Artificial Life Summer 2025

Learning from Nature Evolutionary Algorithms Optimization Inspired by Biology

Master Computer Science [MA-INF 4201] Mon 14:15 – 15:45, HSZ, HS-2

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Overview:

- Some Basics on Optimization
- Evolutionary Computation
- Historic Remarks
- Different Approaches
- Idea of Evolutionary Algorithms (EA)
- EA Steps
 - Individual, Genome, Fitness, Population
 - Parent selection
 - Inheritance
 - Mutation
 - Fitness evaluation
 - External selection

Optimization (some basics):

Depending on the background and the context, optimization is mainly seen as a part of :

- Operations Research
- Artificial Intelligence, or more precise
- Computational Intelligence.

Some Artificial Life approaches are directly working in the following subsets of optimization:

- Stochastic Optimization
- Meta heuristic Optimization

Optimization (some basics):

(Global) optimization is typically based on optimizing a criterion of some objective function **f(s)**:

- minimizing some costs
- maximizing some fitness

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```

$$f(s^*) \ge f(s)$$
 $\forall s \in S$ (in case of maximization)

Minimization vs. Maximization:

Minimization is a kind of optimization with respect to (scalar) costs. Costs are typically defined to have a known lower bound: usually "zero".

Maximization is a kind of optimization with respect to a (scalar) objective function; like **fitness**, profit, or performance. A realistic upper bound for this objective function is often not known in advance.

Re-formulating a maximization problem into a minimization problem is often possible, but not always advisable because of a probable non-linear complete re-scaling of the objective function.

Global vs. Local Optimization:

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- in the objective function,
- in the optimization method as explicit component,
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The stochastic component can be an inevitable property of the application one has to cope with, or can be included deliberately to support the algorithm.

There is a variety of other approaches from the field of Stochastic optimization:

- Random Search
- Random Optimization
- Monte Carlo Methods
- Simulated Annealing
- Single Start
- Multi Start
- Random Search Direction Methods
- Hill Climbing
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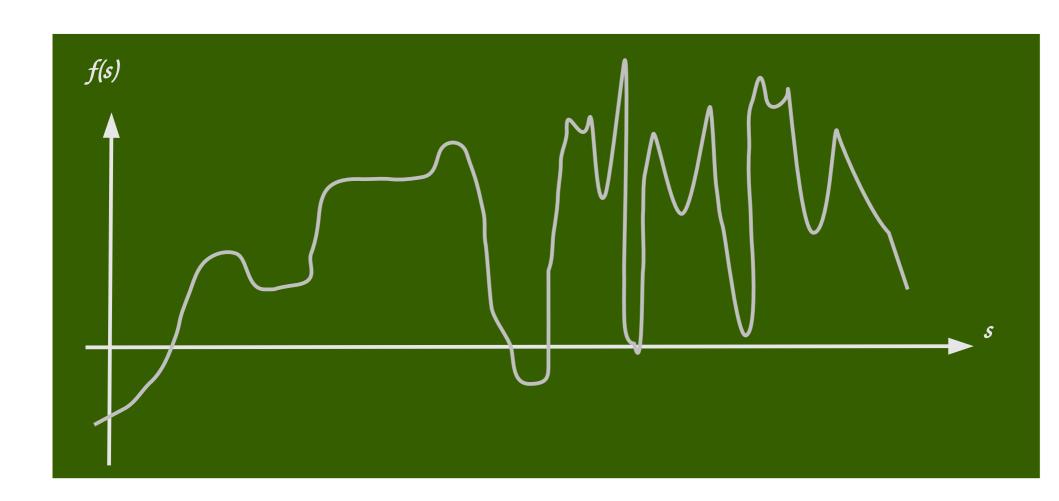


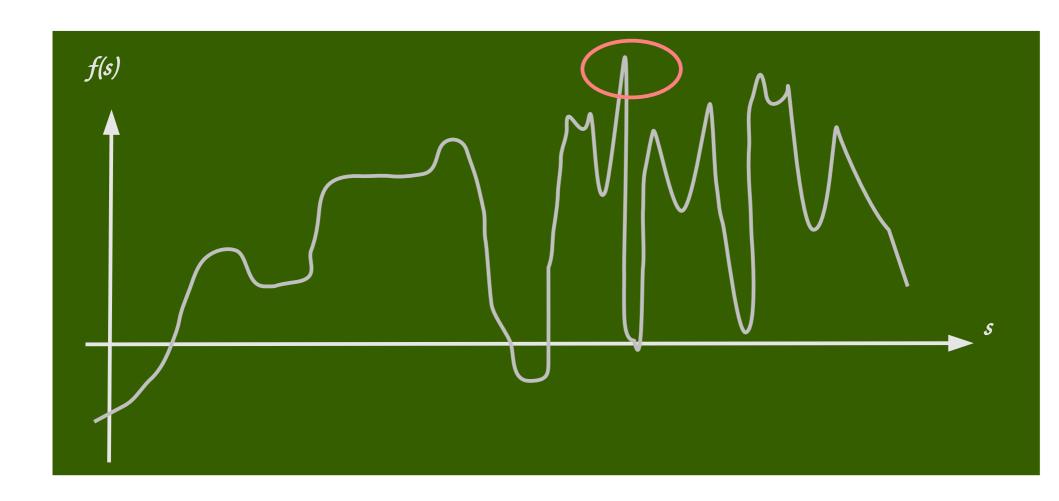












A typical **playground** to investigate the capabilities of optimization methods are **test functions** to be minimized.

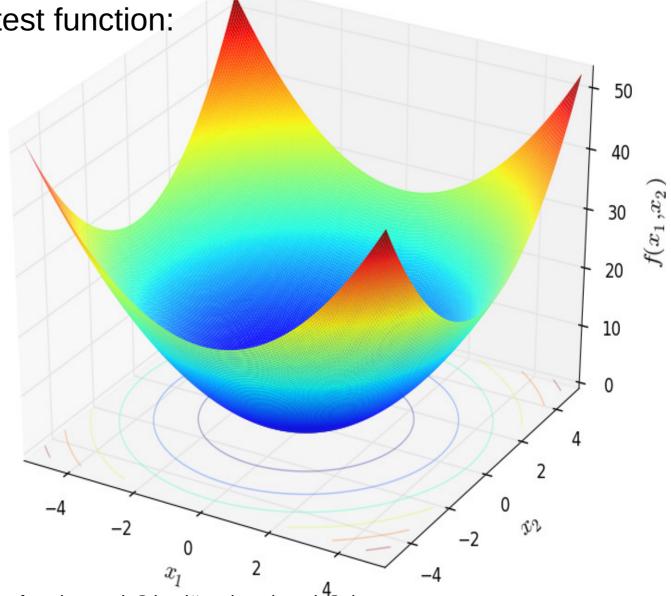
Over the years, many researchers have invested a lot of time to design adequate and appealing test functions to demonstrate and evaluate the results of their optimization methods.

Meanwhile, many collections of such functions can be found. A nice collections is:

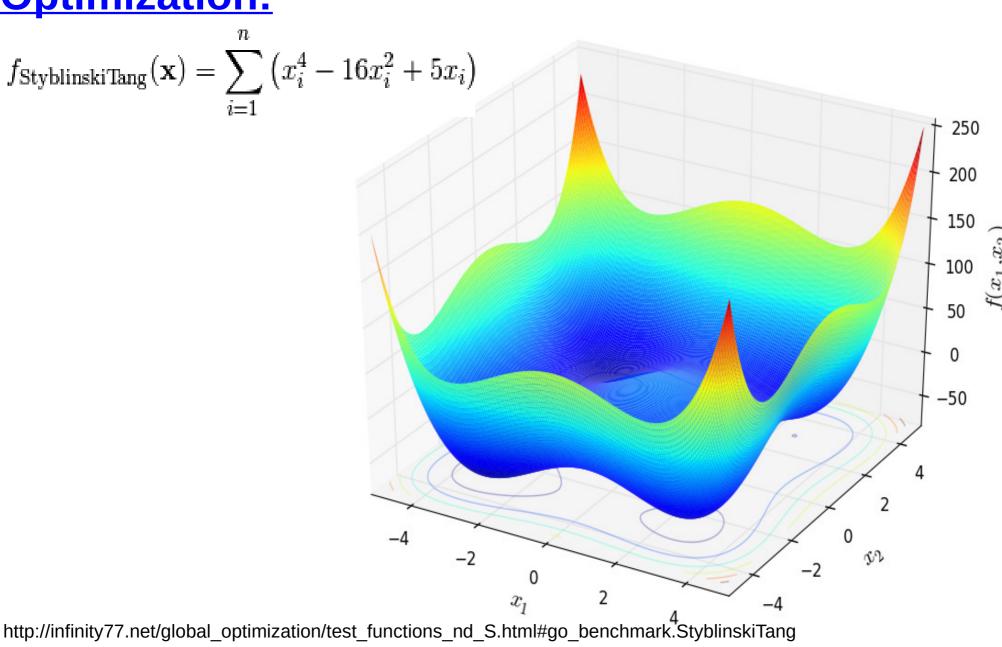
http://infinity77.net/global_optimization/test_functions.html#test-functions-index

An easy to understand test function:

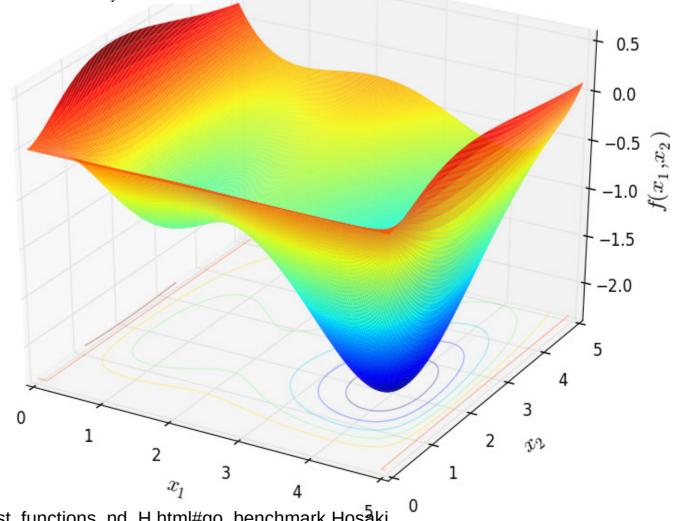
$$f_{\text{Sphere}}(\mathbf{x}) = \sum_{i=1}^{n} x_i^2$$



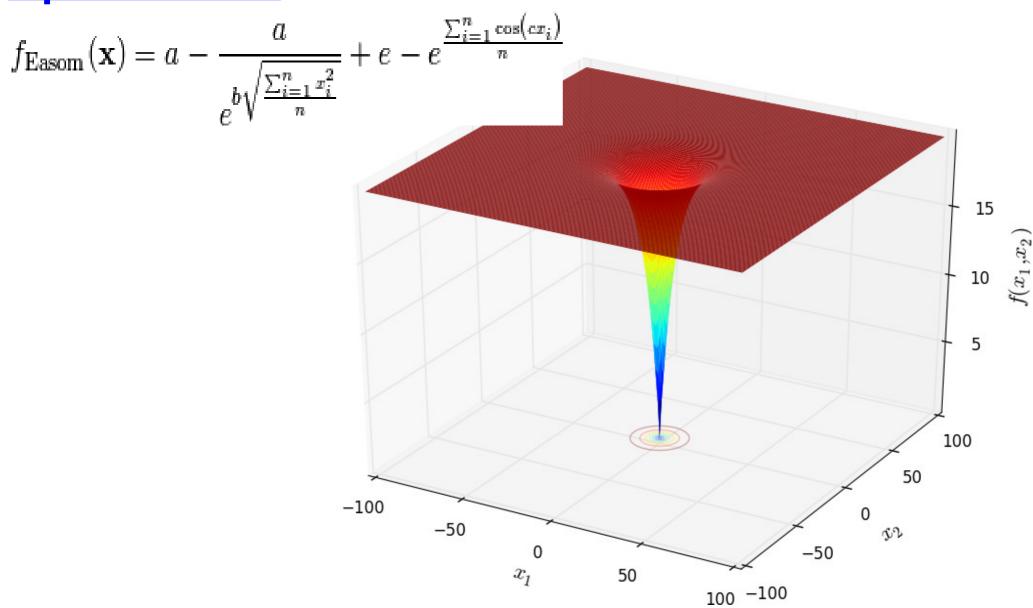
http://infinity77.net/global_optimization/test_functions_nd_S.html#go_benchmark.4Sphere



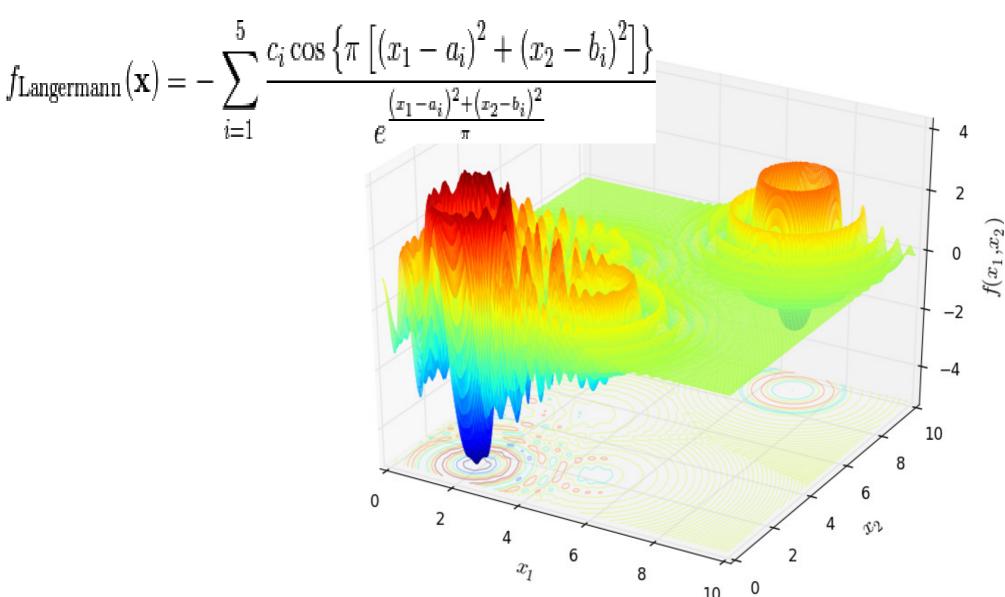
 $f_{\text{Hosaki}}(\mathbf{x}) = \left(1 - 8x_1 + 7x_1^2 - \frac{7}{3}x_1^3 + \frac{1}{4}x_1^4\right)x_2^2e^{-x_1}$



http://infinity77.net/global_optimization/test_functions_nd_H.html#go_benchmark.Hosaki

