

Autonomous Intelligent Systems,  
Institute for Computer Science VI, University of Bonn

Dr. N. Goerke  
Friedrich-Hirzebruch-Allee 8, 53115 Bonn, Tel: (0228) 73-4167  
E-Mail: goerke@ais.uni-bonn.de  
www.ais.uni-bonn.de

Exercises for Artificial Life (MA-INF 4201), SS24

Exercises sheet 7, till: Mon 26. May, 2025

19.5.2025

**Assignment 43** (2 Points)

It is possible to re-formulate a maximization problem into a minimization problem.

Discuss if this is always a favorable idea; give arguments supporting such a transformation and arguments against.

Describe an example for the above mentioned effect.

**Assignment 44** (2 Points)

How many different offspring can be created from the two parents **A** and **B** by using the 1-point-cross-over recombination-operator?

Both genomes (**A** and **B**) are  $L$ -dimensional vectors that consist of  $L = 64$  independent real values; the individual values are not changed by the 1-point-cross-over operator.

**Assignment 45** (2 Points)

Draw the sequence of operations for an Evolutionary Algorithm, name each step, and characterize or explain each step in one short sentence each.

**Assignment 46** (1 Point)

Propose and describe the structure of a genome for an Evolutionary Algorithm that is implementing a seating of students within a lecture hall (e.g. for a written exam).

Suppose the lecture hall has  $r$  rows and  $c$  columns.

It is not necessary (at the moment) to design the Selection process, the Inheritance operators, the Mutation operators or a sensefull Fitness function.

**Assignment 47** (4 Points)

Within an Evolutionary Algorithm a parent individual  $X(i)$  with a genome of  $L$  bit has created  $N$  offspring  $X(i) = Y(i)_n$  identical to the parent  $X(i)$ .

To yield the new generation  $Y(i+1)_n$  the mutation operator is modifying each of these  $N$  offspring  $Y(i)_n$  by flipping each of the  $N * L$  bits with a probability of  $p$ .

Derive a formula that calculates the propability  $Q$  for the case that **at least one** of the  $N$  new individuals  $Y(i+1)_n$  is **different** to the parent  $X(i)$ .

Use your formula, and calculate the probability  $Q$  for the case that  $N = 25, L = 100$  and  $p = 0.02$ .

## Assignment 48 (2 Points)

Compare the methods *Random Search* and *Random Optimization*.

What is different what is common?

## Assignment 49 (2 Points)

One part of a genome of an Evolutionary Algorithm is a binary string, organized as the binary representation of a 32 bit signed integer value  $v$ .

When the mutation operator is flipping one of these bits, the value is changed from  $v$  to  $\tilde{v}$ .

What is the minimal, the maximal and the average difference between  $v$  and  $\tilde{v}$ ?

## Programming Assignment: D (5 Points, due date Mon 26.5.2025)

Write (in Python) a program, that implements a mini-version of an Evolutionary Algorithm. Please implement or at least foresee a slot for every essential step of the EA, even if you do not implement it right now.

The Evolutionary Algorithm shall find the **minimum** of a function  $f(g)$ . Implement a mini population of  $P = 2$  individuals, each with a genome  $g$  (e.g.  $g_1$  and  $g_2$ ) which is a vector of  $L$  real values. The external selection step keeps only the best one of the two individuals, and discards the other one. The implementation of parent selection can thus be omitted, but should be foreseen within the program code. The inheritance step is just copying the surviving genome to be the newly created genome. The mutation step is only performed for the newly created genome. Implement the mutation step by just adding a small random vector  $\mathbf{r}$  to the genome, each of the  $L$  components of  $\mathbf{r}$  shall be either equally distributed between  $-\varepsilon$  and  $+\varepsilon$  or normally distributed.

Fitness evaluation is just calculating the fitness function  $f(g)$  for all  $P$  genomes of the population, and providing the results for the external selection process. Take either the benchmark function *Styblinski Tang* or *Rastrigin* from the lecture 19.5.25 for the dimension 2, or 3 and at least one larger value. Initialize both genomes with random values, and implement a reasonable stopping criterion.

Print out (or visualize) the fitness values of both individuals while the EA is running, and in the end, print the genome of the resulting individual.