



**UiO** : **Department of Informatics**  
University of Oslo

**INF3490/4490**

**Biologically inspired computing**

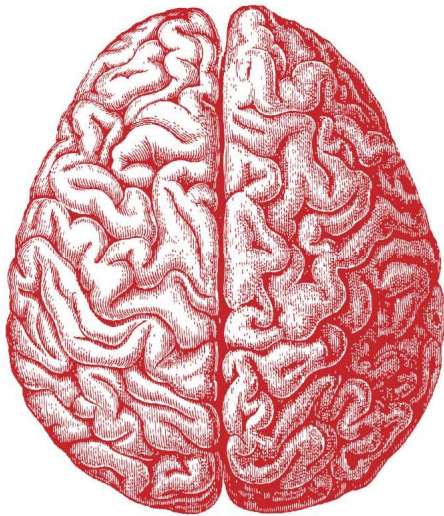
Lecture 2: Eiben and Smith, chapter 1-4

# **Evolutionary Algorithms - Introduction and representation**

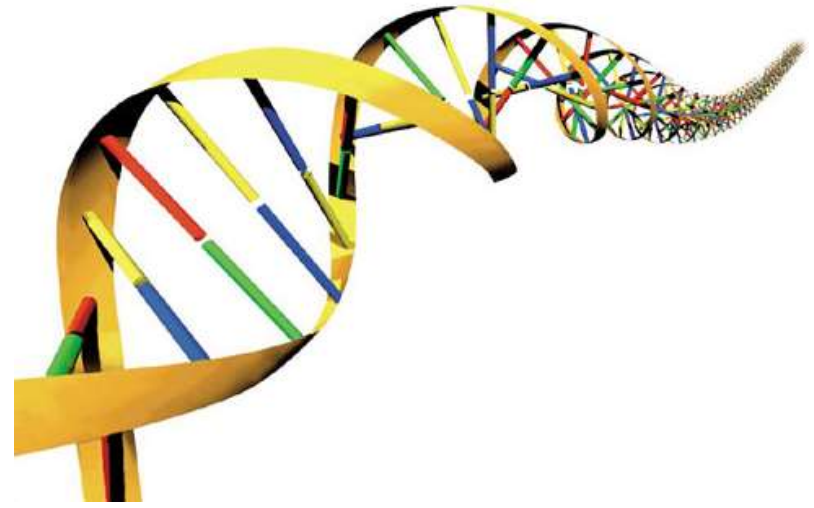
Kai Olav Ellefsen



# Why Draw Inspiration from Evolution?



# Evolution



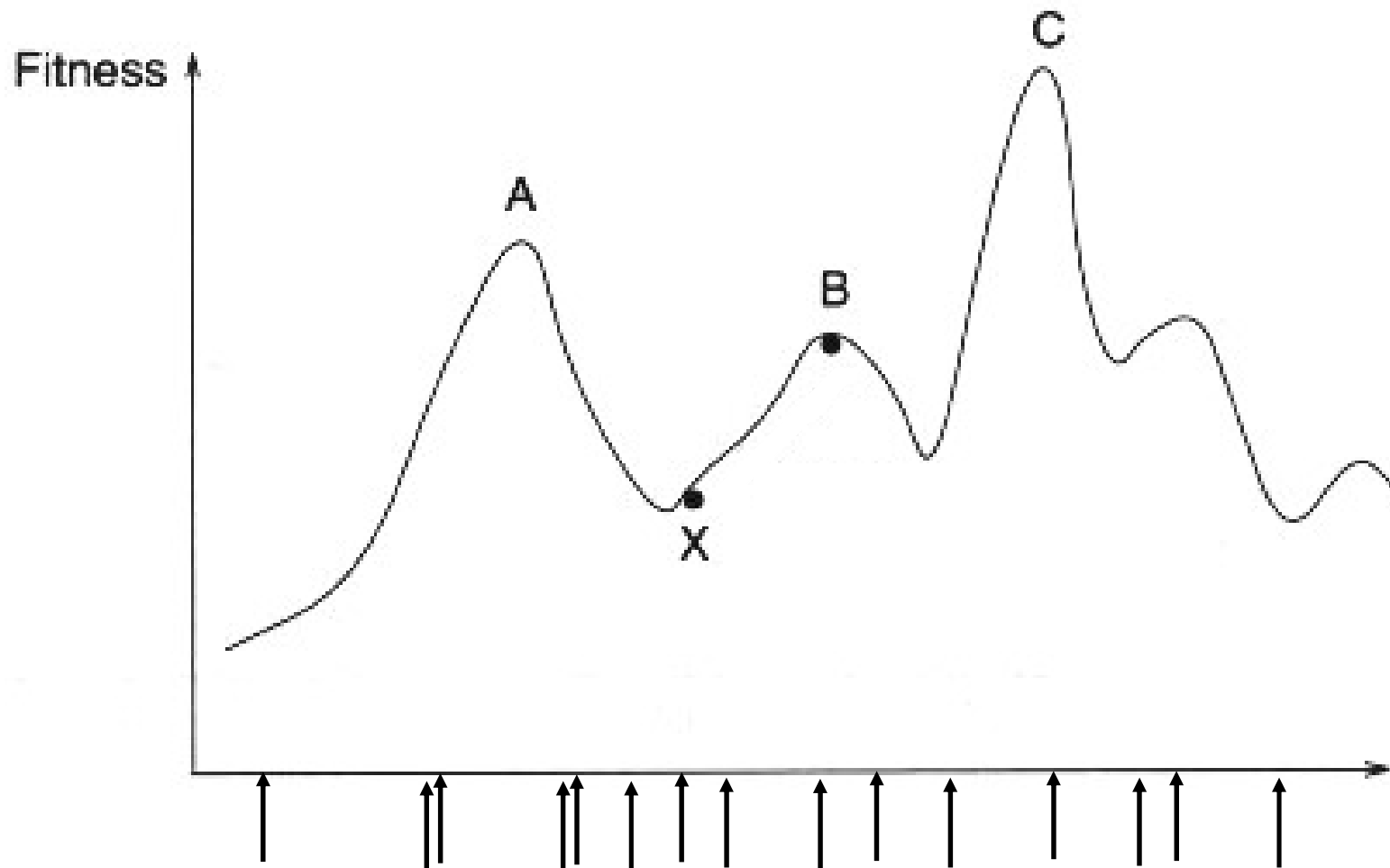
- **Biological evolution:**

- Lifeforms adapt to a particular environment over successive generations.
- Combinations of traits that are better adapted tend to increase representation in population.
- Mechanisms: Variation (Crossover, Mutation) and Selection (Survival of the fittest).

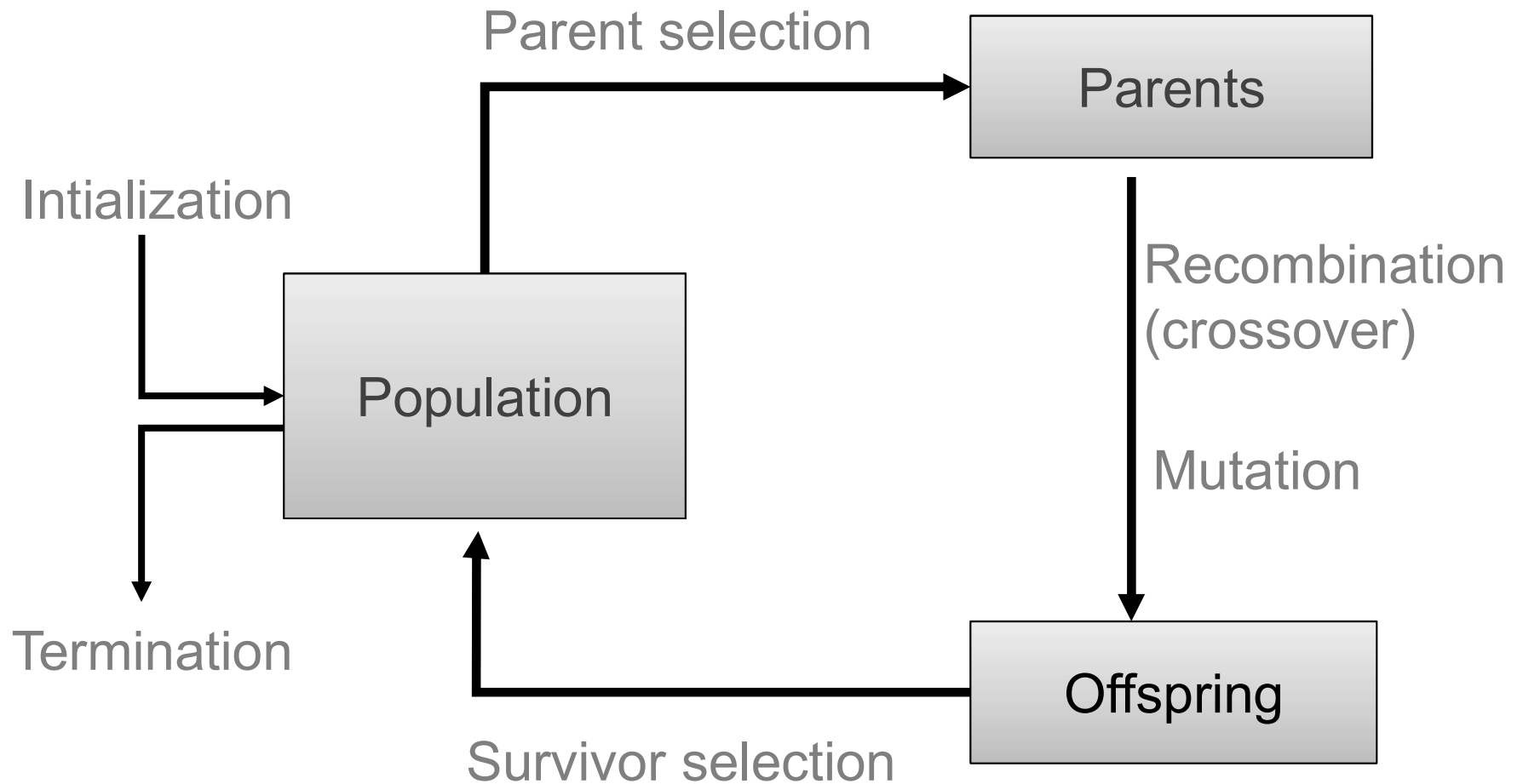
- **Evolutionary Computing (EC):**

- Mimic the biological evolution to optimize solutions to a wide variety of complex problems.
- In every new generation, a new set of solutions is created using bits and pieces of the fittest of the old.