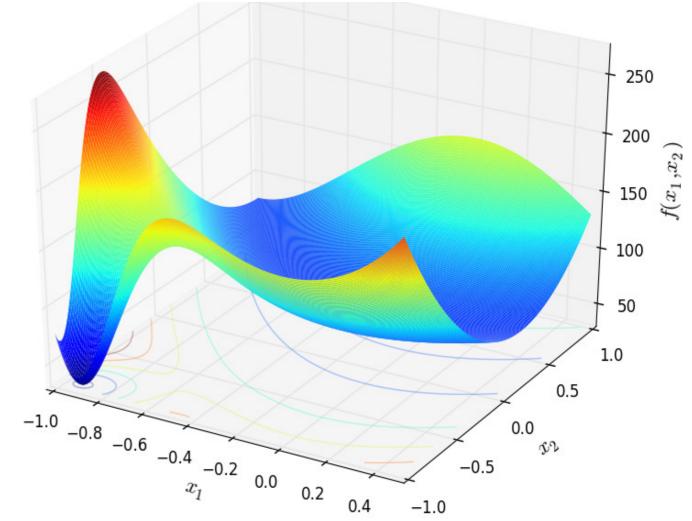


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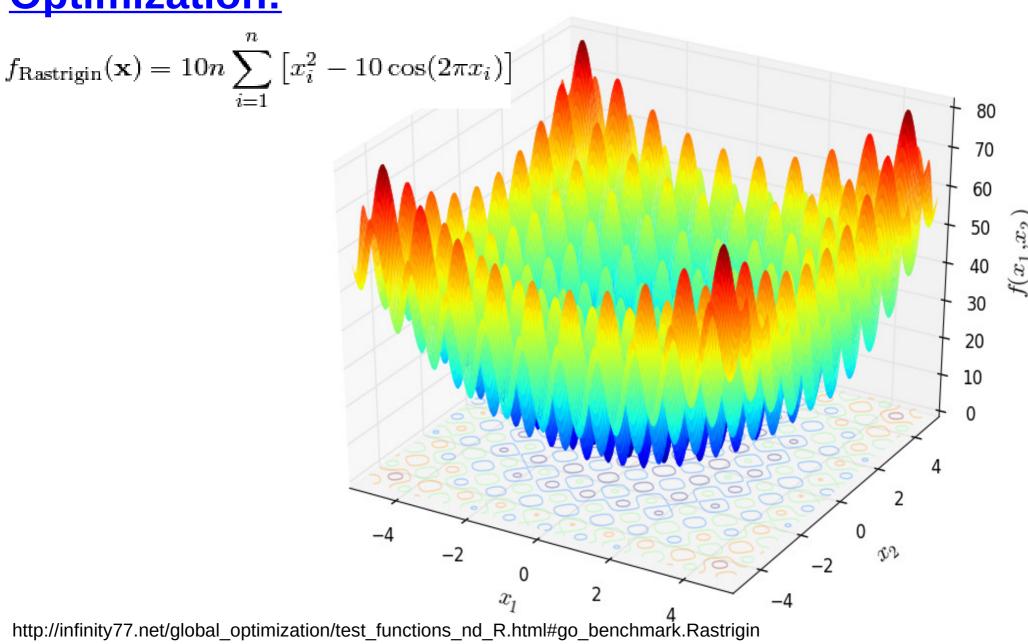


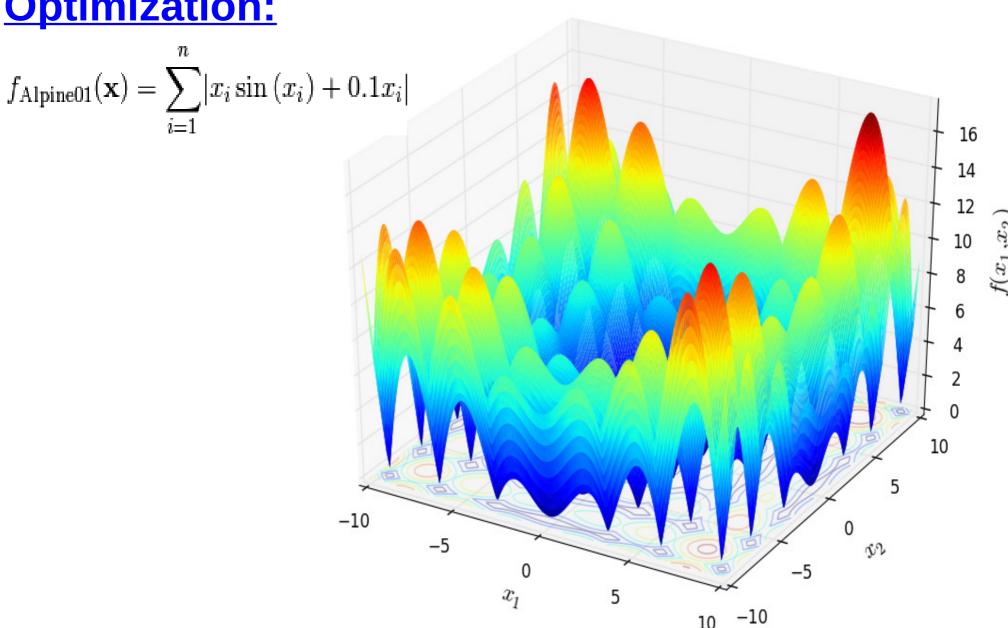
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$$f_{\text{RosenbrockModified}}(\mathbf{x}) = 74 + 100(x_2 - x_1^2)^2 + (1 - x_1)^2 - 400e^{-\frac{(x_1+1)^2 + (x_2+1)^2}{0.1}}$$

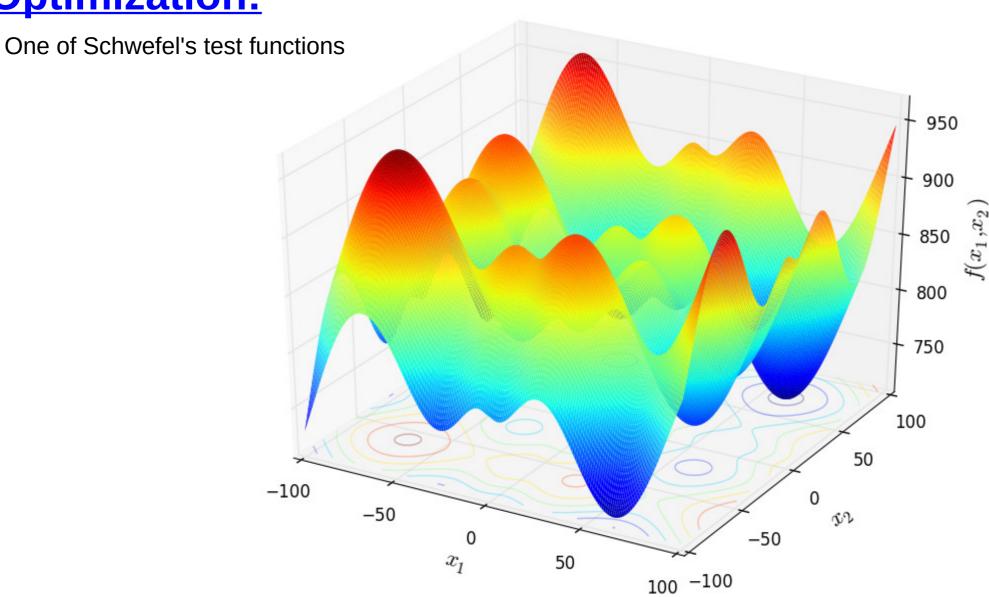


http://infinity77.net/global optimization/test functions nd R.html#go benchmark.RosenbrockModified





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http://infinity77.net/global_optimization/test_functions_nd_A.html#go_benchmark.Schwefel26

Below is a list of common **test functions (to minimize)** that are used to investigate the capabilities of optimization methods:

- Schwefel's Function
- Generalized Rosenbrock's Function
- Rastrigin's Function
- Ackley's (path) Function
- Langermann's Function
- Michalewicz's Function
- Easoms Function
- Griewangk's Function
- Bohachevsky's Function
- Watson's Function
- Colville's Function

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Evolutionary Computation:

Optimization inspired by Biology

Evolutionary Computation (EC):

What is it?

Where does it come from?

Where can it be found?

Why is it interesting for Computer Science?

Historic Remarks, Different Approaches:

The field is at the moment denominated as **Evolutionary Computation (EC)**.

EC comprises several approaches and ideas

- that have been developed independently (60ies),
- that follow the same basic guideline and
- that have (later) been found to be so closely related to each other,
- that they can be seen as different variants or dialects of the same basic principles.

Historic Remarks, Different Approaches:

Evolutionary Computation (EC)

Swarm Behavior / Swarm Intelligence

- Ant Algorithm
- Ant Colony Optimization
- Particle Swarm Optimization

Evolutionary Algorithms (EA)

- Genetic Algorithms (GA)
- Genetic Programming (GP)
- Evolutionary Strategies (ES)
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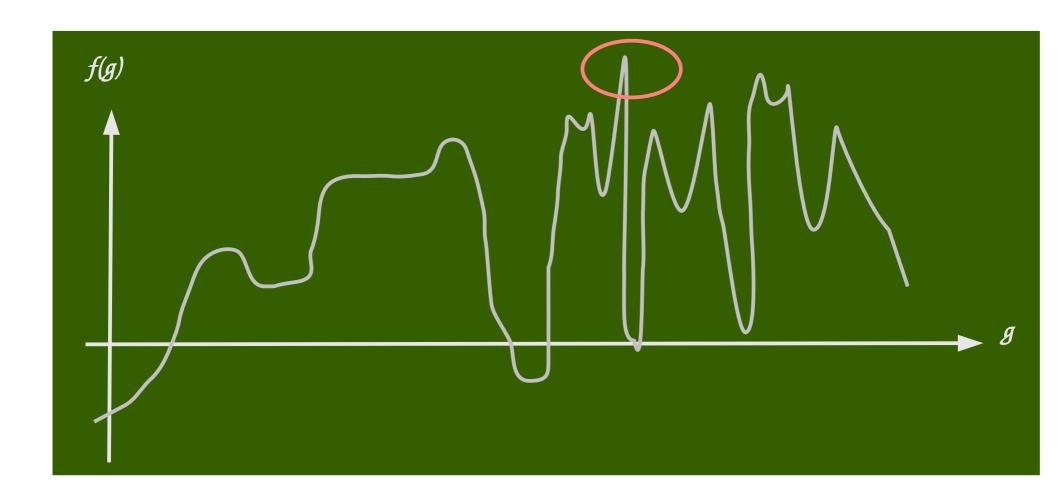
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Optimization:

Draw a **nasty fitness function** on the blackboard:



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Example: Fkt Maximum

I. Rechenbergs tubing problem

The fuel flows into the tube from the left. The fuel should leave the tube (top right) such that the resistance of the fluid is minimized.

The question is how the two tubes should be connected, i.e. what is the shape of the connecting tube?



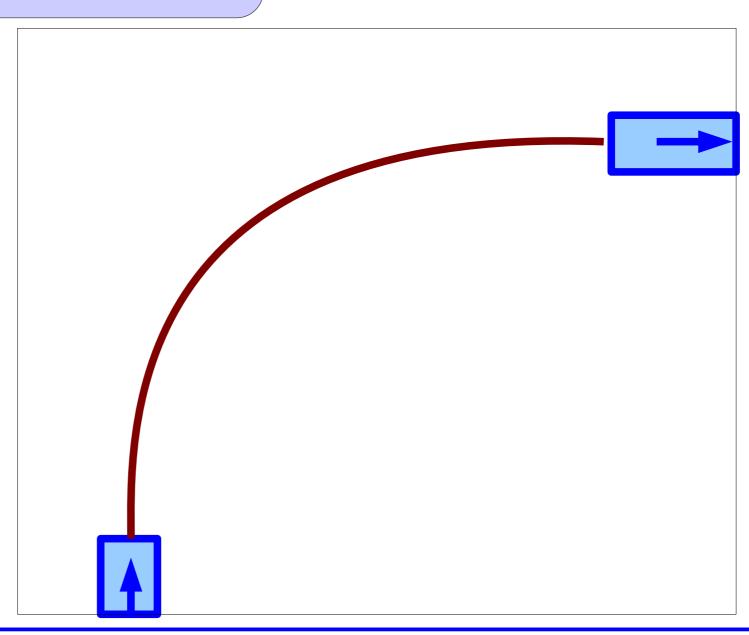


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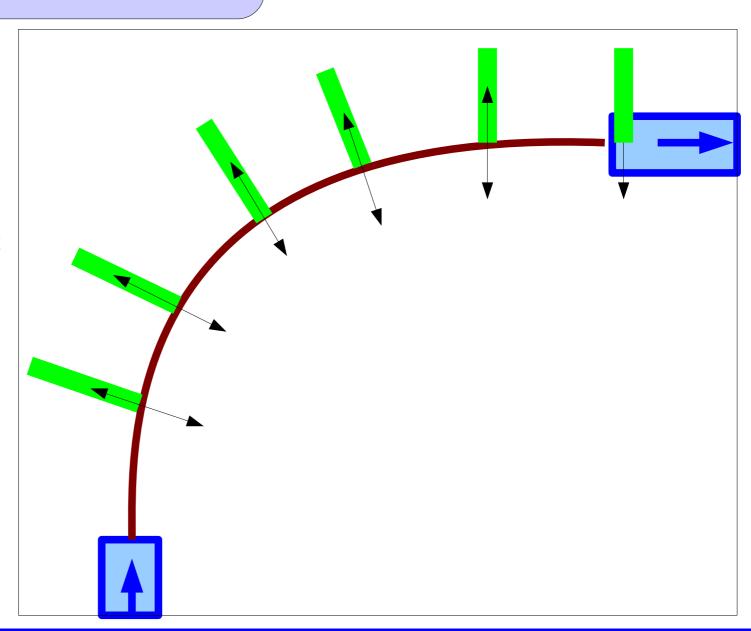


