

**Autonomous Intelligent Systems,
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Exercises for Artificial Life (MA-INF 4201), SS11

Exercises sheet 7, due: Mon 6.06.2011



30.5.2011

Group	Name	41	42	43	44	45	46	47	Σ

Assignment 41 (3 Point)

Describe how you would design an evolutionary algorithm to implement the method of stochastic optimization called *Random Search (RS)*.

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

Please include at least, the population size, the fitness function, the parameters μ and λ , the inheritance, the mutation, and the fitness evaluation into your explanation.

Assignment 42 (2 Points)

To optimize a week based plan of recreation (e.g. going to the movies), an evolutionary algorithm shall be used. On every day, two time slots (8pm and 10pm) and three possible movie-theaters are available. Since the Artificial Life Lecture is so time consuming this year, it is only possible to go to the movies once per week.

Thus, the binary genome is coding the day, the time and the location in a one-out-of-N matter (exactly one bit is set, all the others are zero).

Please describe how you would structure the genome, and determine the length L of this genome.

Assignment 43 (2 Points)

Check, if the N-point cross over recombination operators of inheritance (for an EA) are capable of generating all possible genomes for binary genomes of length L.

Assignment 44 (2 Point)

An evolutionary algorithm is proposed to find a solution for a salesman who has to plan a cyclic journey, visiting all cities from a given set of L cities exactly once. For this application the genome has been structured as a sequence of all L cities to visit.

An easy to implement mutation operator would be to swap two cities within this list.

Is it possible to generate all possible sequences of cities by this mutation operator?

Assignment 45 (2 Point)

The inheritance procedure of an evolutionary algorithm is implemented as recombination of $k=2$ parents, by 1-point cross over. The size of the population is P , the size of the pool of parents is μ , and the strategy is $(\mu + \lambda)$; thus the inheritance operator has to generate $\lambda = P - \mu$ individuals.

A closer investigation of the pool of parents revealed, that the better half of these individuals have identical genomes, all the other genomes are different from each other.

How many new genomes are produced if the two parents are drawn equally distributed randomly from the pool of possible parents? Derive a formula.

If mutation is omitted, what might happen to the population after some steps?.

Assignment 46 (2 Points)

Evaluating the fitness function can be really time consuming. Except from this part, which step of an evolutionary algorithm will require the most computing resources?

Please do not just guess, but argue in a proper scientific way.

Assignment 47 (2 Points)

Describe two operators for an evolutionary algorithm: one that is implementing a pure *exploration* strategy, and a second one implementing a pure *exploitation* strategy.

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 cannot reach all of them neither through 1-point or 2-point crossover.

1-point crossover	1-point crossover	2-point crossover
Parents: 11 0	Parents: 1 10	Parents: 1 1 0

00 1	0 01	0 0 1
Offsprings:	Offsprings:	Offsprings:
111	101	100
000	010	011
110	110	110
001	001	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 p of such an event is $\frac{1}{2} * \frac{1}{2} = \frac{1}{4}$. The probability that a **new** genome is produced is $1 - p = \frac{3}{4}$. i.e. 75% of all produced genomes are new. So in total there will be $\lambda * \frac{3}{4} = (P - \mu) \frac{3}{4}$ new and $\lambda * \frac{1}{4} = (P - \mu) \frac{1}{4}$ 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 round. **After some time all genomes are identical.**

Assignment 46

Complexity estimations with a population size $P = \mu + \lambda$ where μ is the number of parents and λ is the number of new individuals (offspring). Size of the genome is L

Parent Selection

If the parent selection is fitness based, the complexity is $O(\mu)$

Inheritance

Depending on how the k parents are selected, the complexity of the parent selection can be between $O(\lambda)$ if the parents are (randomly) chosen in $O(1)$ complexity. Otherwise the complexity can be up to $O(\lambda * \mu^k)$ if all parents are considered for each new individual.

Mutation

The complexity of the mutation should usually be $O(\lambda)$.

External Selection

If the external selection is e.g. fitness based, the complexity is $O(P) = O(\mu + \lambda)$

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.