# The Problem with Hillclimbing



# General scheme of EAs



## EA scheme in pseudo-code

```
BEGIN
  INITIALISE population with random candidate solutions;
  EVALUATE each candidate;
  REPEAT UNTIL ( TERMINATION CONDITION is satisfied ) DO
    1 SELECT parents;
    2 RECOMBINE pairs of parents;
    3 MUTATE the resulting offspring;
    4 EVALUATE new candidates;
    5 SELECT individuals for the next generation;
  OD
END
```



# Scheme of an EA:

## Two pillars of evolution

There are two competing forces

**Increasing** population  
**diversity** by genetic operators

- mutation
- recombination

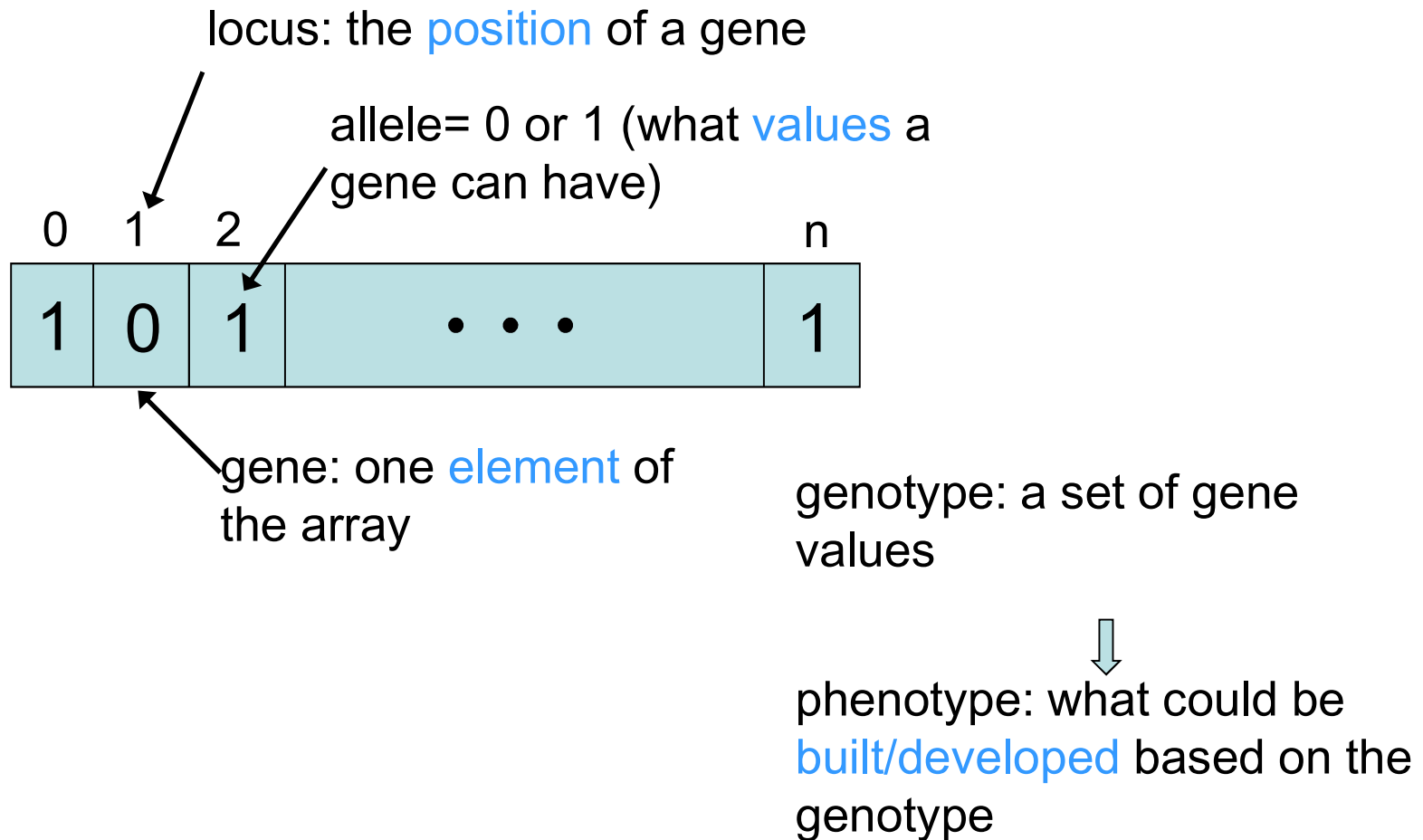
Push towards **novelty**

**Decreasing** population **diversity**  
by selection

- of parents
- of survivors

Push towards **quality**

# Representation: EA terms

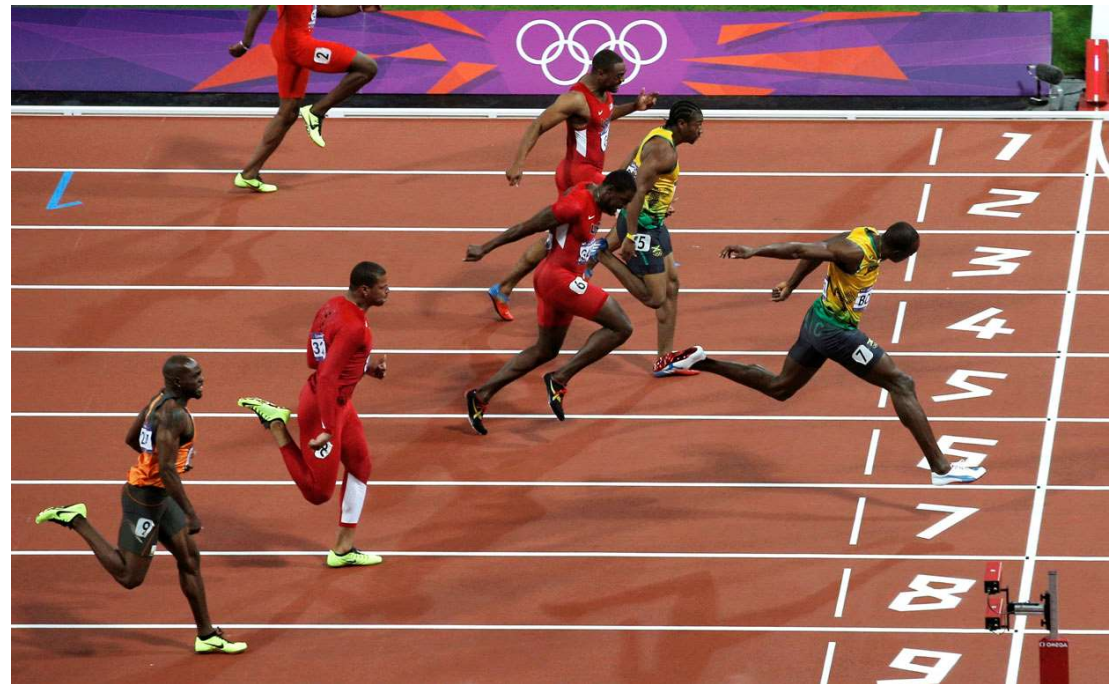




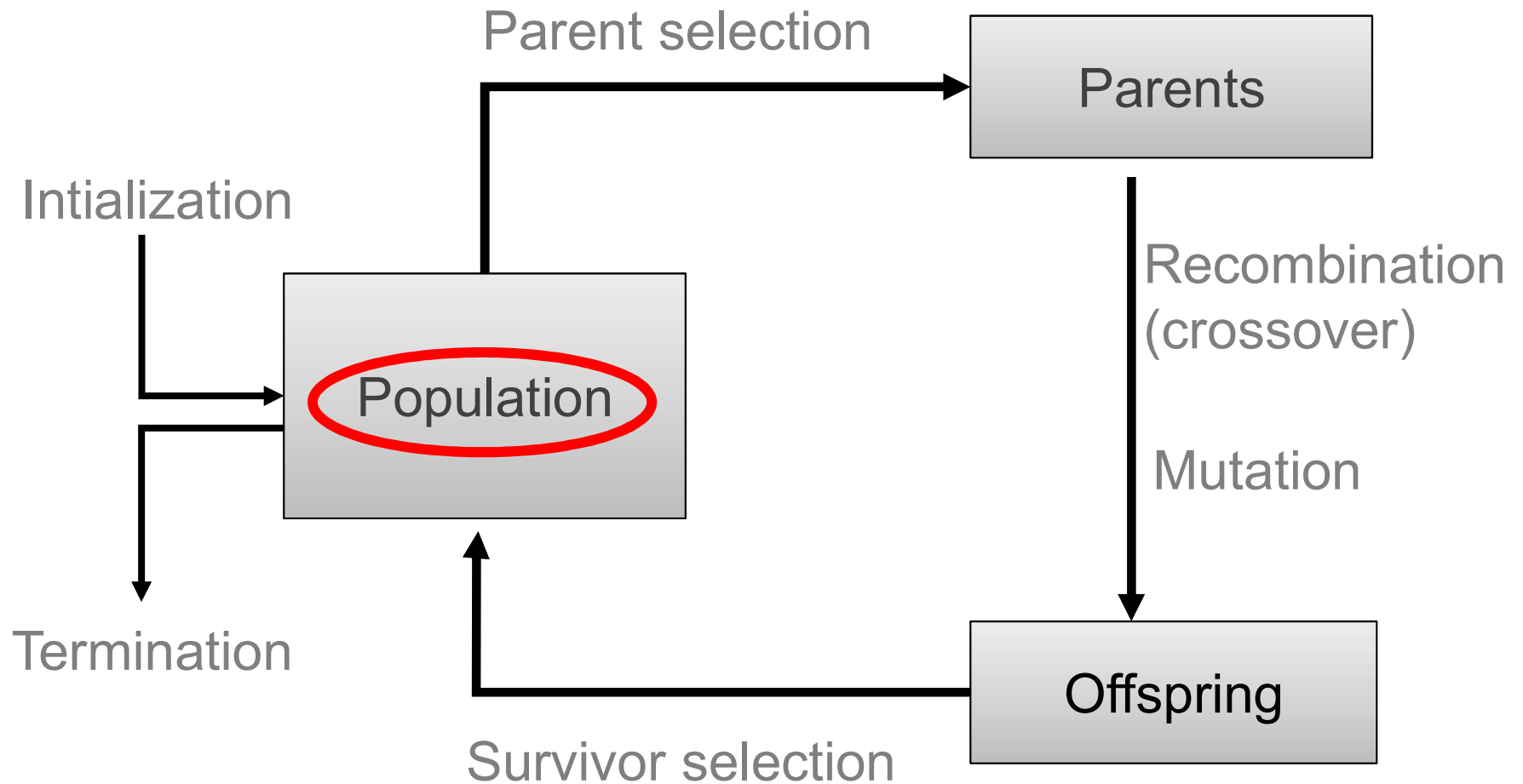
# Main EA components:

## Evaluation (fitness) function

- Represents the task to solve
- Enables selection (provides basis for comparison)
- Assigns a single real-valued fitness to each phenotype



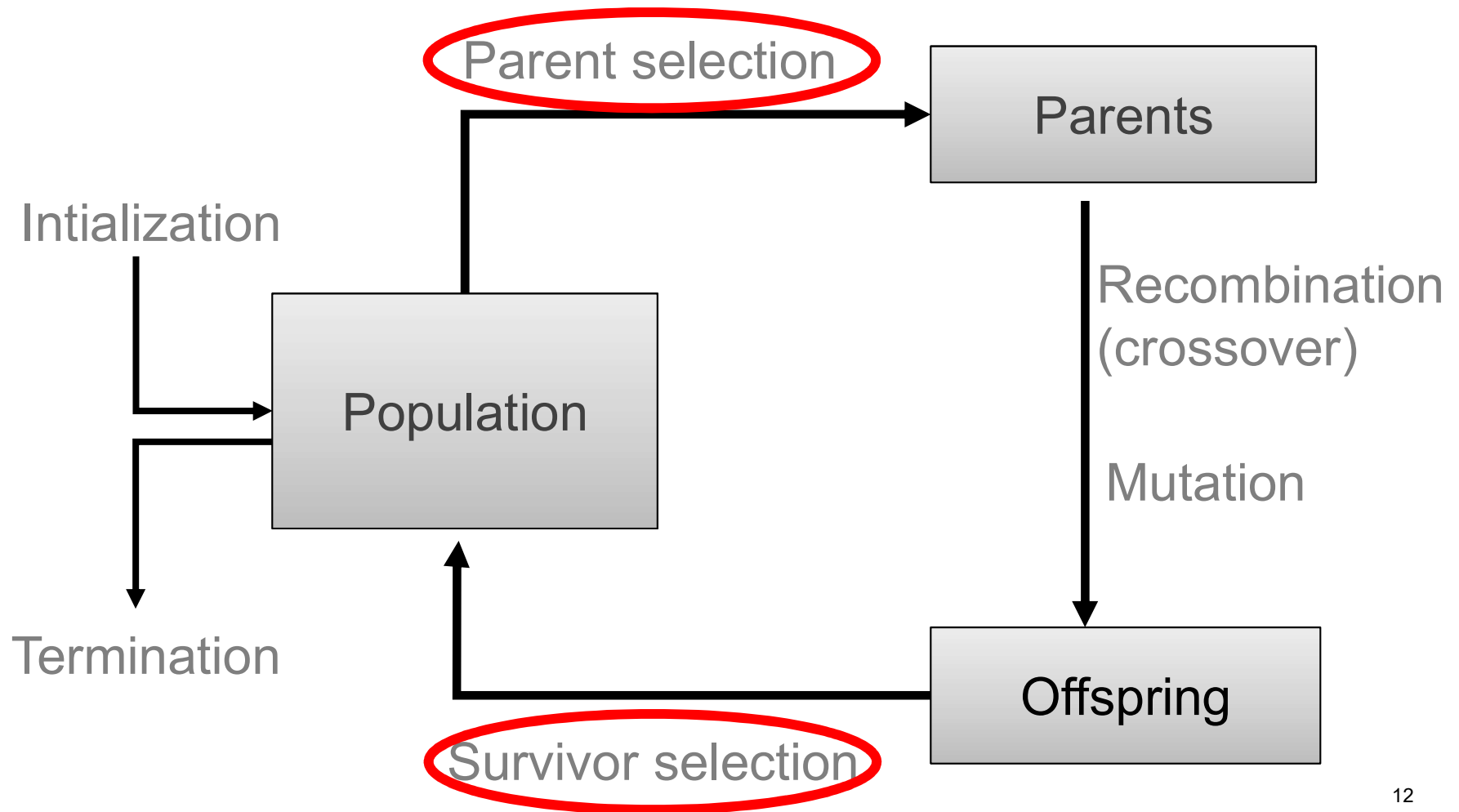
# General scheme of EAs



## Main EA components: Population

- The **candidate solutions (individuals)** of the problem
- Population is the basic unit of evolution, i.e., the **population is evolving**, not the individuals
- **Selection** operators act on **population level**
- **Variation** operators act on **individual level**

# General scheme of EAs



## Main EA components: Selection mechanism (1/3)

- Identifies individuals
  - to become parents
  - to survive
- Pushes population towards higher fitness
- Parent selection is usually probabilistic
  - high quality solutions more likely to be selected than low quality, but not guaranteed
  - This *stochastic* nature can aid escape from local optima

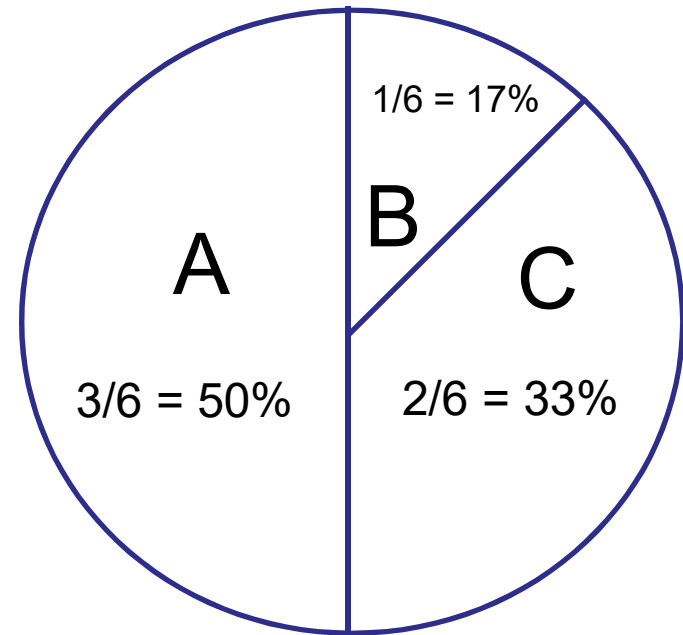
## Main EA components: Selection mechanism (2/3)

Example: roulette wheel selection

$\text{fitness}(A) = 3$

$\text{fitness}(B) = 1$

$\text{fitness}(C) = 2$



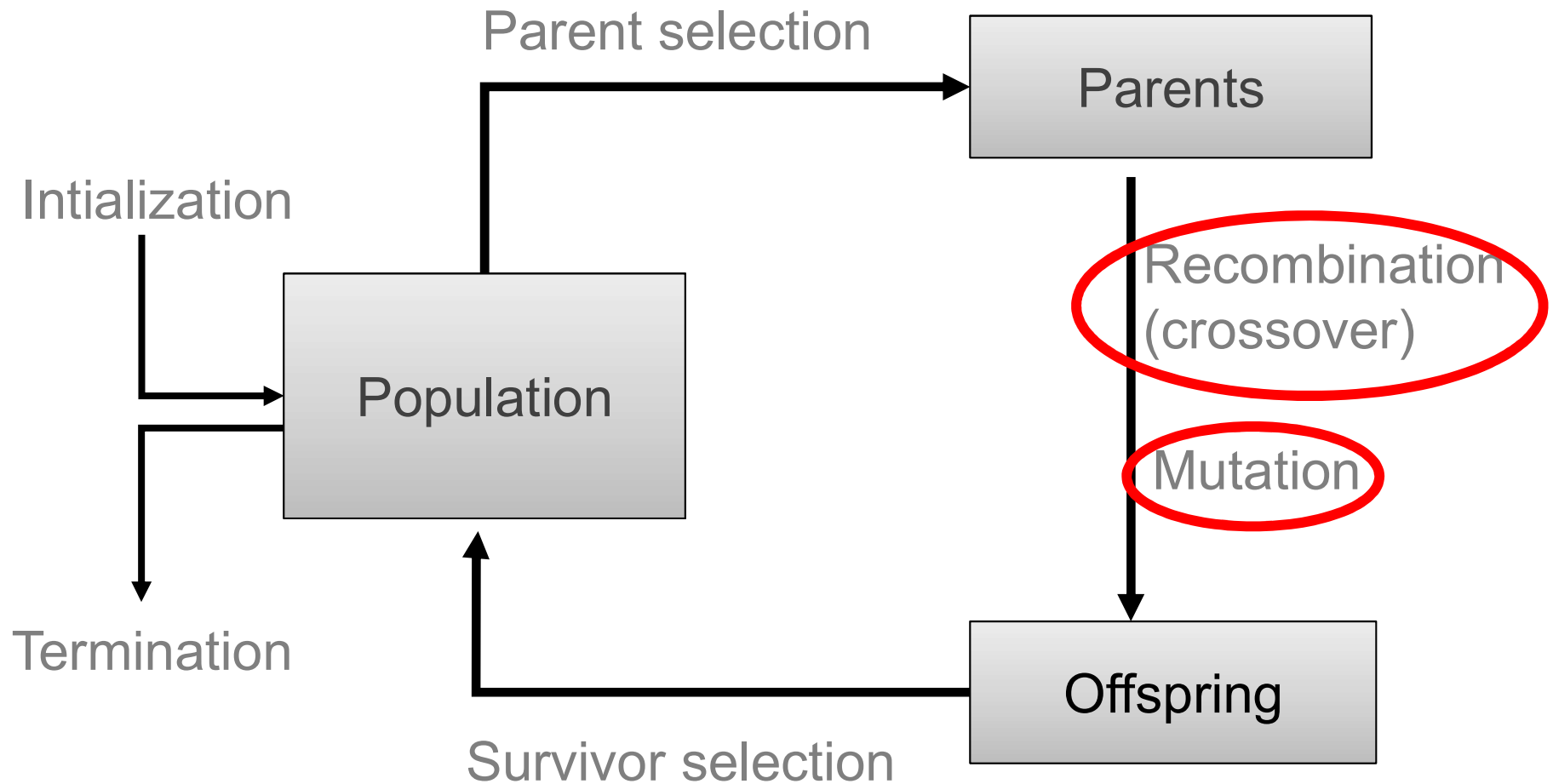
## Main EA components: Selection mechanism (3/3)