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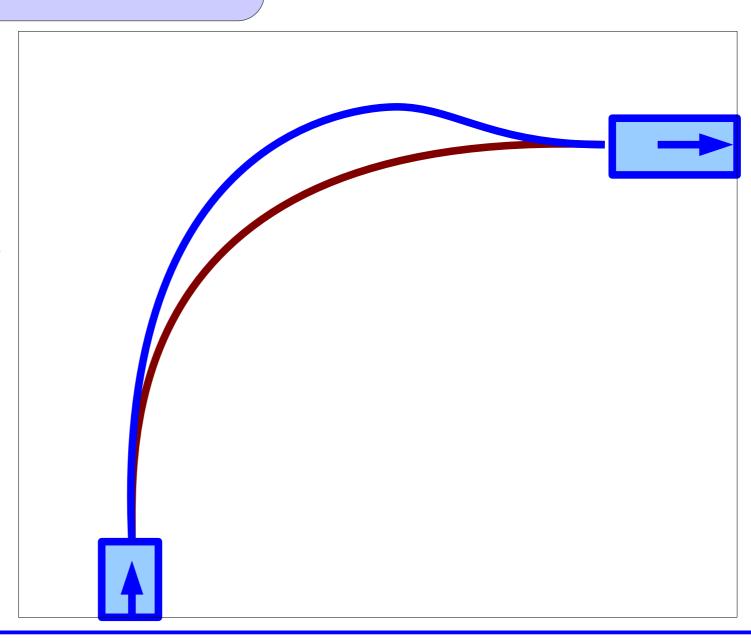


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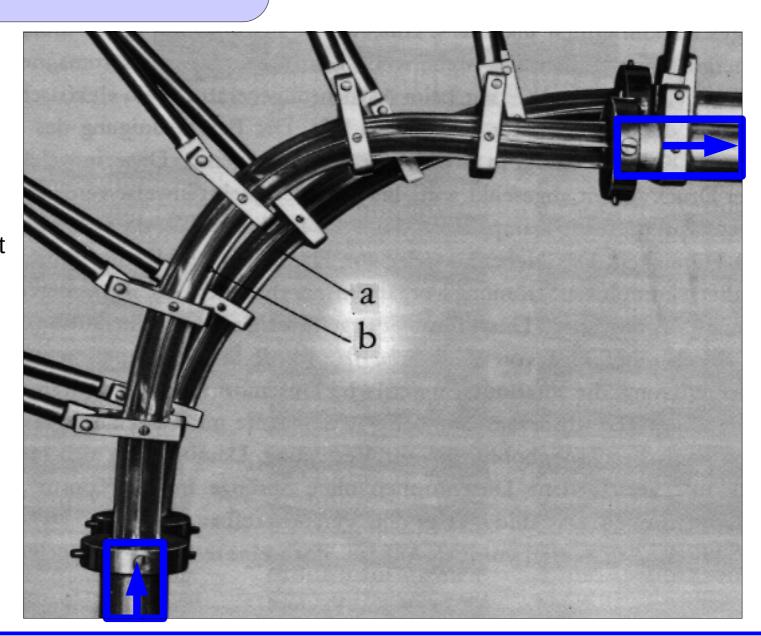


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The whole family of algorithms denominated as **Evolutionary Algorithms** was inspired by a series of ideas and principles from living nature.

Especially the principles of Evolution (C.Darwin) and Reproduction and Inheritance (G.Mendel) and the discovery of the Genome, and the DNA (1953, J.Watson, F.Crick) have inspired the development of EAs in the 50ies and 60ies of the last century.

Thus, major parts of EAs are designed in analogy to the biological role model.

Different Approaches:

Evolutionary Computation (EC)

Evolutionary Algorithms (EA)

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Several aspects and terms of Evolutionary Algorithms are directly borrowed from biology:

- Population of Individuals
- Survival of the fittest
- Selection
- Inheritance
- Reproduction
- Mating
- Recombination
- Cross-Over
- Mutation
- Genome

Evolutionary Algorithms perform a stochastic optimization using a modified Multi-Start approach, (Multi-Hypothesis approach).

Instead of working with one single hypothesis, several different hypotheses will be regarded at the same time (working "quasi" in parallel).

Within an Evolutionary Algorithm, each of the multihypotheses is called an Individual.

The collective of all Individuals is called the **Population** of the **Evolutionary Algorithm**.

Each Individual of the Population will typically have a different position s_p in search space s_p , and thus, a different fitness s_p .

The position s_p in search space is defining the individual p; s_p is called the Genome of p.

Some of the Individuals might represent acceptable solutions, close to a local optimum, or even close to the global one.

Some of them represent mediocre solutions.

Some might represent just rubbish (most will).

The entire **Population** carries more information about the objective function than, any of those single **Individuals** alone.

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Keep the good ones. Discard the bad ones.

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This is the implementation of the biological principle:

Selection

"Survival of the fittest"

The **Selection** (whom to keep, whom to discard) is performed with respect to the result achieved by the objective function **f(s)**.

This is called "External Selection", because the objective function f(s) is provided by the environment from external the EA.

(sometimes called "Environmental Selection")

The result of this **External Selection** is a reduced population, with only the best individuals surviving.

The individuals, that survived the external selection process, are now entitled to restock the population to it's original size. They are called parents, allowed to generate offspring.

Re-stocking the population could in principle be done by generating complete new individuals.

But it is assumed (and proven) that using some of the already acquired information for the new individuals is preferable.

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Reproduction and Inheritance

To transport some of the information from the previous generation, into the next generation (inheritance), the offspring are generated out of the genome of the parents.

The most popular way in Evolutionary Algorithms is to select two parents from the remaining population (parent selection), and to generate offspring by mixing, or combining the genome of these parents.

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This way of <u>exploration</u> is implemented in EAs using a random alteration of the existing <u>genomes</u>. It is called:

Mutation

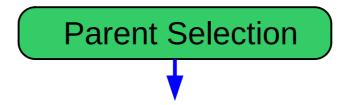
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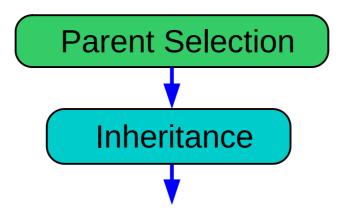
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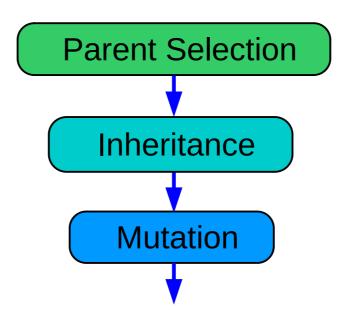
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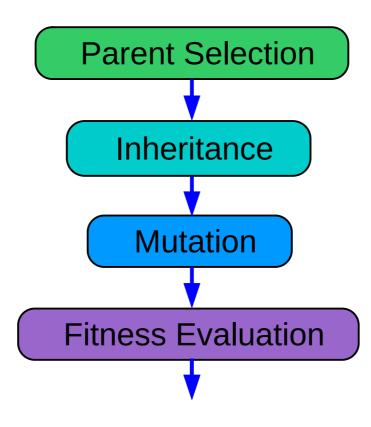
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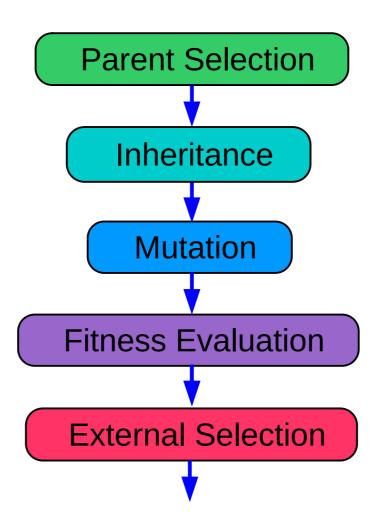


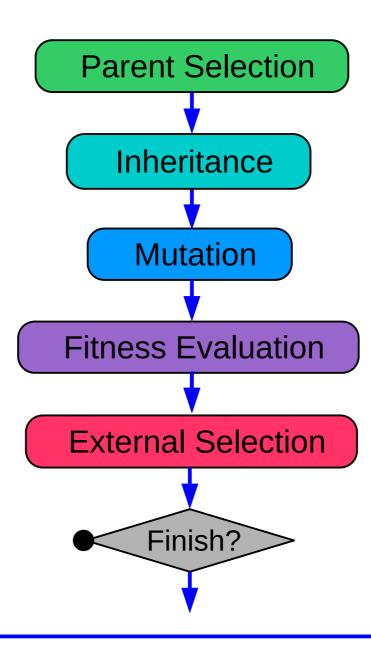
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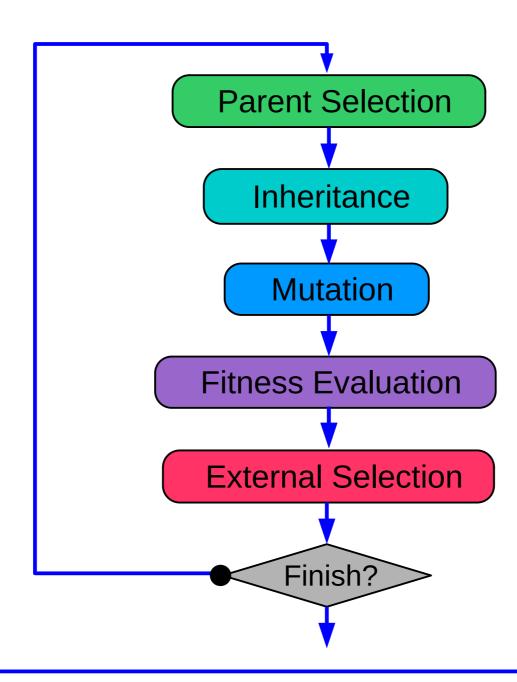


