5, 7, 1, 5, 5, 4] \quad \text{and} \quad [4, 6, 4, 9, 2, 7, 9, 0, 8, 8, 6, 5].$$

Construct two children of these chromosomes with the help of shuffle crossover using the permutation (3, 1, 6, 7, 4, 11, 8, 12, 5, 10, 2, 9) and a cut between the fifth and the sixth gene!

How may shuffle crossover be implemented efficiently?

(Hint: Is it actually necessary to execute the shuffling and unshuffling explicitly?)

- b) Consider the two chromosomes

$$[8, 3, 5, 7, 0, 4, 11, 1, 9, 6, 10, 2] \quad \text{and} \quad [2, 8, 0, 1, 6, 10, 9, 3, 5, 7, 4, 11].$$

Construct two children of these chromosomes with the help of uniform order-based crossover using the bit mask [1, 1, 0, 0, 0, 1, 0, 1, 1, 1, 0, 1]!

- c) Consider the two chromosomes

$$[5, 1, 6, 7, 0, 8, 9, 3, 10, 11, 2, 4] \quad \text{and} \quad [7, 11, 8, 0, 10, 1, 5, 4, 9, 3, 6, 2].$$

Construct one child of these chromosomes with the help of the method of edge recombination!

Exercise 18 Interpretation of a Schema

In the lecture schemata were illustrated in two different ways: as hyperplanes in a unit hypercube and as “stripe patterns” of a one-dimensional function, which indicated the regions of captured argument values. The latter illustration assumed a standard binary encoding of the numbers. In this exercise, however, we want to consider a Gray code instead. Represent the schemata

a) 0 * * * ... *

b) * * 1 * ... *

c) * 1 * 0 * ... *

for Gray codes and a one-dimensional function in the interval $[0, 1]$!

(In order to compute Gray codes, use the method that was discussed in the lecture.)

Exercise 19 Defining Length of a Schema

In the schema theorem the *defining length* of a schema h is used to measure the probability that a chromosome that fits a schema h before crossover, no longer fits this schema after crossover. For this we assumed in the definition of the defining length that one-point crossover is used. How does one have to change the definition of the defining length if

- a) two-point crossover
- b) uniform crossover

are used instead? (Hint: How can one measure the distance of genes in the two parts that end up in the same child with two-point crossover?)

Exercise 20 Order of a Schema

In the schema theorem the *order* of a schema h is used to measure the probability that a chromosome that fits a schema h before mutation, no longer fits this schema after mutation. Which corresponding quantities may one use for the one-parent genetic operators

- a) pair swap
- b) moving a subsequence (of genes)

in order to assess their effect on the fit to a schema?