### Survivor selection:

- N old solutions + K new solutions (offspring) -> N individuals (new population)
- Often deterministic:
  - **Fitness based**: e.g., rank old population + offspring and take best
  - **Age based**: make N offspring and delete all old solutions
- Sometimes a combination of stochastic and deterministic (elitism)



# General scheme of EAs



# Main EA components:

## Variation operators

- Role: to generate new candidate solutions
- Usually divided into two types according to their **arity** (number of inputs to the variation operator):
  - Arity 1 : **mutation** operators
  - Arity  $>1$  : **recombination** operators
  - Arity = 2 typically called **crossover**
  - Arity  $> 2$  is formally possible, seldom used in EC

# Main EA components:

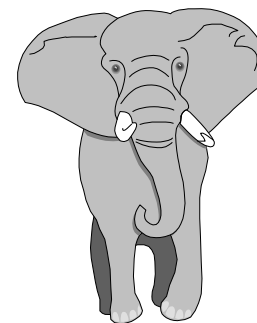
## Mutation (1/2)

- Role: cause small, random variance to a genotype
- Element of randomness is essential and differentiates it from other unary heuristic operators
- Importance ascribed depends on representation and historical dialect:
  - Binary Genetic Algorithms – background operator responsible for preserving and introducing diversity
  - Evolutionary Programming for continuous variables – the only search operator
  - Genetic Programming – hardly used

## Main EA components: Mutation (2/2)

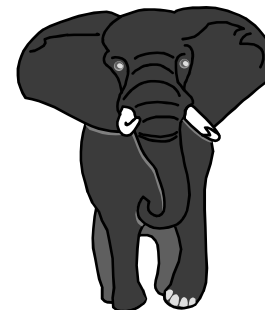
before

1 1 1 1 1 1 1

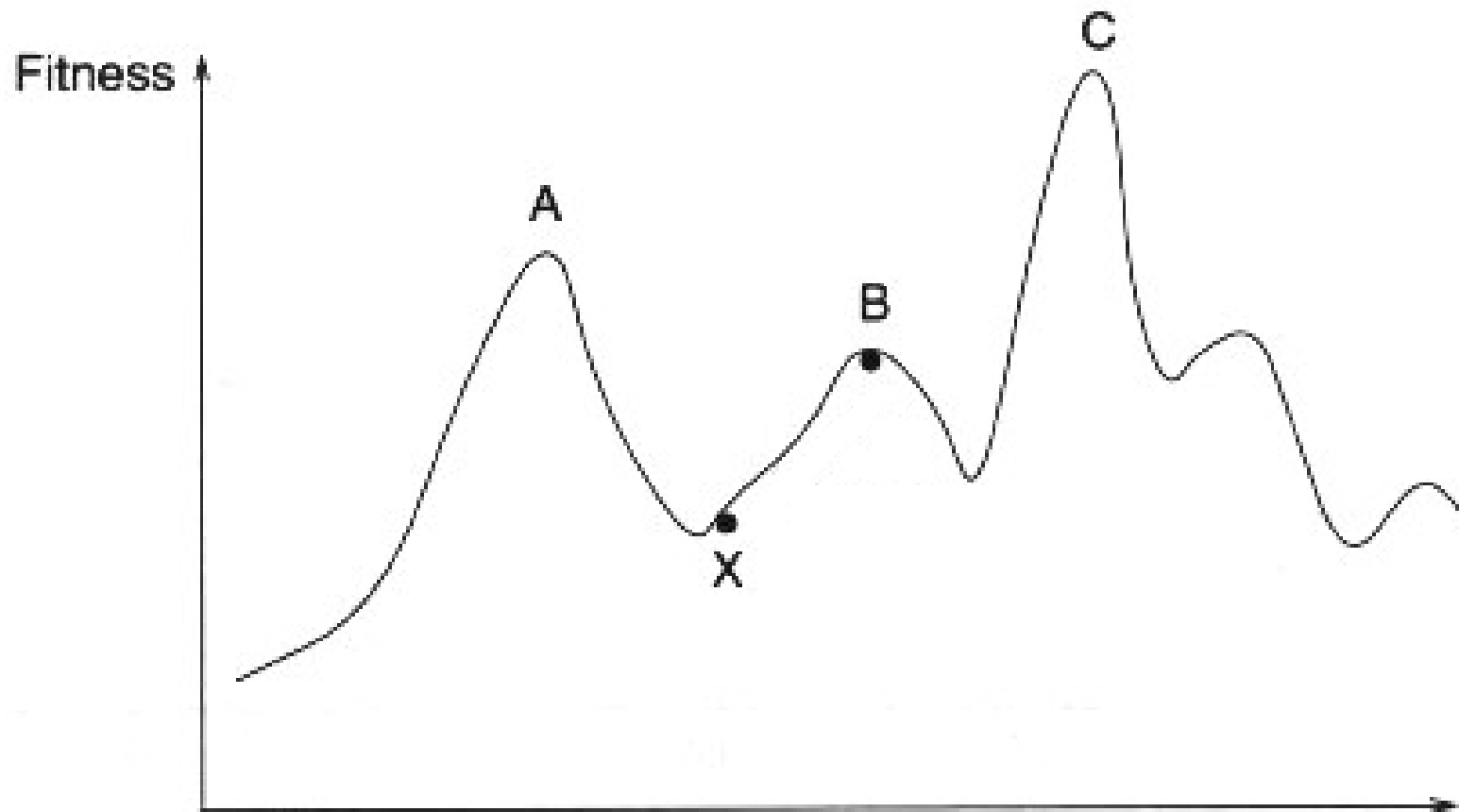


after

1 1 1 0 1 1 1



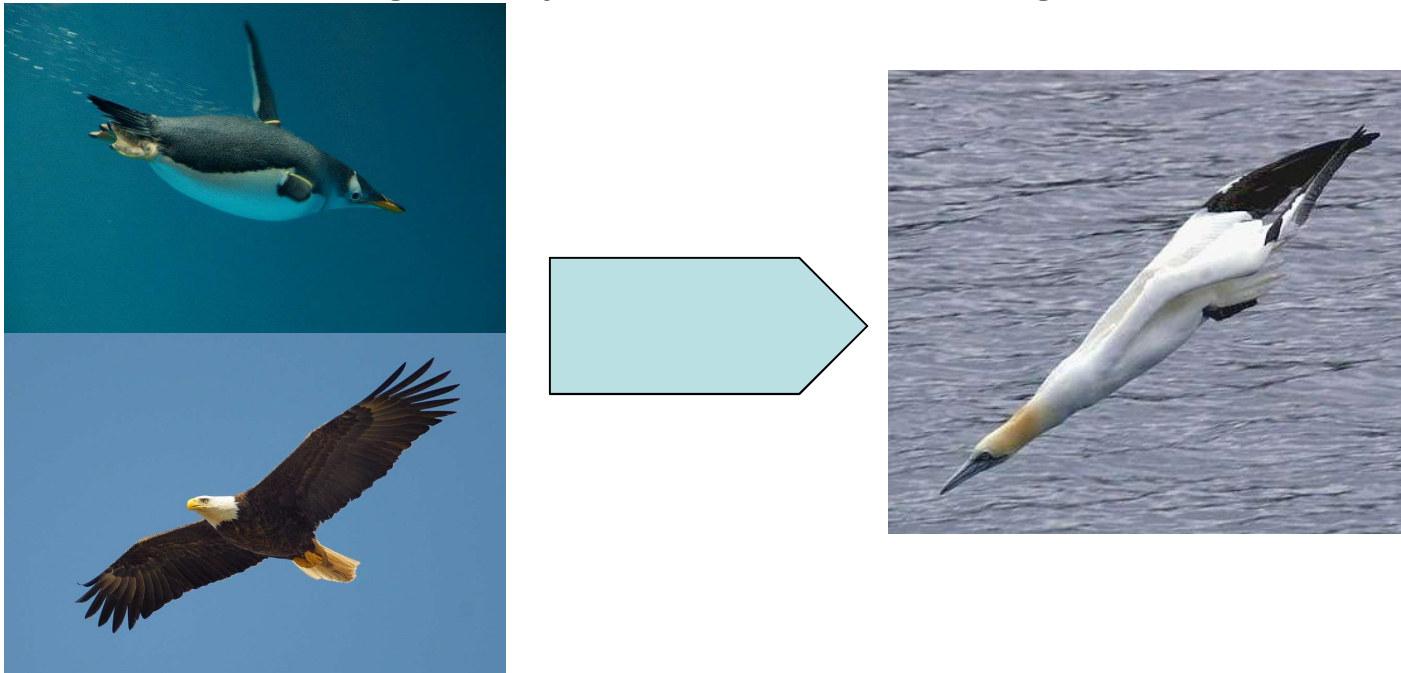
# Why do we do Random Mutation?