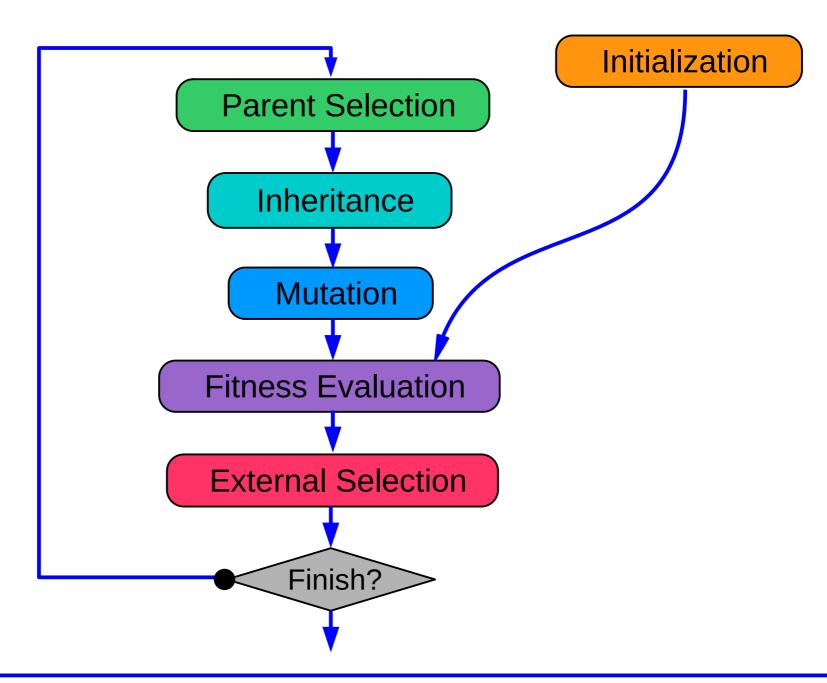




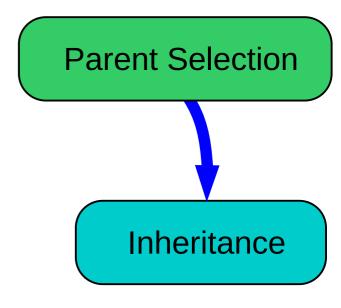


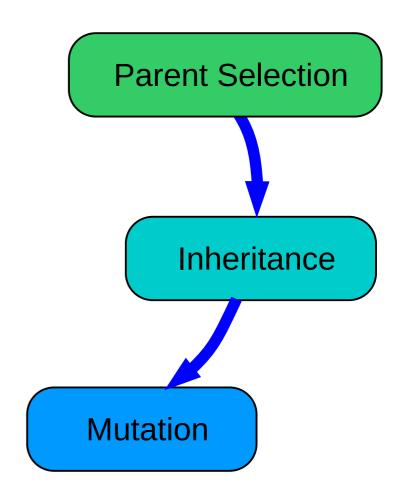


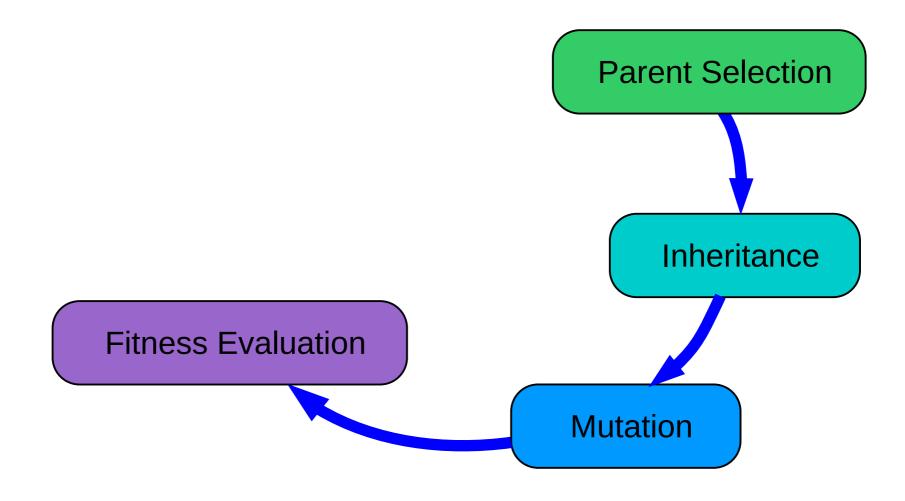


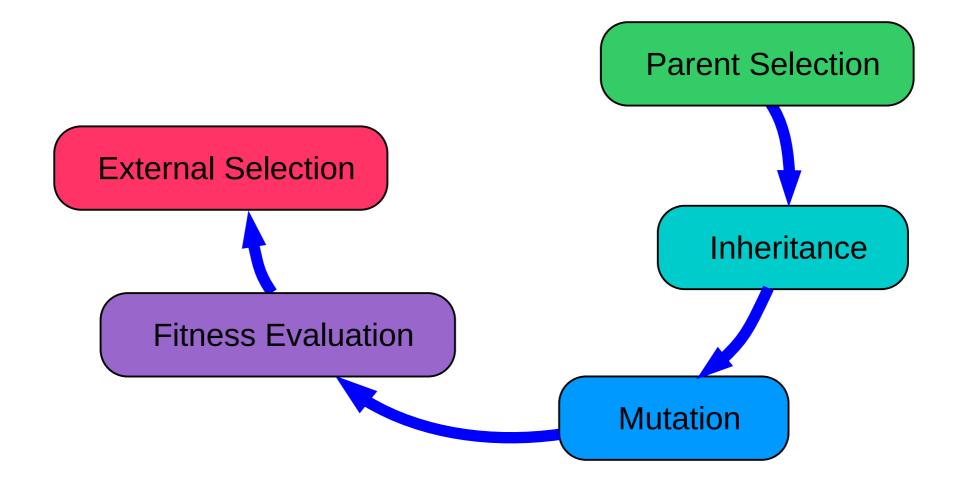


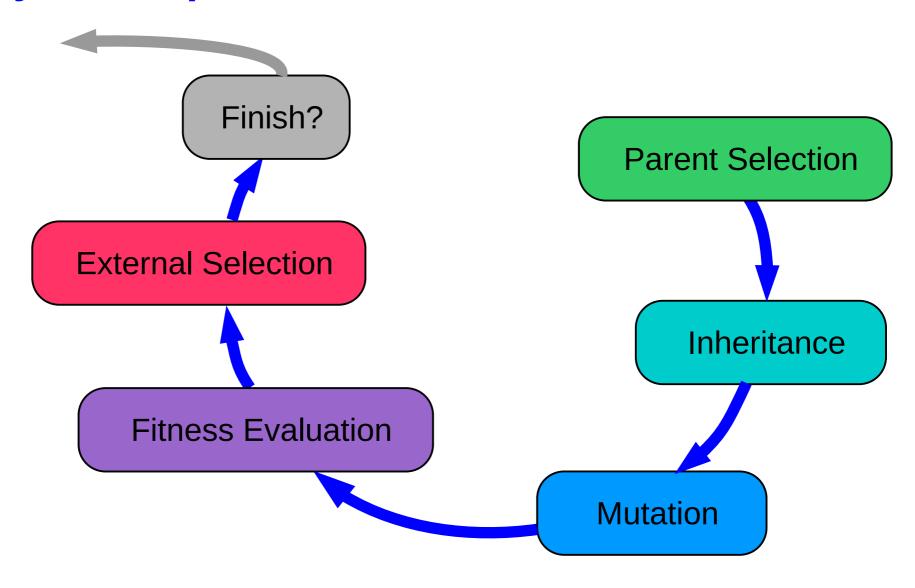
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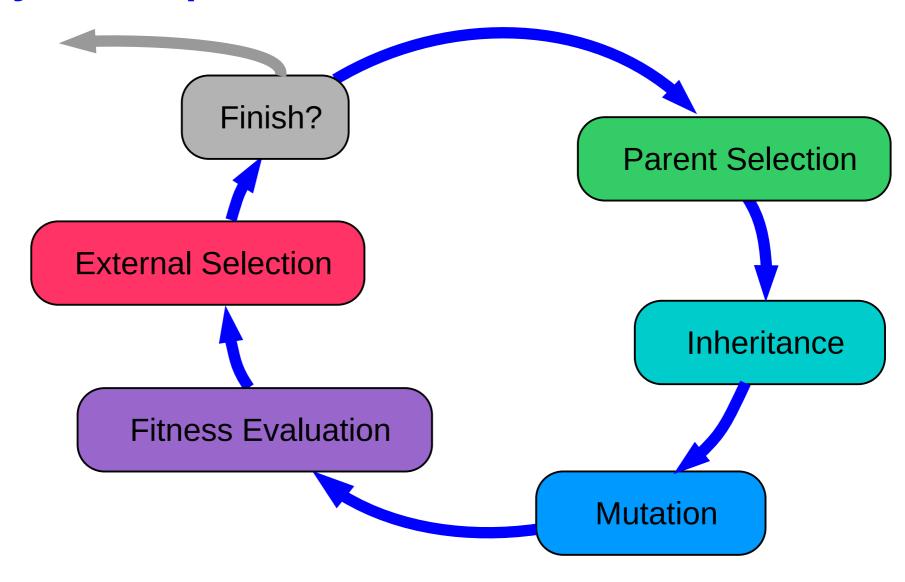


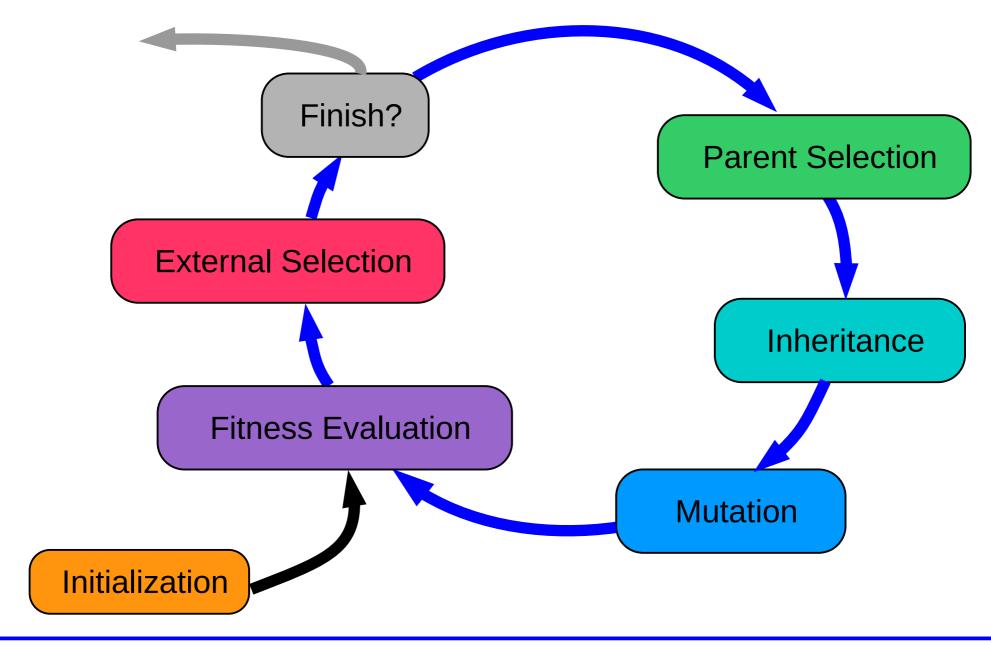


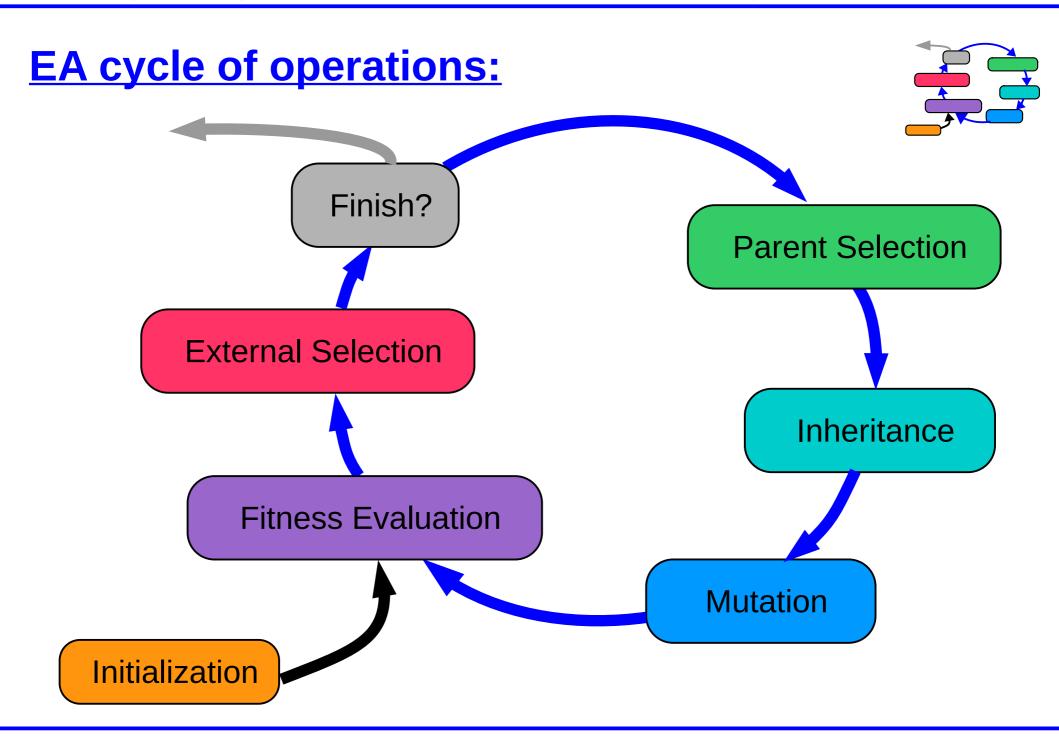










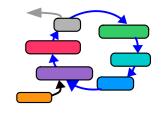


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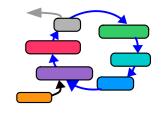
Population, Individual, Genome, Fitness



An Evolutionary Algorithm works with a **population** of single **individuals**.



Population, Individual, Genome, Fitness

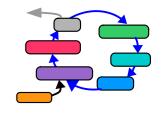


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Each individual owns a genome.



Population, Individual, Genome, Fitness

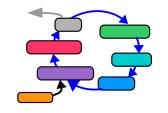


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A genome is a set of parameters s out of a search space S.

Population, Individual, Genome, Fitness



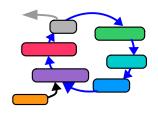
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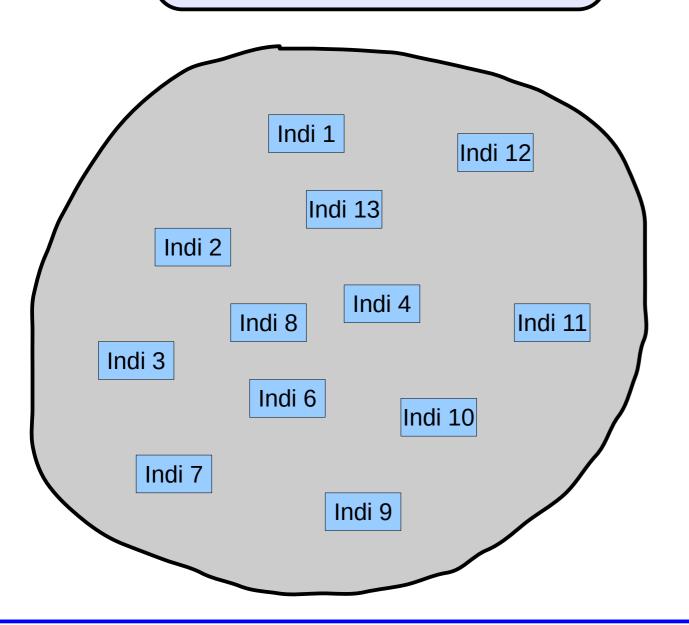
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A genome is a set of parameters s out of a search space S.

The genome s_p of an individual p is evaluated with respect to a fitness function f (objective function). The result $f(s_p)$ of this evaluation is called f_p fitness of the individual p.

Population of Individuals





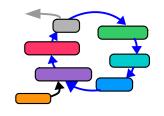
A population is a set or group of individuals.

Indi 1 Indi 2 ...

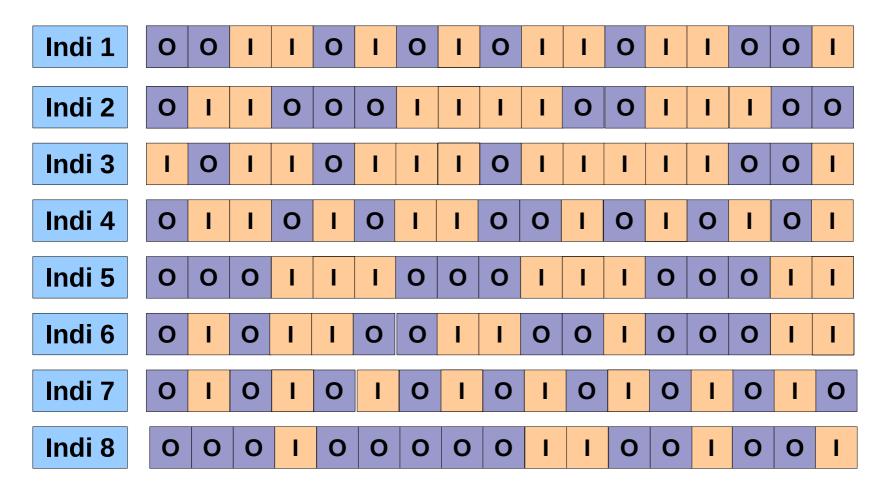
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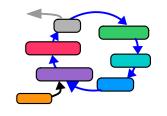
Population of Individuals



A population of individuals with individual genomes.



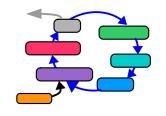




A **genome** is a set of parameters **s** out of a search space **S**. The genome determines the properties and capabilities of an individual (phenotype).

Indi 1 OOIIOIOIOOIOO



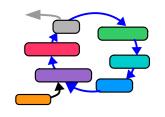


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The implementation of a **genome** can be a simple string of bits, can be a vector of integer or real values, or can be a set of items, (or something else).

A genome can even be a string of characters, like a computer program, or a complete text.





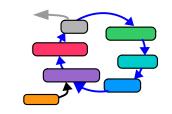
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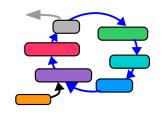
A genome does not even has to have a fixed length. The length can change during the optimization of the EA.





A genome can be



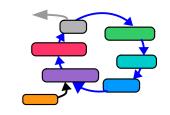


A genome can be

a simple string of bits:







A genome can be

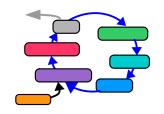
a simple string of bits:

0 0 1 1 0 1 0 1 0 1 0

a vector of values:

17 0.38 2.0e-7 42 3.141





A genome can be

a simple string of bits:

0 0 1 1 0 1 0 1 0 1 0

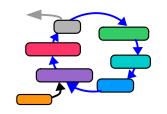
a vector of values:

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a set of items:

{ Car, Banana, Monday, USB-Stick }





A **genome** can be

a simple string of bits:

17 0.38 2.0e-7 42 3.141

a vector of values:

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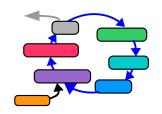
{ Car, Banana, Monday, USB-Stick }

a string of characters:

"Throatwobbler Mangrove"

From: Monty Python's Flying Circus: Episode 22, Cosmetic surgery





A **genome** can be

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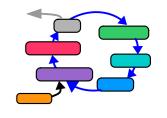
From: Monty Python's Flying Circus: Episode 22, Cosmetic surgery

a complete computer program.

```
#include "Evolutionary_Algorithms.h"
int main()
{
  int P = 1000;  // size of population
  int L= 20;  // length of genome
```



Fitnessfunction



The fitness function f calculates the fitness value f(s) for each individual genome s.

