# ***Artificial Life - Exercise 7* *Jaana Takis, Benedikt Waldvogel***

## **Assignment 41**

Population size n = 100

Fitness fn: f(x) = n - x

Inheritance: k=1, ie. a copy of the parent

no. of offsprings generated = 1

no. of best parents kept = 100

fitness evaluation: random probability

mutation: none

*What would be different if you should implement Random Optimization (RO) with the evolutionary algorithm?*

We would allow the population size decrease in time, keeping only the best 50% of parents at all times.

## **Assignment 42**

We would structure the genome as a table where each of the 7 column represents the weekday. The 6 rows represent the cinema and the timeslot (i.e. 2 rows per cinema). The genome can be also represented as sequence of bits with a length of L=7\*6=42 by concatenating each row (row1 || row2 || row3 || row4 || row5 || row6)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | Mon | Tue | Wed | Thu | Fri | Sat | Sun |
| Cinema 1  8pm | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Cinema 1  10pm | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Cinema 2  8pm | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Cinema 2  10pm | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Cinema 3  8pm | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| Cinema 3  10pm | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

The example the table corresponds to the genome 000000000000000000000000000000001000000000.

## **Assignment 43**

No, N point crossover is not capable of producing all of the binary genomes of length L.

Eg. We can show that a hypercube with two parent binary genomes labelled 110 and 001 have the following possible offsprings: 111, 011, 010, 100, 101, 000. Yet we cannnot reach all of them neither through 1-point or 2-point crossover.

|  |  |  |
| --- | --- | --- |
| 1-point crossover | 1-point crossover | 2-point crossover |
| Parents:  11|0  00|1  Offsprings:  111  000  110  001 | Parents:  1|10  0|01  Offsprings:  101  010  110  001 | Parents:  1|1|0  0|0|1  Offsprings:  100  011  110  001 |

For neither of the 3 approaches above can recombination of the found offsprings with the same type of crossover provide us with the missing 4 genomes (or in this case with any new information). The only way we can explore the search space further would be through the use of mutation.

## **Assignment 44**

Yes! One can prove it by comparing it to a sorting algorithm like Quicksort. Quicksort also only swaps two elements for each operation and one can proof that quicksort returns an ordered permutation for every possible input.

## **Assignment 45**

An identical genome is produced if **both** parents belong to that half of the pool that has identical genomes. The probability of such an event is . The probability that a **new** genome is produced is . I.e. 75% of all produced genomes are new. So in total there will be new and genomes produced.

If the parent selection is done in such a way that always half of the pool is identical, the absolute number of identical genomes will be monotonously increasing on each ronud. **After some time all genomes are identical**.

## **Assignment 46**

Complexity estimations with a population size where is the number of parents and is the number of new individuals (offspring). Size of the genome is

###### **Parent Selection**

If the parent selection is fitness based, the complexity is

###### **Inheritance**

Depending on how the parents are selected, the complexity of the parent selection can be between if the parents are (randomly) chosen in complexity. Otherwise the complexity can be up to if all parents are considered for each new individual.

###### **Mutation**

The complexity of the mutation should usually be .

###### **External Selection**

If the external selection is e.g. fitness based, the complexity is

So usually the inheritance is a very time consuming part but depends on how the parents are selected.

## **Assignment 47**

Exploration strategy is implemented by a mutation operator. Mutation (implemented by the stochastic component) allows us to explore the search space further and maintains genetic diversity. Eg. a popular method in binary genome would be flipping a bit at random positions.

Exploitation strategy is implemented through inheritance and reproduction. This take advantage of the information already acquired. Eg. a popular method is recombining the genomes of 2 parents through crossover in order to produce new offsprings.