# Main EA components:

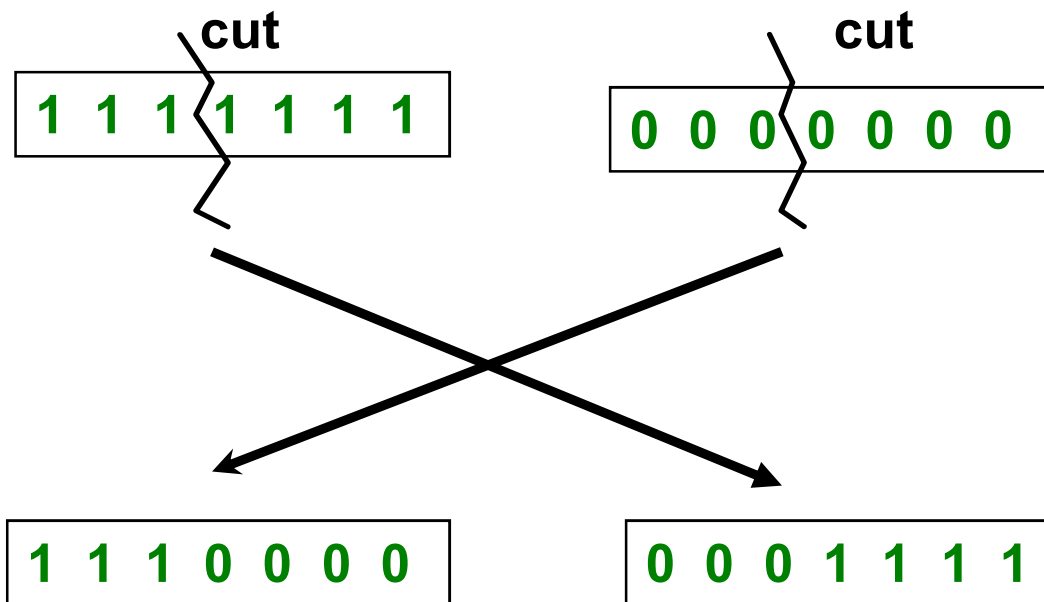
## Recombination (1/2)

- Role: merges information from parents into offspring
- Choice of what information to merge is stochastic
- Hope is that some offspring are better by combining elements of genotypes that lead to good traits