The fitness value is a scalar value.

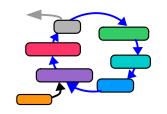
Larger fitness is indicating a better individual.

The fitness is heavily depending on the application!

The mapping from **genome** to **fitness value** can be directly, e.g. by a mathematical function, or can be a complicated process, e.g. the performance of a soccer playing, walking robot.



Fitness value



The fitness function f calculates the fitness value f(s) for each individual genome.

Indi 1























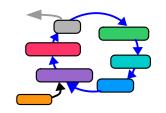






f(1) = 9

Fitness value

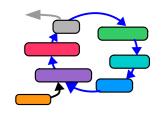


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Indi 1	0	0	I	I	0	I	0	I	0	I	I	0	I	I	0	0	ı
Indi 2	0	I	I	0	0	0	I	I	I	I	0	0	I	I	I	0	0
Indi 3	I	0	I	I	0	I	I	I	0	I	I	I	I	I	0	0	I
Indi 4	0	I		0	I	0	I	I	0	0	I	0	I	0	I	0	I
Indi 5	0	0	0	I	I	I	0	0	0	I	I	I	0	0	0	I	I
Indi 6	0	I	0	I	I	0	0		I	0	0	I	0	0	0	I	I
Indi 7	0	I	0	I	0		0	I	0	I	0	I	0	I	0	I	0
Indi 8	0	0	0	I	0	0	0	0	0	I	I	0	0	I	0	0	I



Fitness value



The fitness function f calculates the fitness value f(s) for each individual genome.

Indi 1























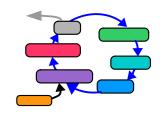




0

f'(1) = 2

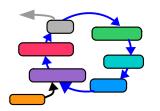
Fitness value



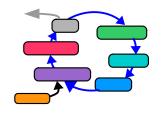
The fitness function f calculates the fitness value f(s) for each individual genome.

	ndi 1	0	0	I	I	0	I	0	I	0	I	I	0	I	I	0	0	I
	ndi 2	0	I	I	0	0	0	I			I	0	0	I	I	I	0	0
I	ndi 3	I	0	I	I	0			I	0	I	I		I	I	0	0	I
I	ndi 4	0	I	I	0	I	0	I	I	0	0	I	0	I	0	I	0	I
	ndi 5	0	0	0	I	I		0	0	0	I	I		0	0	0	I	
I	ndi 6	0	I	0	I	I	0	0	I	I	0	0	I	0	0	0	I	
I	ndi 7	0	I	0	I	0		0	I	0	I	0	I	0	I	0	I	0
	ndi 8	0	0	0	I	0	0	0	0	0	I	I	0	0	I	0	0	I



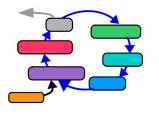






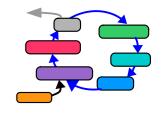
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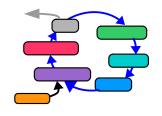


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In general, it is a good advise, to keep the size of the population fixed; but it is possible to change P.





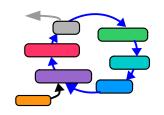
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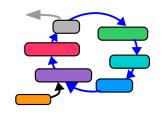
Special approaches and extensions of EAs divide the population into several **sub-populations**, that may be treated differently.





How large shall the size of the **population** be?



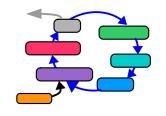


How large shall the size of the population be?

There are several aspects that influence the choice of P:

- enough richness, diversity of hypothesis
- costs for evaluating the individuals
- computing costs for the entire algorithm





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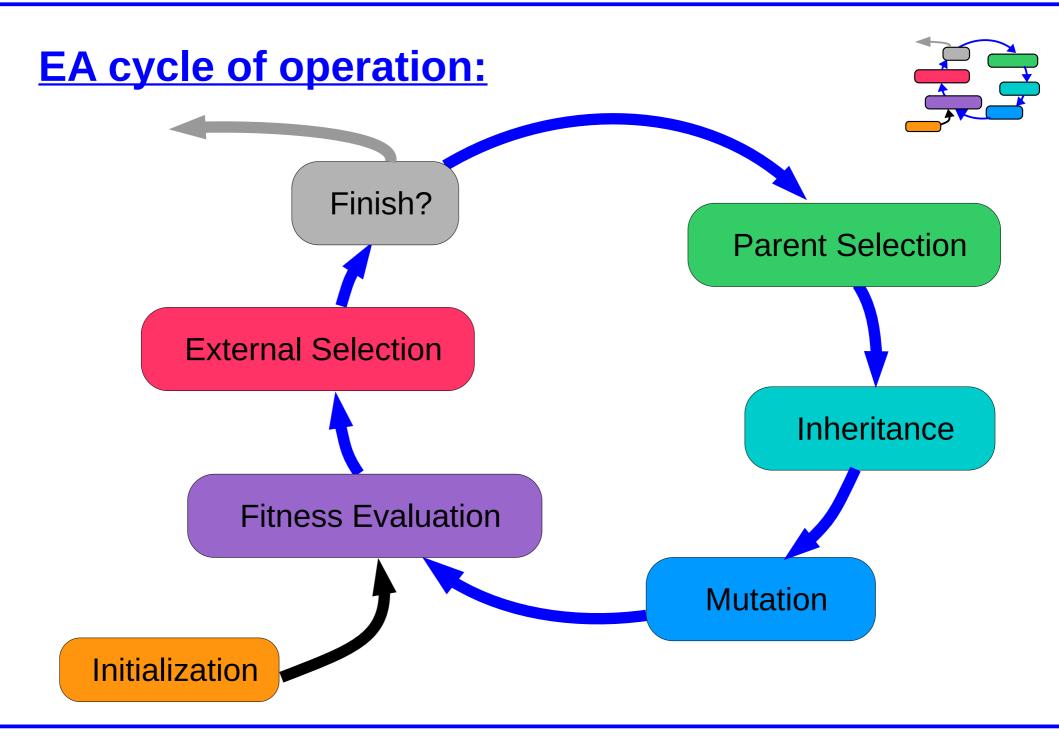
- enough richness, diversity of hypothesis
- costs for evaluating the individuals
- computing costs for the entire algorithm
- keep it simple, keep it small

```
P = 50 ... 1000 (simulations)
```

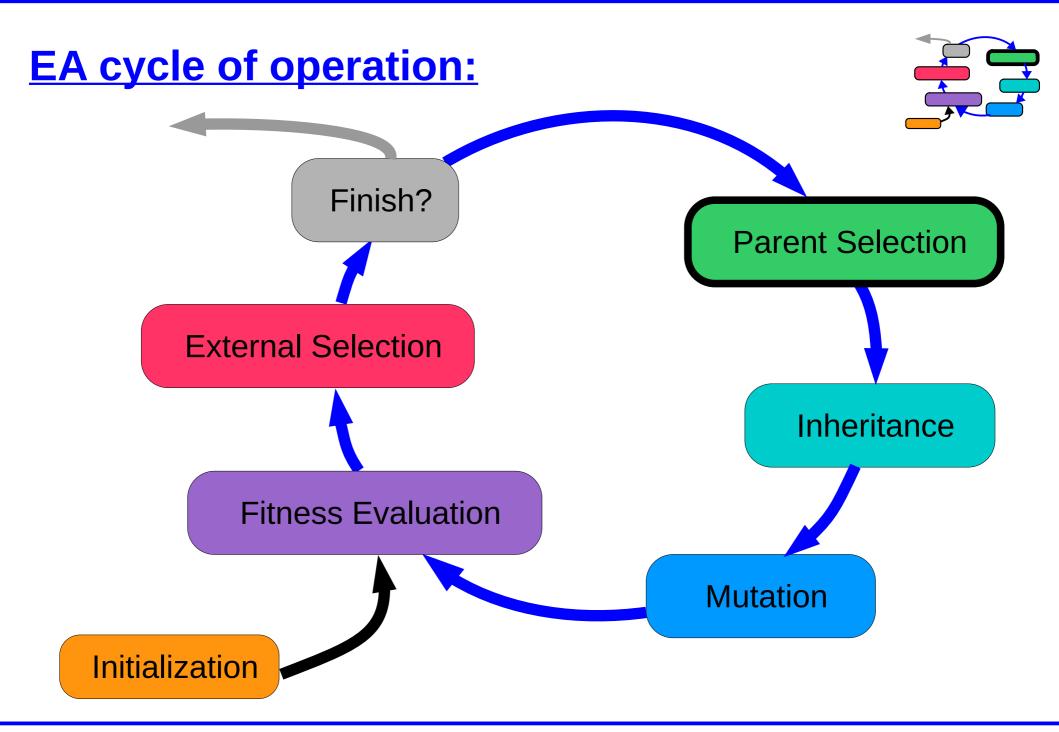
P = 5 ... 50 (real world experiments)

Overview:

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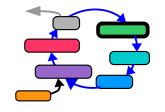


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Parent Selection



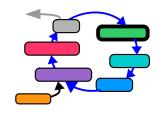
The μ individuals that survived the external selection process, are the pool to select the parents from.

Those parents selected, will have to generate λ offspring.

For every inheritance process, a number of k individuals (parents) are selected from the pool of possible parents for mating + recombination.



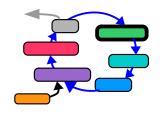
Parent Selection



Out of the μ remaining individuals the **k**-parents are chosen for the inheritance step to generate λ offspring.

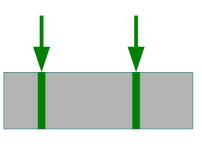
pool of µ possible parents

Parent Selection



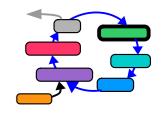
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pool of µ possible parents



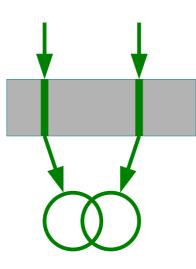
parent selection

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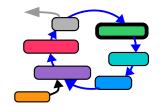
pool of µ possible parents



parent selection

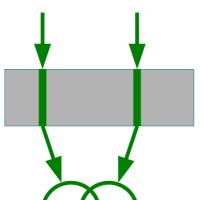
mating, recombination

Parent Selection



Out of the μ remaining individuals the k-parents are chosen for the inheritance step to generate λ offspring.

pool of μ possible parents



parent selection

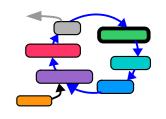
mating, recombination

λ offspring inheritance





Parent Selection

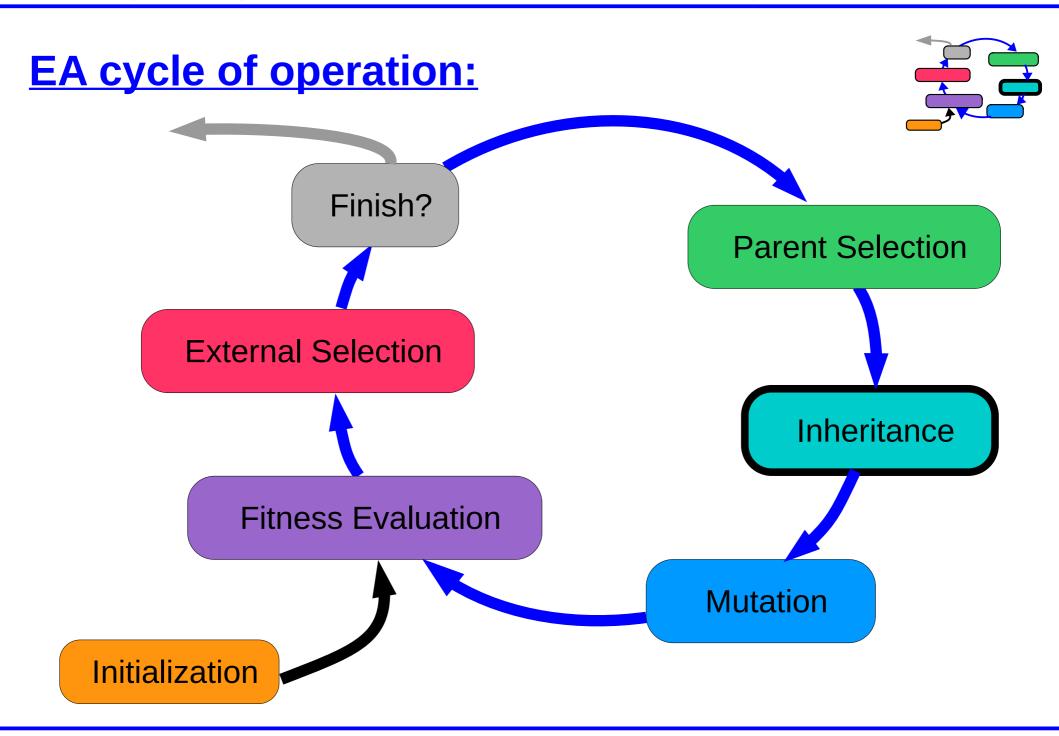


Common strategies for the parent selection are:

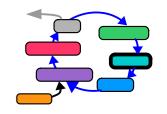
- random choice
- schedule based, e.g. round robin
- fitness based elitism: fitness proportional choice rank proportional choice
- fitness based stochastic: fitness proportionate, probabilistic choice rank proportionate, probabilistic choice
- combinations of the above

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Inheritance



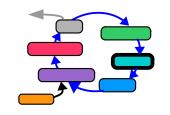
Inheritance is the principle of transporting some of the information from the previous generation (parents), into the next generation, by generating the offspring out of the parents genomes.

Thus, generating offspring means to create new individuals with new genomes.

Inheritance in the context of Evolutionary Algorithms means to use the genomes of those parents that have been selected.

There is a wide variety of possible ways to generate offspring.

Inheritance



The most popular mechanism to implement the inheritance principle is to use k=2 parents and to combine their genomes (mostly called recombination).

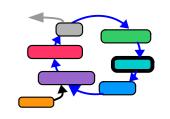
The most popular mechanism to implement recombination of 2 genomes is cross over:

Inheritance:

- recombination
 - by cross over
 - (other recombination operators)
- (other inheritance mechanism)
 - (other inheritance operators)
 - ...