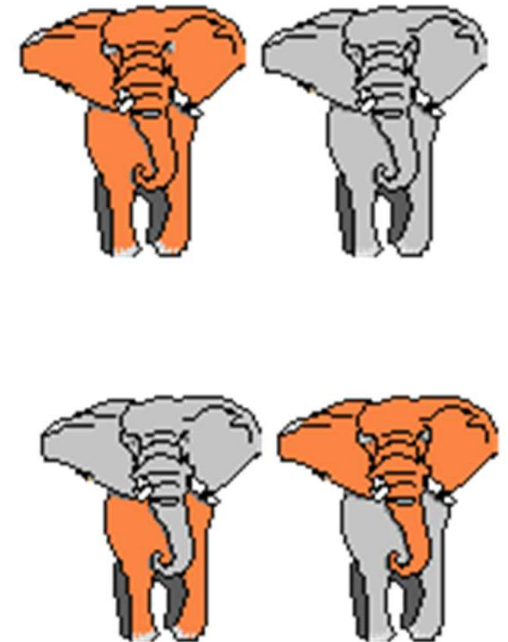


# Main EA components: Recombination (2/2)

Parents

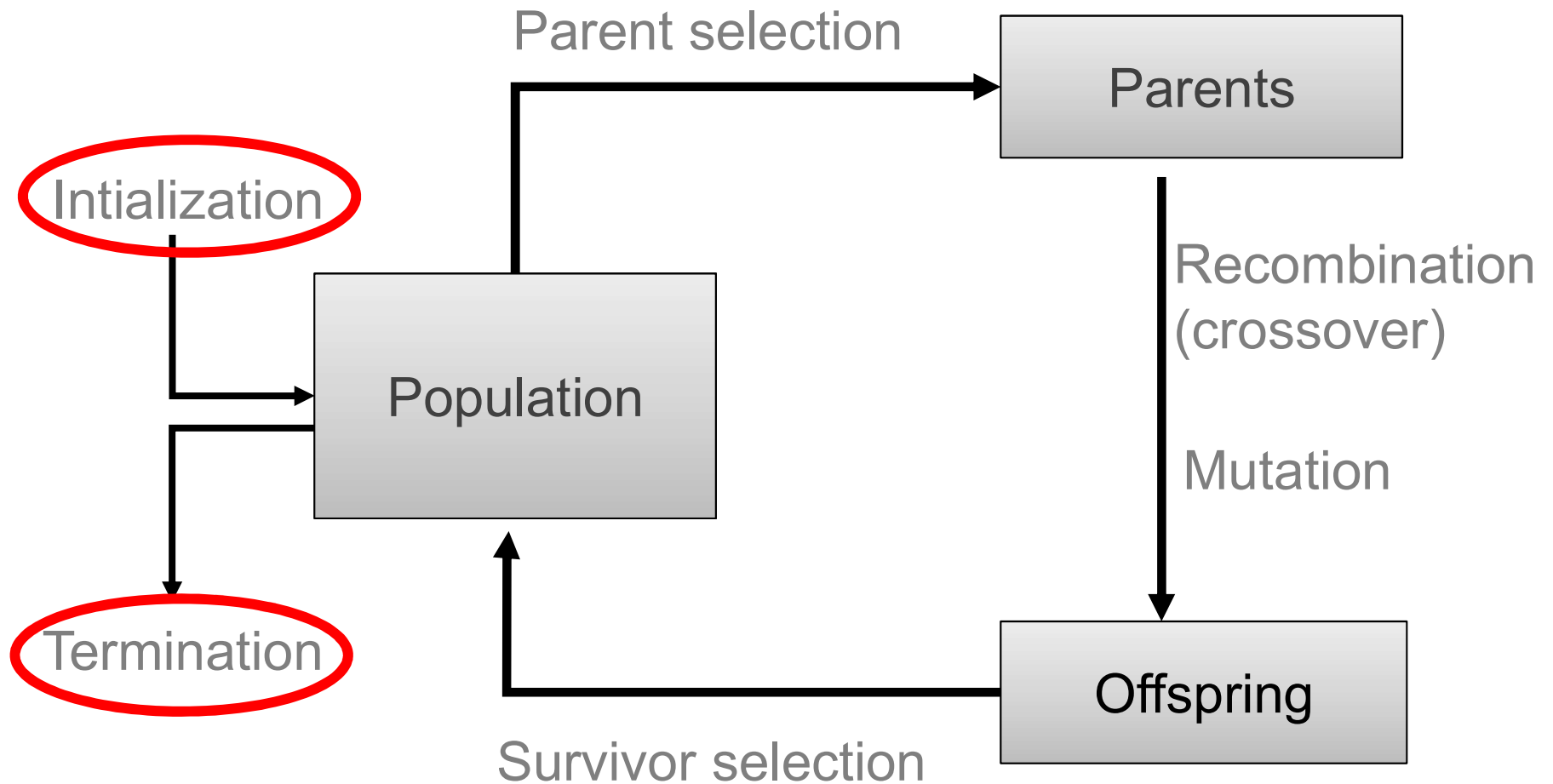


Offspring





# General scheme of EAs

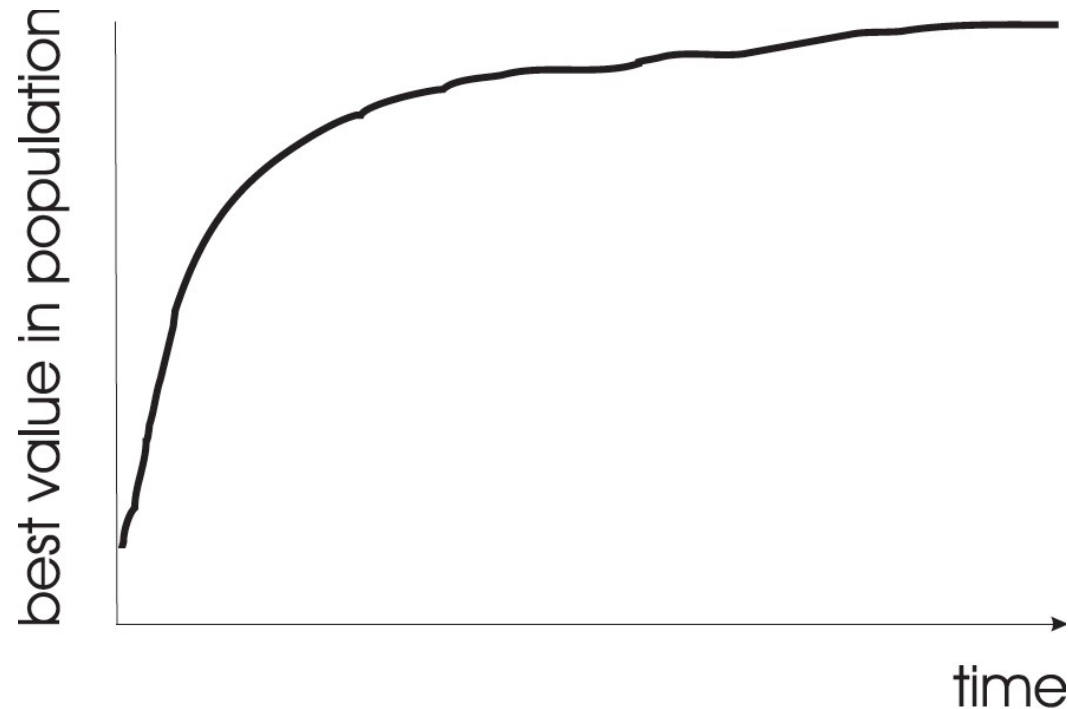


# Main EA components:

## Initialisation / Termination

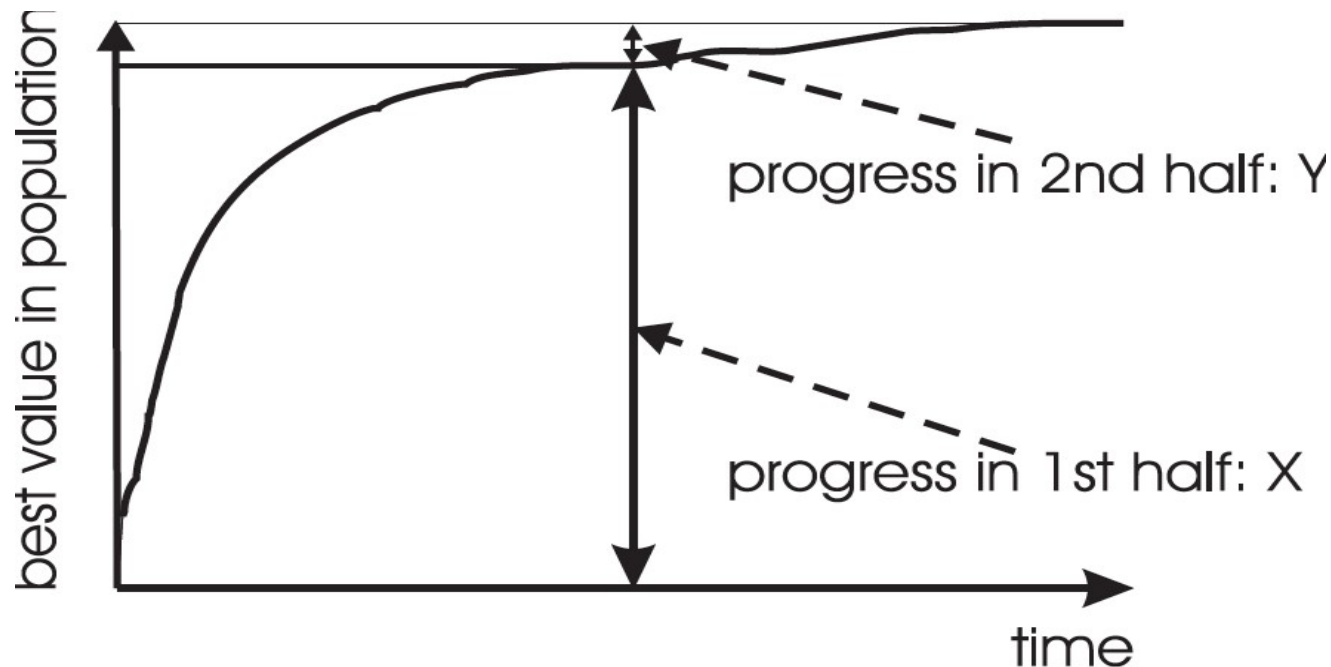
- Initialisation usually done at random,
  - Need to ensure even spread and mixture of possible allele values
  - Can include existing solutions, or use problem-specific heuristics, to “seed” the population
- Termination condition checked every generation
  - Reaching some (known/hoped for) fitness
  - Reaching some maximum allowed number of generations
  - Reaching some minimum level of diversity
  - Reaching some specified number of generations without fitness improvement

# Typical EA behaviour: Typical run: progression of fitness



# Typical EA behaviour: Are long runs beneficial?

- Answer:
  - It depends on how much you want the last bit of progress



# Chapter 4: Representation, Mutation, and Recombination

- Role of **representation** and **variation operators**
- Most common representation of genomes:
  - Binary
  - Integer
  - Real-Valued or Floating-Point
  - Permutation
  - Tree

# Role of representation and variation operators

- First stage of building an EA and most difficult one: choose *right* representation for the problem
- Type of variation operators needed depends on chosen representation

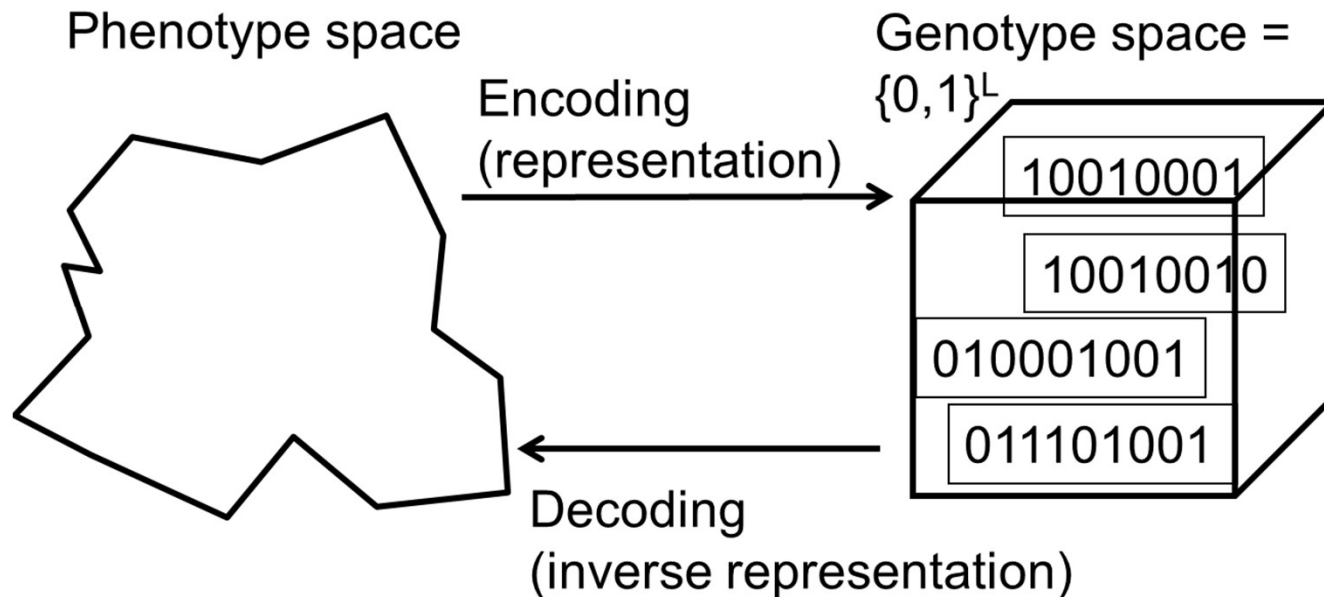
# TSP: How to represent?





# Binary Representation

- One of the earliest representations
- Genotype consists of a string of binary digits



# Binary Representation: Mutation

- Alter each gene independently with a probability  $p_m$
- $p_m$  is called the mutation rate

parent

1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

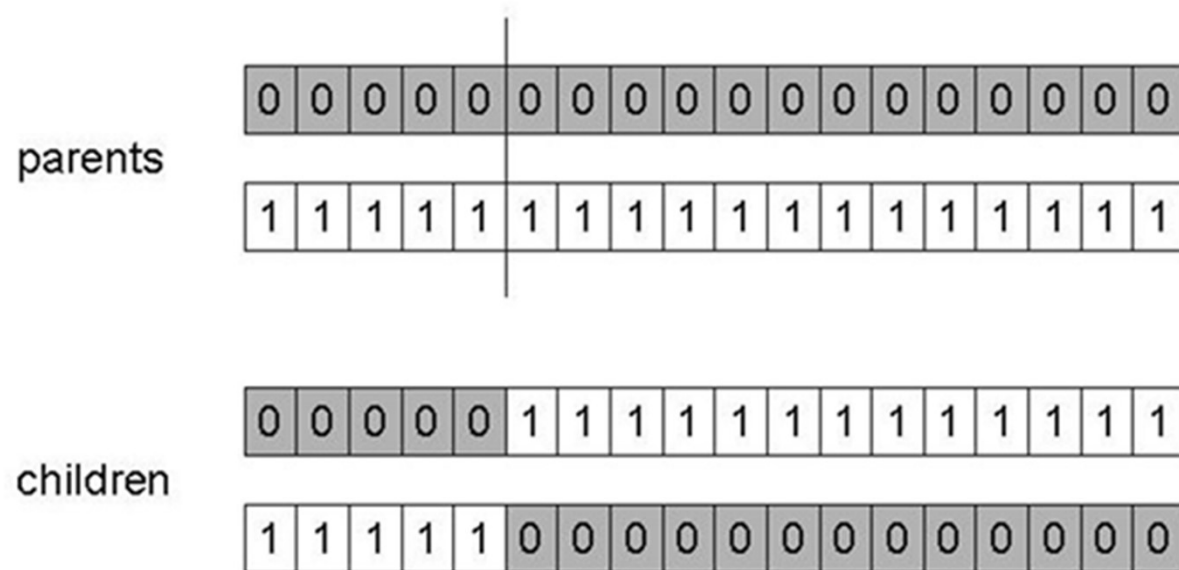
child

0	1	0	0	1	0	1	1	0	0	0	1	0	1	1	0	0	1
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

# Binary Representation:

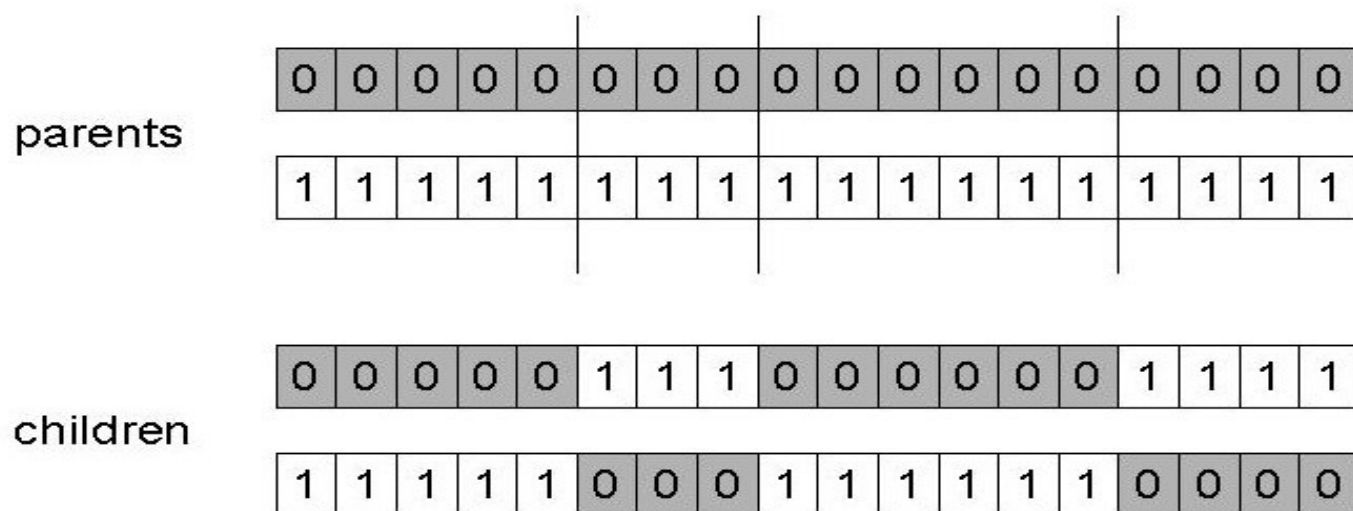
## 1-point crossover

- Choose a random point on the two parents
- Split parents at this crossover point
- Create children by exchanging tails