<u>EA:</u>

Inheritance



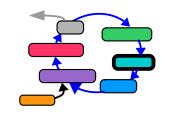
Recombination by **1-point cross over**:

Select two parents, A and B and recombine their genomes by taking one part form parent A and the other part from parent B

Choose a random point C where to split the genomes, and recombine the four remaining fractions to build new individuals, containing partial information from both parents.



Inheritance



Recombination by **1-point cross over**:

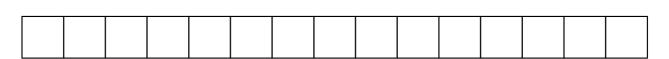
Parent A:



Parent B:

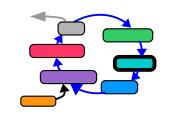


Child 1:





Inheritance



Recombination by **1-point cross over**:

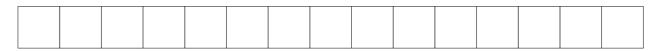


Parent A:

Parent B:

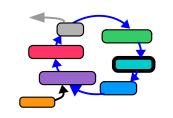


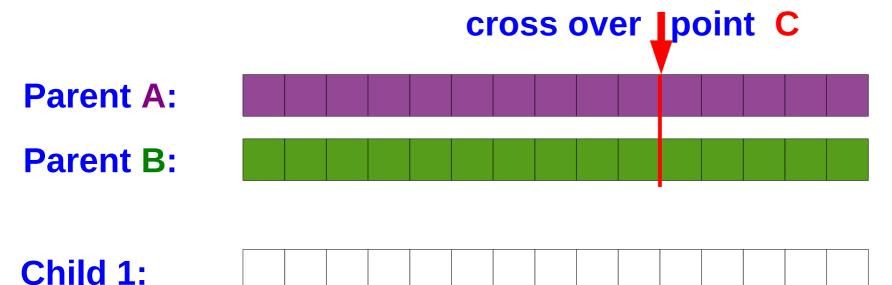
Child 1:



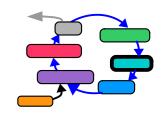


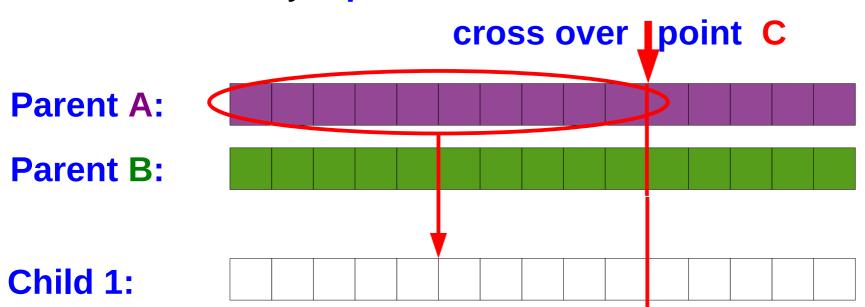
Inheritance



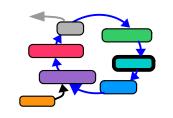


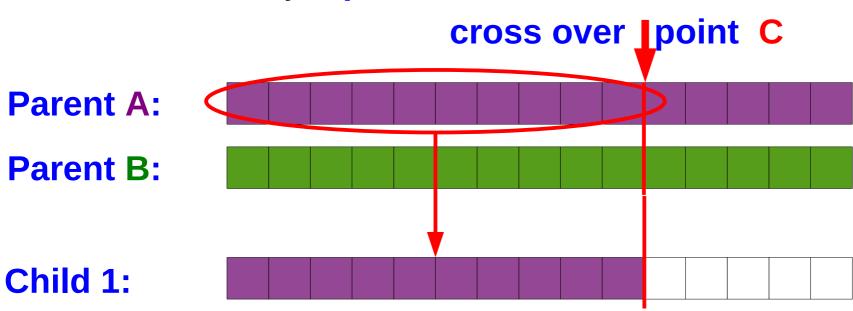
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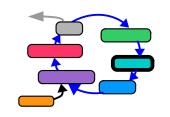


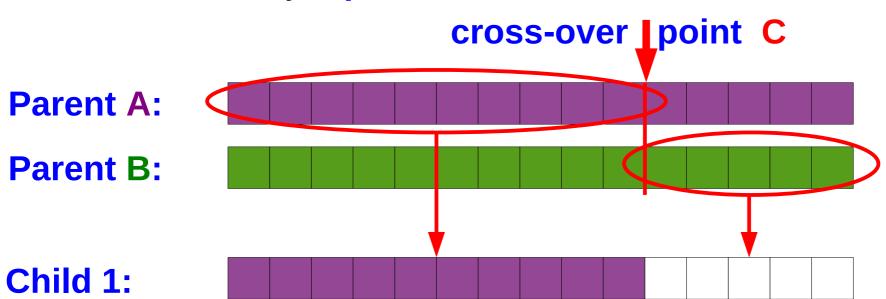
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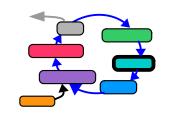


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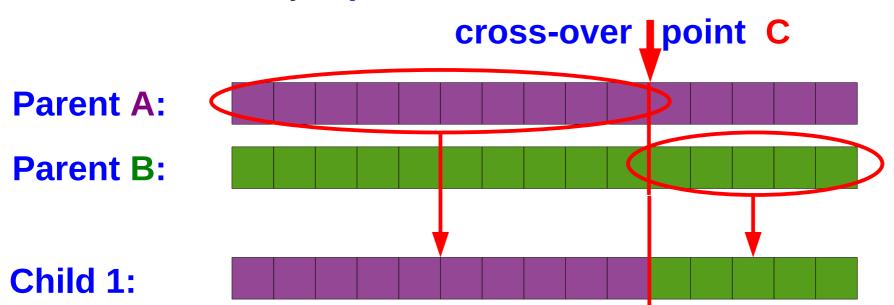




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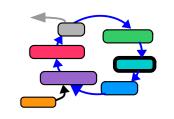


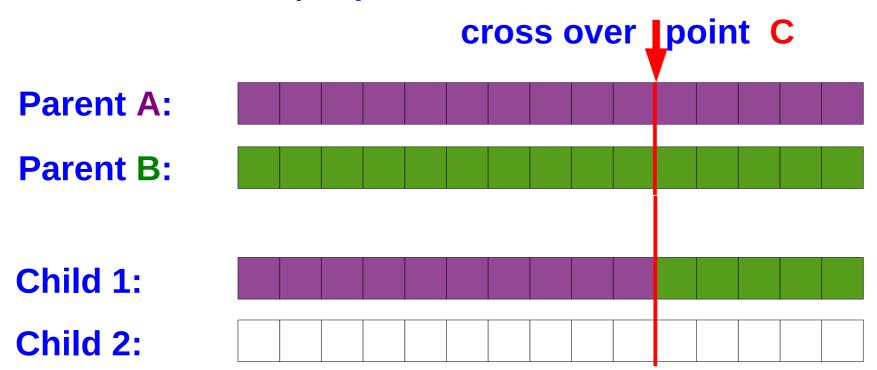
Recombination by **1-point cross-over**:



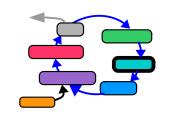
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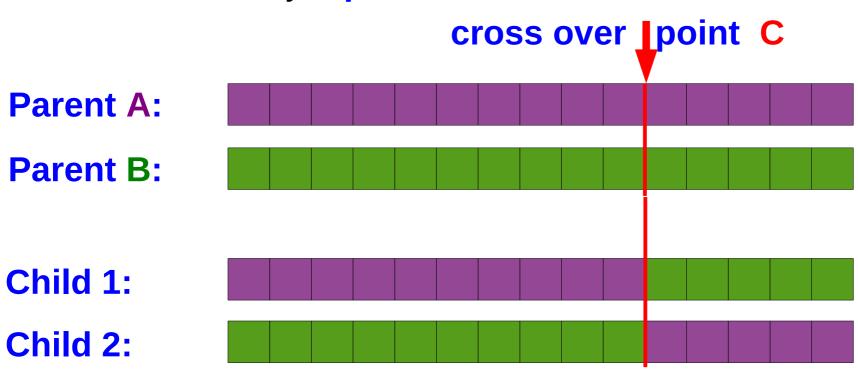
Inheritance



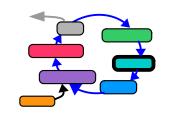


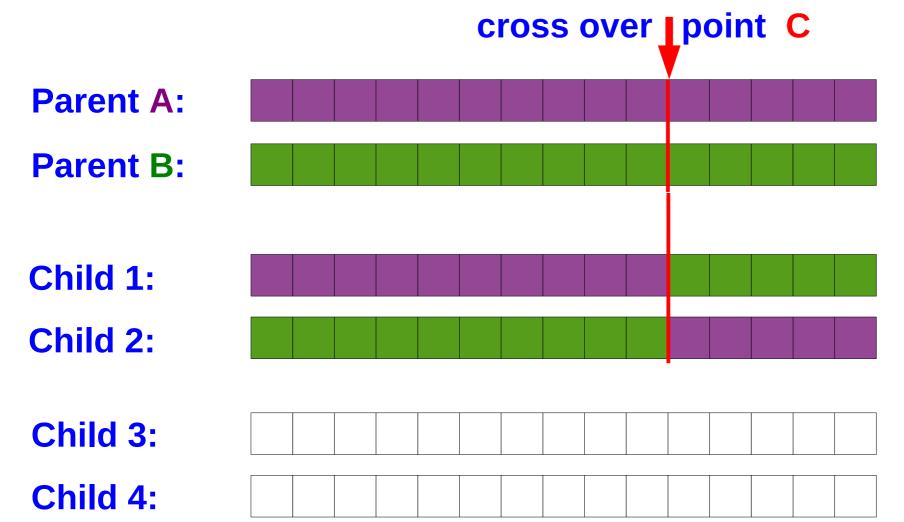
Inheritance



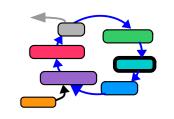


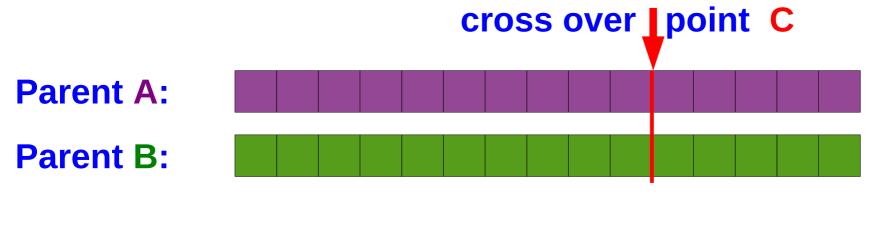
Inheritance





Inheritance





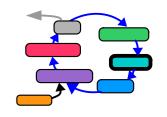








Inheritance



k=2 and k>2, recombination with k parents

Several ways to combine (or re-combine) the genomes of the k parents have been proposed.

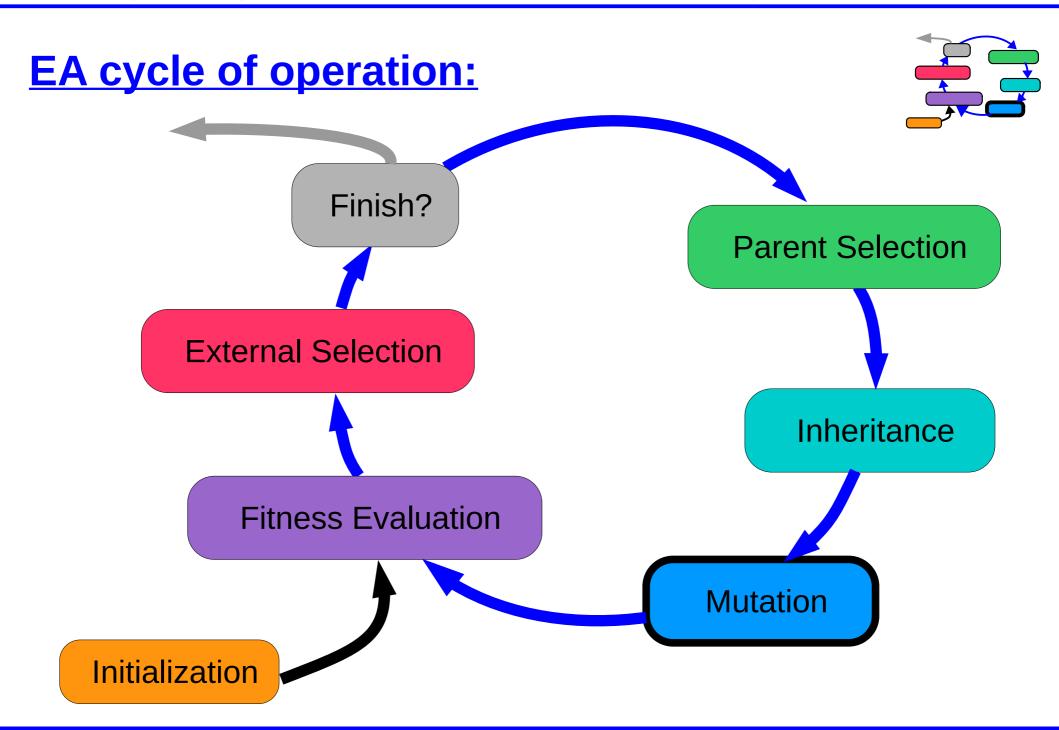
Some of them rely on a special structure of the genome.

- N-point cross over (the most popular)
- mean-values, one component, all components
- max, min, sum, difference of values
- union, intersection of sets of items
- concatenate (strings)

•

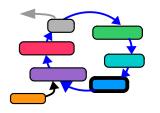
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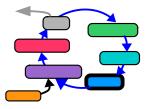


The job of the mutation step is to maintain the diversity of the genomes within the population:

Different positions in search space sample the fitness function at different points.

Changing the genome by **mutation** is implementing the **exploration** principle of **stochastic optimization**.

Mutation



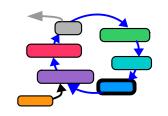
Depending on the different way the information is coded in the genome, the layout of the **mutation** step is to be designed differently.

Some common mutation operators are:

- Binary genome: a bit-flip
- Vector of parameters: change of value
- Set of items: replace a single item
- String of characters: replace a single character
- Sequence: change order within sequence
- Other: other method

Special codings of the genome will require that the mutation is paying respect to this coding.