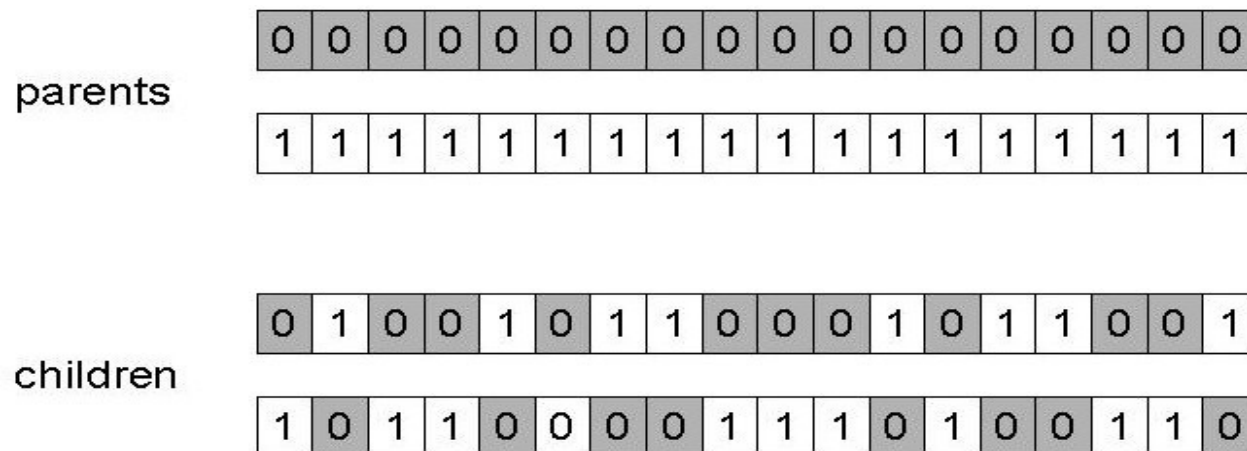
# Binary Representation: n-point crossover

- Choose n random crossover points
- Split along those points
- Glue parts, alternating between parents



## Binary Representation: Uniform crossover

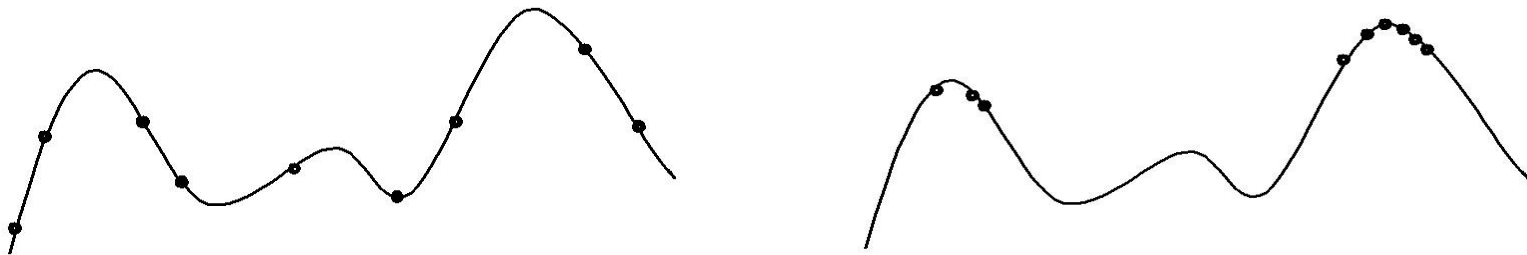
- Assign 'heads' to one parent, 'tails' to the other
- Flip a coin for each gene of the first child
- Make an inverse copy of the gene for the second child
- Breaks more “links” in the genome



# Binary Representation: Crossover and/or mutation?

There is co-operation AND competition between them:

- **Crossover** is **explorative**, it makes a *big* jump to an area somewhere “in between” two (parent) areas
- **Mutation** is **exploitative**, it creates random *small* diversions, thereby staying near (in the area of) the parent



# Integer Representation

- Some problems naturally have integer variables,
  - e.g. image processing parameters
- Others take categorical values from a fixed set
  - e.g. {blue, green, yellow, pink}
- N-point / uniform crossover operators work
- Extend bit-flipping mutation to make:
  - “creep” i.e. more likely to move to similar value
    - Adding a small (positive or negative) value to each gene with probability  $p$ .
  - Random resetting (esp. categorical variables)
    - With probability  $p_m$  a new value is chosen at random



# Real-Valued or Floating-Point Representation: Uniform Mutation

- General scheme of floating point mutations

$$\bar{x} = \langle x_1, \dots, x_l \rangle \rightarrow \bar{x}' = \langle x'_1, \dots, x'_l \rangle$$

$$x_i, x'_i \in [LB_i, UB_i]$$

- **Uniform Mutation**

$x'_i$  drawn randomly (uniform) from  $[LB_i, UB_i]$

- Analogous to bit-flipping (binary) or random resetting (integers)

# Real-Valued or Floating-Point Representation: Nonuniform Mutation

- Non-uniform mutations:
  - Most common method is to add random deviate to each variable separately, taken from  $N(0, \sigma)$  **Gaussian distribution** and then curtail to range
$$x'_i = x_i + N(0, \sigma)$$
  - Standard deviation  $\sigma$ , **mutation step size**, controls amount of change (2/3 of drawings will lie in range  $(-\sigma \text{ to } +\sigma)$ )

# Real-Valued or Floating-Point Representation:

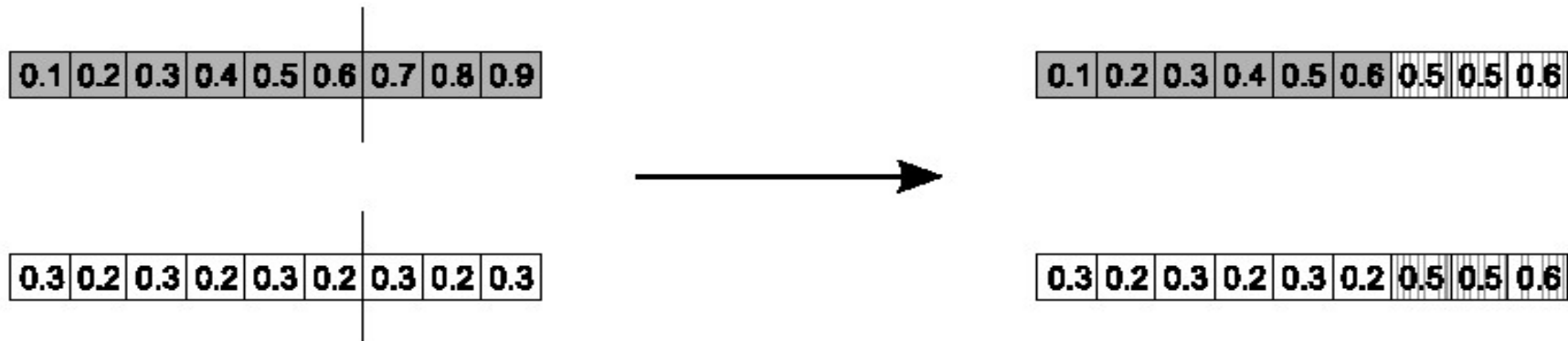
## Crossover operators

- Discrete recombination:
  - each allele value in offspring  $z$  comes from one of its parents  $(x,y)$  with equal probability:  $z_i = x_i$  or  $y_i$
  - Could use **n-point** or **uniform**
- Intermediate recombination:
  - exploits idea of creating children “between” parents (hence a.k.a. *arithmetic* recombination)
  - $z_i = \alpha x_i + (1 - \alpha) y_i$  where  $\alpha : 0 \leq \alpha \leq 1$ .
  - The parameter  $\alpha$  can be:
    - constant:  $\alpha = 0.5$  -> uniform arithmetical crossover
    - variable (e.g. depend on the age of the population)
    - picked at random every time

## Real-Valued or Floating-Point Representation: Simple arithmetic crossover

- Parents:  $\langle x_1, \dots, x_n \rangle$  and  $\langle y_1, \dots, y_n \rangle$
- Pick a random gene (k) after this point mix values
- child<sub>1</sub> is:

$$\left\langle x_1, \dots, x_k, \alpha \cdot y_{k+1} + (1 - \alpha) \cdot x_{k+1}, \dots, \alpha \cdot y_n + (1 - \alpha) \cdot x_n \right\rangle$$



## Real-Valued or Floating-Point Representation: Single arithmetic crossover

- Parents:  $\langle x_1, \dots, x_n \rangle$  and  $\langle y_1, \dots, y_n \rangle$
- Pick a single gene (k) at random,
- child<sub>1</sub> is:  $\langle x_1, \dots, x_k, \alpha \cdot y_k + (1 - \alpha) \cdot x_k, \dots, x_n \rangle$
- Reverse for other child. e.g. with  $\alpha = 0.5$

0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9
-----	-----	-----	-----	-----	-----	-----	-----	-----

0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.5	0.9
-----	-----	-----	-----	-----	-----	-----	-----	-----



0.3	0.2	0.3	0.2	0.3	0.2	0.3	0.2	0.3
-----	-----	-----	-----	-----	-----	-----	-----	-----

0.3	0.2	0.3	0.2	0.3	0.2	0.3	0.5	0.3
-----	-----	-----	-----	-----	-----	-----	-----	-----

## Real-Valued or Floating-Point Representation:

### Whole arithmetic crossover

- Most commonly used
- Parents:  $\langle x_1, \dots, x_n \rangle$  and  $\langle y_1, \dots, y_n \rangle$

- Child<sub>1</sub> is:

$$a \cdot \bar{x} + (1 - a) \cdot \bar{y}$$

- reverse for other child. e.g. with  $\alpha = 0.5$

0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9
-----	-----	-----	-----	-----	-----	-----	-----	-----

0.2	0.2	0.3	0.3	0.4	0.4	0.5	0.5	0.6
-----	-----	-----	-----	-----	-----	-----	-----	-----



0.3	0.2	0.3	0.2	0.3	0.2	0.3	0.2	0.3
-----	-----	-----	-----	-----	-----	-----	-----	-----

0.2	0.2	0.3	0.3	0.4	0.4	0.5	0.5	0.6
-----	-----	-----	-----	-----	-----	-----	-----	-----

EA Example: [http://rednuht.org/genetic\\_cars\\_2/](http://rednuht.org/genetic_cars_2/)

- Representation
- Fitness function
- Selection
- Variation
- Initialization and termination

# Permutation Representations

- Useful in ordering/sequencing problems
- Task is (or can be solved by) arranging some objects in a certain order. Examples:
  - production scheduling: important thing is which elements are scheduled before others (order)
  - Travelling Salesman Problem (TSP) : important thing is which elements occur next to each other (adjacency)
- if there are  $n$  variables then the representation is as a list of  $n$  integers, each of which occurs exactly once