The mutation for a binary genome is typically implemented as one or more bit-flips:

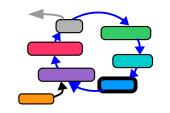
Method 1:

Choose a random position r in the genome and flip that bit. This yields a 100% chance that the genome is changed; the resulting Hamming distance is always exactly 1.

Before:





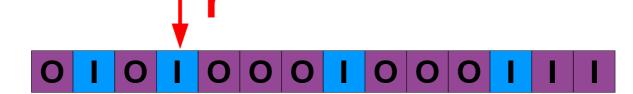


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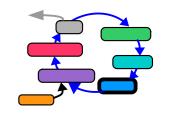
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Before:



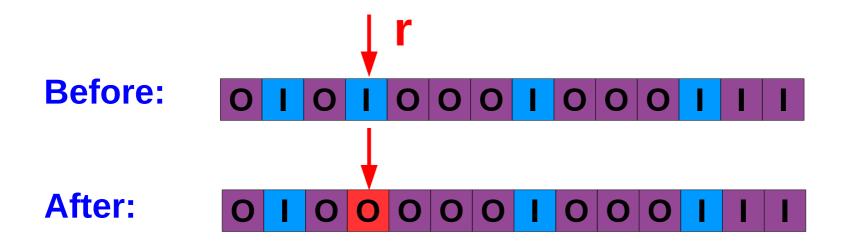




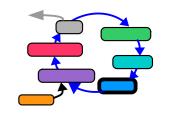
The mutation for a binary genome is typically implemented as one or more bit-flips:

Method 1:

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The mutation for a binary genome is typically implemented as one or more bit-flips:

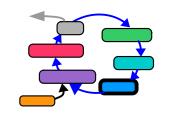
Method 2:

Go through all positions in the genome, and flip each bit with a given bit-flip-probability ω . There is a chance, that all bits are flipped, and a chance that none is flipped.

Before:







The mutation for a binary genome is typically implemented as one or more bit-flips:

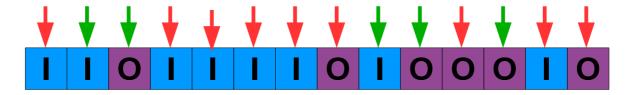
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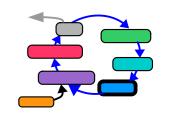
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 $0.0 < \omega < 1.0$

Before:







The mutation for a binary genome is typically implemented as one or more bit-flips:

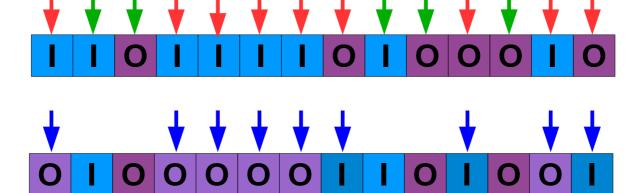
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There is a chance, that all bits are flipped, and a chance that none is flipped.

 $0.0 < \omega < 1.0$

Before:



After:





Inheritance

It is possible, that the inheritance and the mutation process yield invalid genomes, which represent hypotheses **s** from outside the allowed search space **S**.

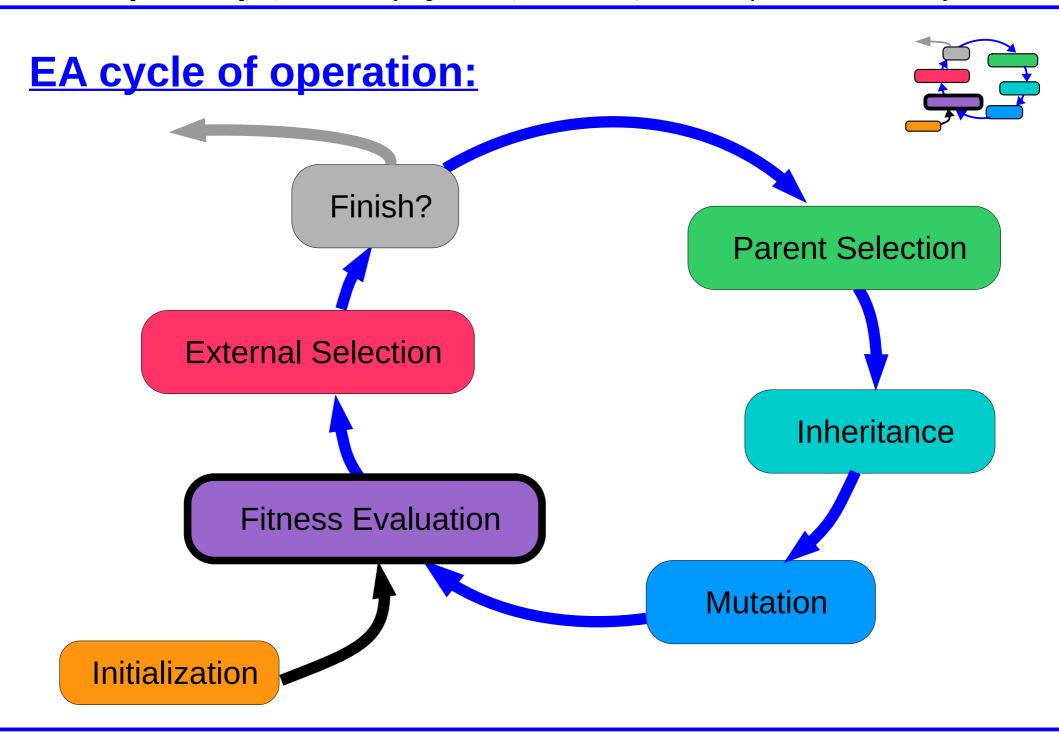
Those illegal genomes would stress the optimization process in an unwanted way.

Therefore, it is a good advise, to take precautions against illegal genomes (if possible, and economic):

- shape the structure of the genome,
- shape the structure of the inheritance,
- shape the structure of the mutation.

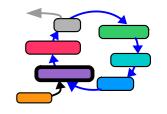
Overview:

- Evolutionary Computation
- Historic Remarks
- Different Approaches
- Idea of Evolutionary Algorithms (EA)
- EA Steps
 - Individual, Genome, Fitness, Population
 - Parent selection
 - Inheritance
 - Mutation
 - Fitness evaluation
 - External selection





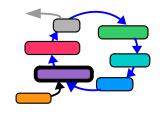
Fitness Evaluation



The fitness of each individual is evaluated with respect to the fitness-function (most case identical to the objective function). For Evolutionary Algorithms, it is usual to have a fitness function that is to be maximized.



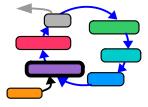
Fitness Evaluation



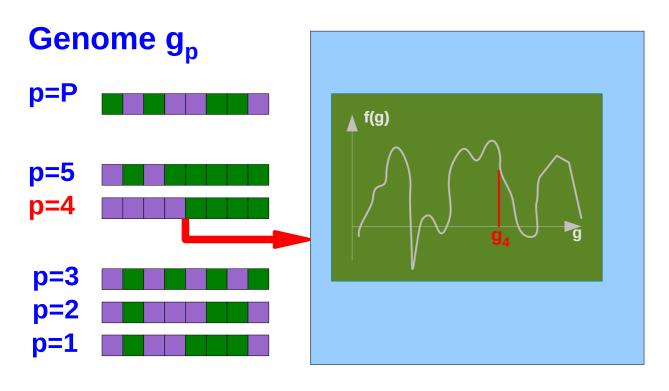
The **fitness** of each individual is evaluated with respect to the **fitness-function** (most case identical to the objective function). For Evolutionary Algorithms, it is usual to have a **fitness** function that is to be maximized.

If the **fitness evaluation** is expensive, it is a good idea to process only the new individuals/genomes from the inheritance step, including those individuals/genomes that have changed during mutation.

Fitness Evaluation



The fitness $f(g_p)$ of each individual p is evaluated with respect to the application using the given fitness-function f(g).



Fitness Value f(g_p)

$$f(g_p) =$$

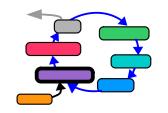
$$f(g_4) = ???$$

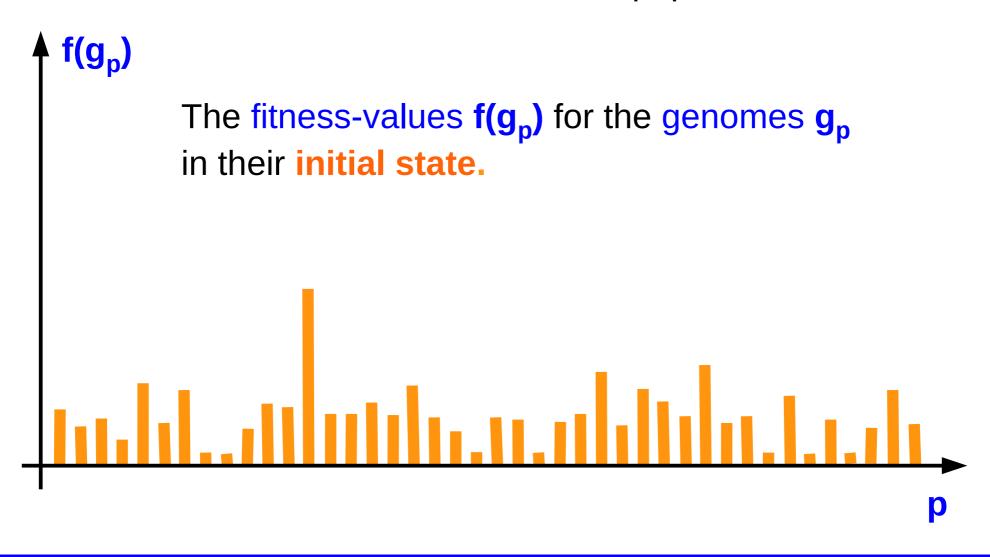
$$f(g_3) = 0.228$$

$$f(g_2) = -171.0$$

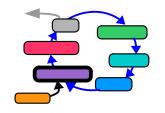
$$f(g_1) = 0.5$$

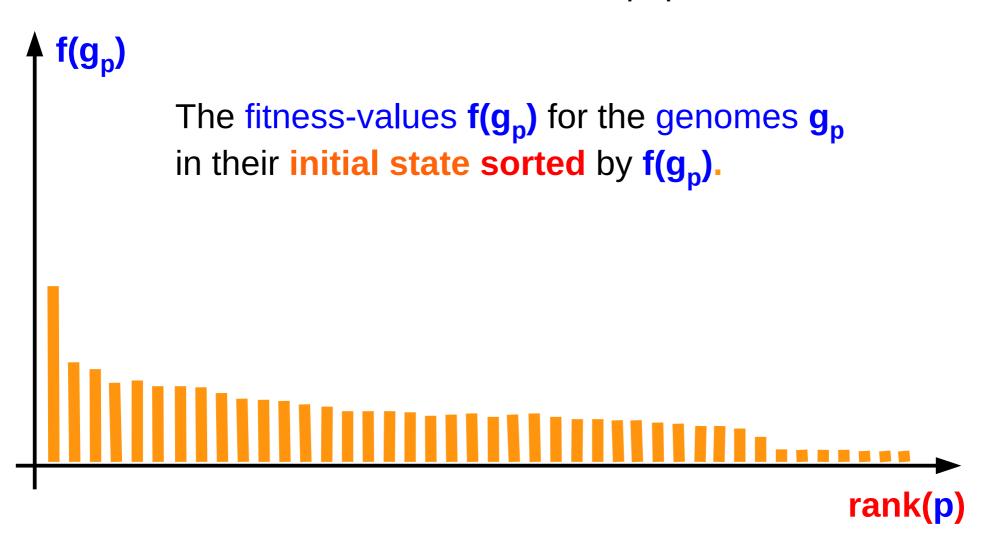
Fitness Evaluation



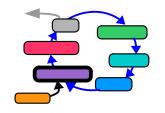


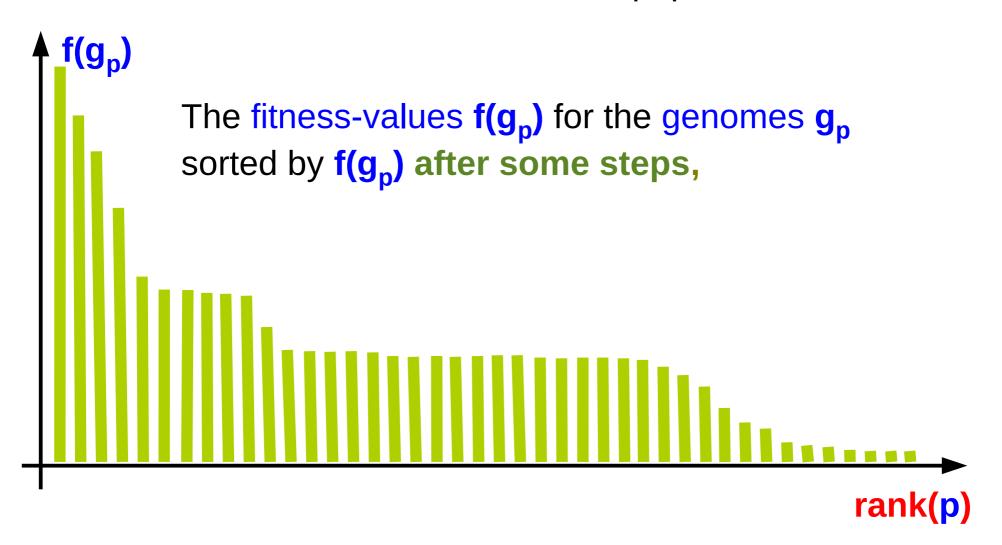
Fitness Evaluation



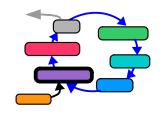


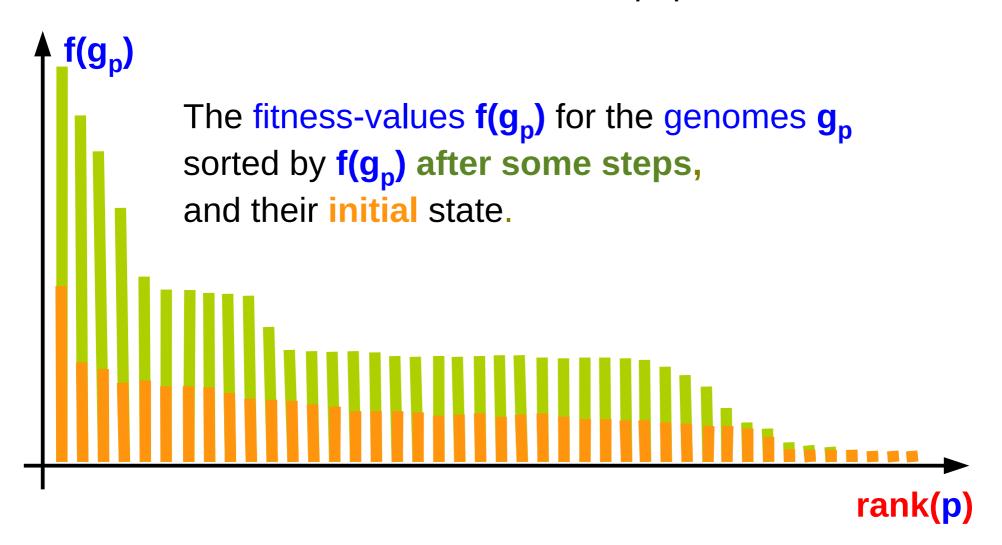
Fitness Evaluation





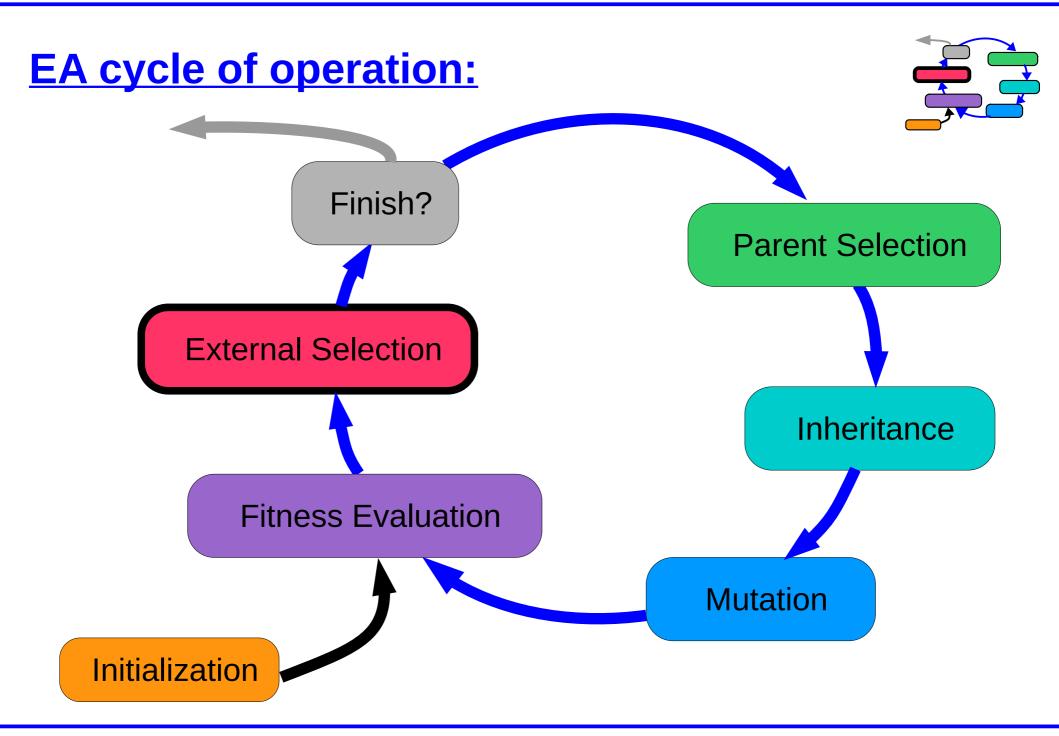
Fitness Evaluation



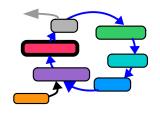


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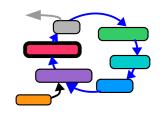




The purpose of the **selection process** is to keep the "Best", and discard the "Losers". The **selection** is based on the achieved fitness, which is obtained by the fitness function, quasi from **external** to the EA.

The μ individuals that survive the external selection process, will be the pool for the parents of the next generation. Later on, from these μ parents the λ offspring will be generated through the inheritance process.

External Selection



The two questions for the **external selection** are:

How many (μ) of the individuals shall survive?

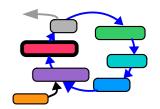
and

Which are the ones to keep?

A common way is to keep the population constant to P individuals.

discard λ by external selection and keep μ as pool for the parents, then generate λ offspring for the next generation.

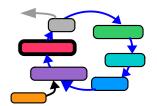




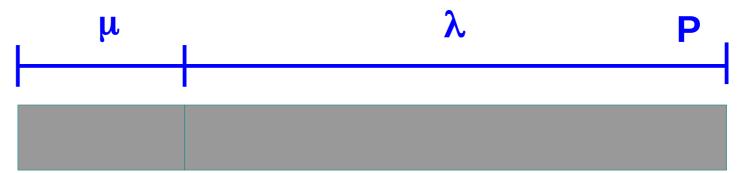
Have P, keep μ , generate λ offspring



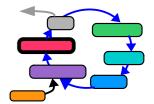




Have P, keep μ , generate λ offspring



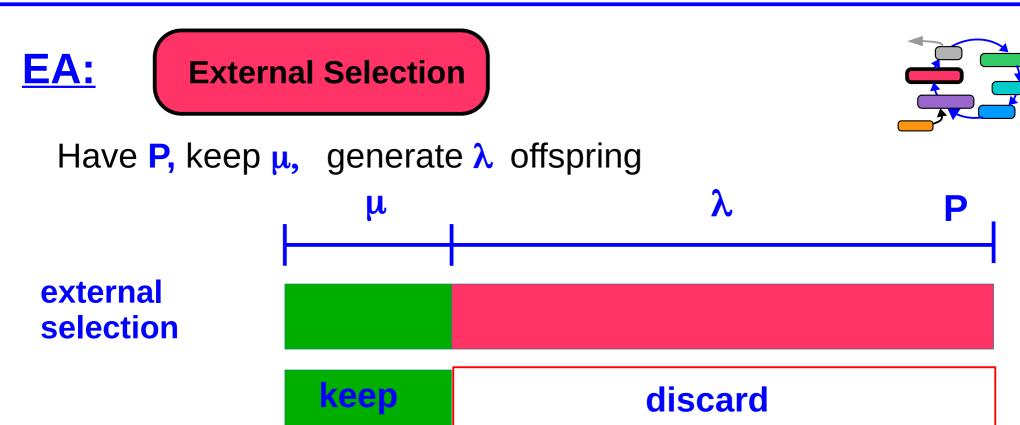


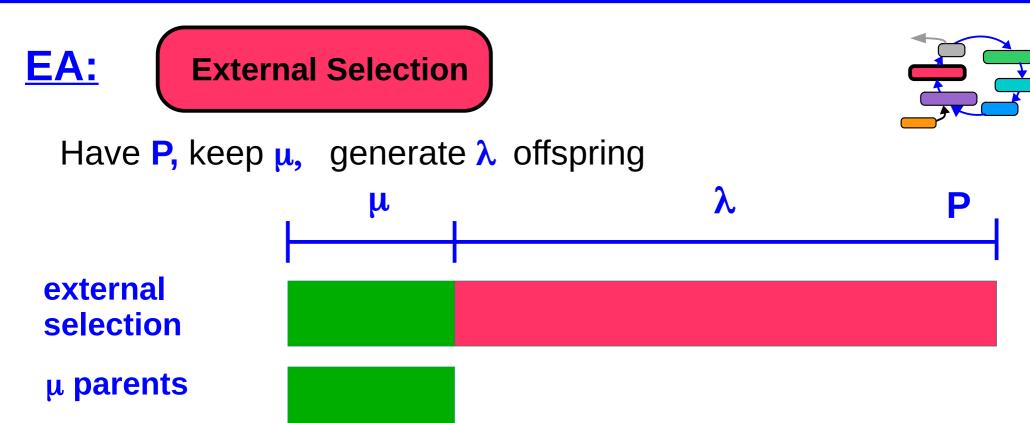


Have P, keep μ , generate λ offspring

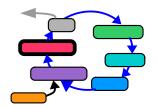


external selection

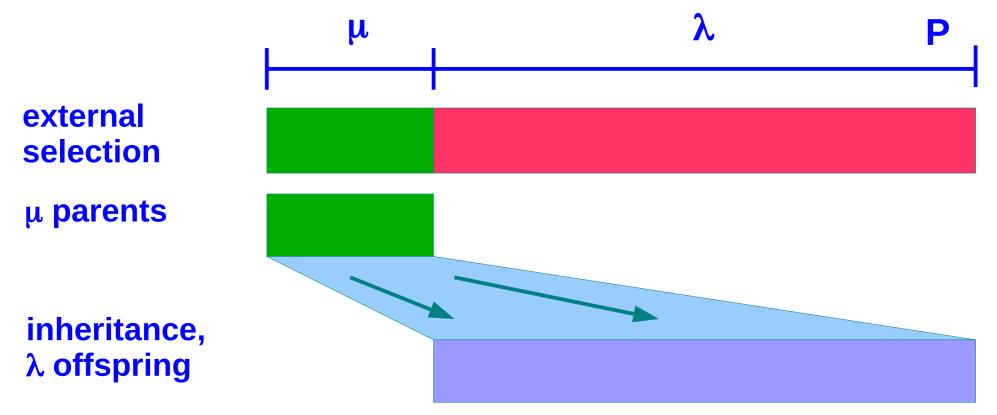




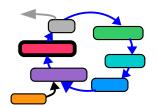




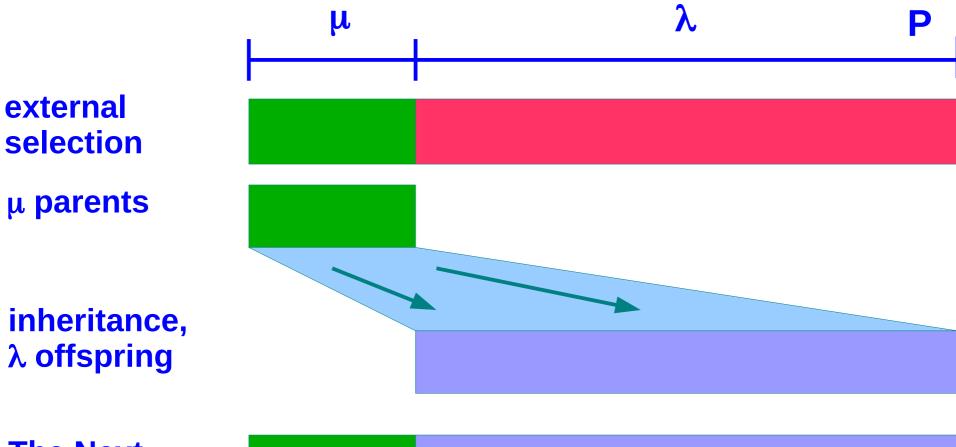
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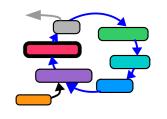
Have P, keep μ , generate λ offspring



The Next Generation

TNG

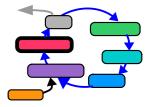
External Selection



Common strategies for the external selection are:

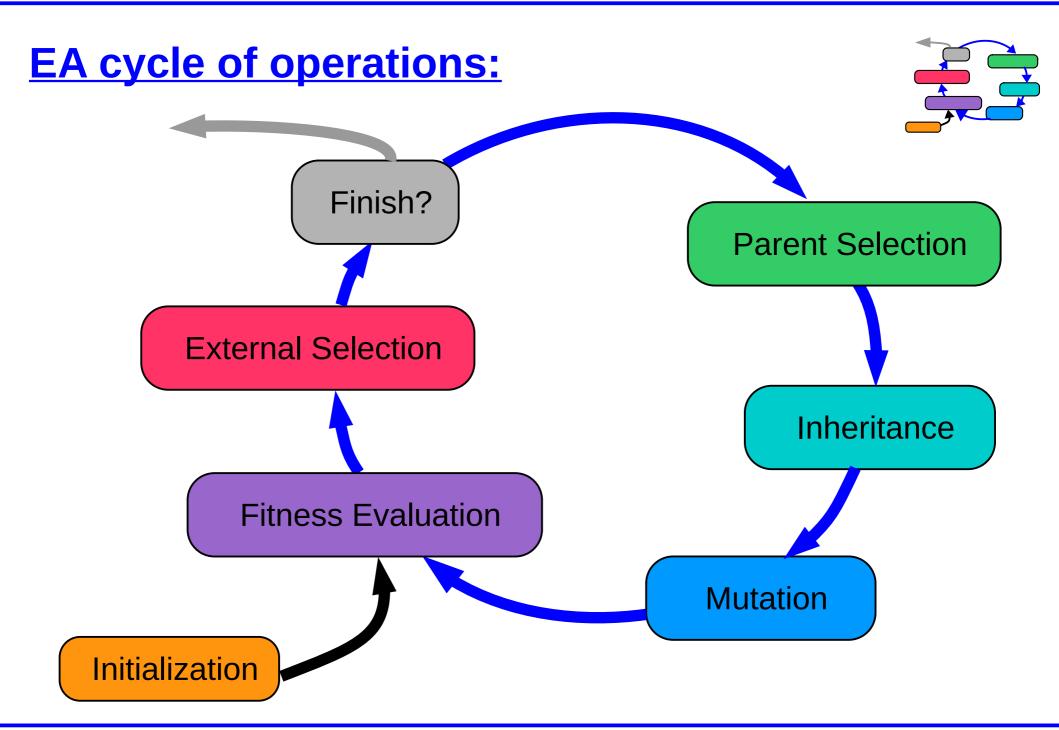
- random choice
- schedule based, e.g. round robin
- fitness based elitism: fitness proportional choice rank proportional choice
- fitness based stochastic:
 fitness proportionate, probabilistic choice
 rank proportionate, probabilistic choice
- combinations of the above

External Selection



There are different ideas and principles behind the selection of the μ possible parents from the population, with special pros and cons.

- deterministic or stochastic selection
- fitness dependent selection
- fitness proportional selection
- rank-based selection
- tournament selection
- life-time based selection
- combinations of the above + more



Artificial Life Summer 2025

Learning from Nature Evolutionary Algorithms Optimization Inspired by Biology

Master Computer Science [MA-INF 4201] Mon 14:15 – 15:45, HSZ, HS-2

Dr. Nils Goerke, Autonomous Intelligent Systems, Department of Computer Science, University of Bonn

Artificial Life Summer 2025

Learning from Nature

Evolutionary Algorithms

Optimization Inspired by Biology

Thank you for attending the lecture

Dr. Nils Goerke, Autonomous Intelligent Systems, Department of Computer Science, University of Bonn