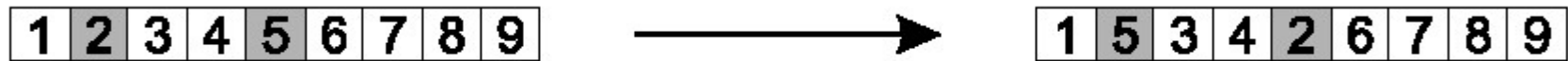


# Permutation Representations: Mutation

- Normal mutation operators lead to inadmissible solutions
  - Mutating a single gene destroys the permutation
- Therefore must change at least two values
- Mutation probability now reflects the probability that some operator is applied once to the whole string, rather than individually in each position

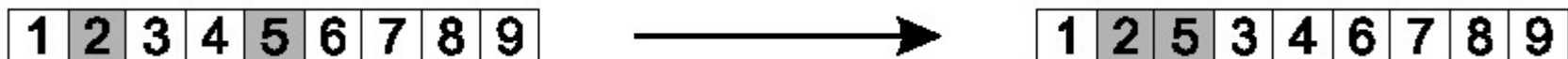
# Permutation Representations: Swap mutation

- Pick two alleles at random and swap their positions



## Permutation Representations: Insert Mutation

- Pick two allele values at random
- Move the second to follow the first, shifting the rest along to accommodate
- Note that this preserves most of the order and the adjacency information



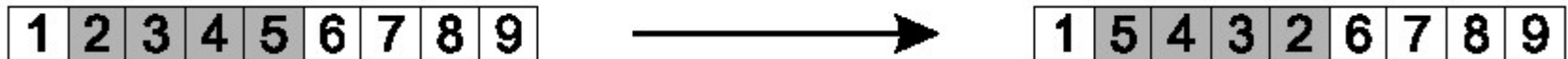
## Permutation Representations: Scramble mutation

- Pick a subset of genes at random
- Randomly rearrange the alleles in those positions



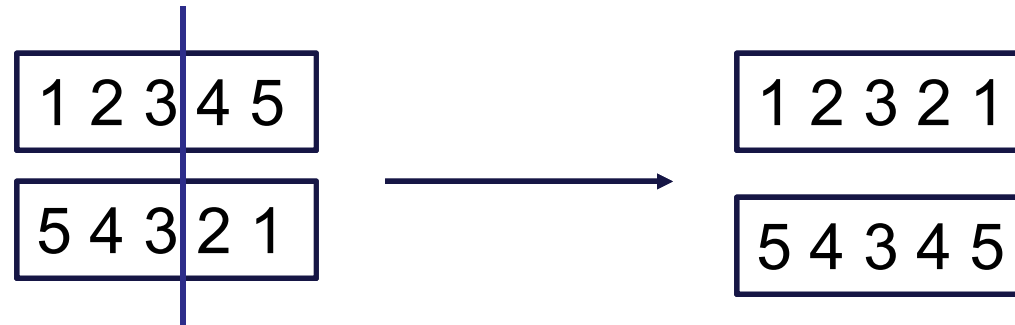
## Permutation Representations: Inversion mutation

- Pick two alleles at random and then invert the substring between them.
- Preserves most adjacency information (only breaks two links) but disruptive of order information



## Permutation Representations: Crossover operators

- “Normal” crossover operators will often lead to inadmissible solutions



- Many specialised operators have been devised which focus on combining order or adjacency information from the two parents

# Permutation Representations: Conserving Adjacency

- Important for problems where adjacency between elements decides quality (e.g. TSP)



## Permutation Representations: Conserving Adjacency

- Important for problems where adjacency between elements decides quality (e.g. TSP)
  - [1,2,3,4,5] is same plan as [5,4,3,2,1] -> order and position not important, but adjacency is.
- Partially Mapped Crossover and Edge Recombination are example operators





# Permutation Representations: Conserving Order

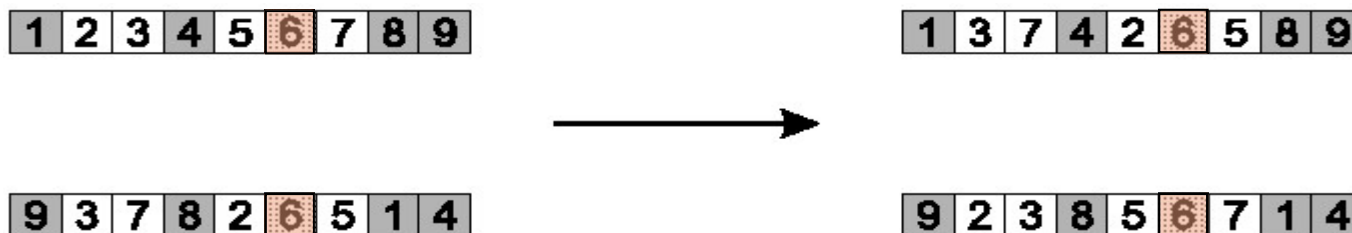
- Important for problems where **order** of elements decide performance (e.g. production scheduling)

Making breakfast:

1. Start brewing coffee
2. Toast bread
3. Apply butter
4. Add jam
5. Pour hot coffee

# Permutation Representations: Conserving Order

- Important for problems order of elements decide performance (e.g. production scheduling)
  - Now,  $[1,2,3,4,5]$  is a very different plan than  $[5,4,3,2,1]$
- Order Crossover and Cycle Crossover are example operators



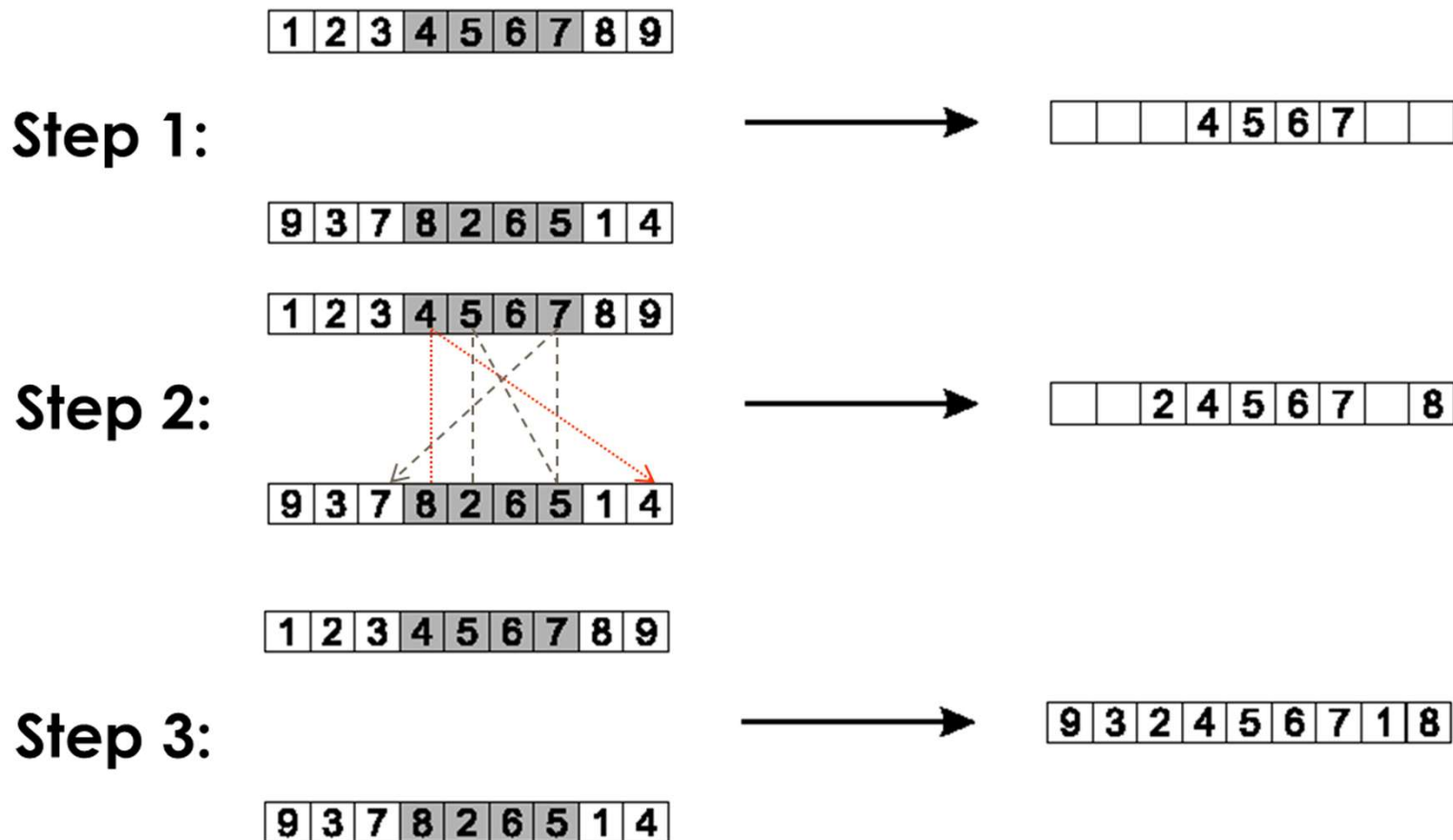
## Permutation Representations: Partially Mapped Crossover (PMX) (1/2)

Informal procedure for parents P1 and P2:

1. Choose random segment and copy it from P1
2. Starting from the first crossover point look for elements in that segment of P2 that have not been copied
3. For each of these  $i$  look in the offspring to see what element  $j$  has been copied in its place from P1
4. Place  $i$  into the position occupied  $j$  in P2, since we know that we will not be putting  $j$  there (as is already in offspring)
5. If the place occupied by  $j$  in P2 has already been filled in the offspring  $k$ , put  $i$  in the position occupied by  $k$  in P2
6. Having dealt with the elements from the crossover segment, the rest of the offspring can be filled from P2.

Second child is created analogously

# Permutation Representations: Partially Mapped Crossover (PMX) (2/2)



## Permutation Representations: Edge Recombination (1/3)

- Works by constructing a table listing which edges are present in the two parents, if an edge is common to both, mark with a +
- e.g. [1 2 3 4 5 6 7 8 9] and [9 3 7 8 2 6 5 1 4]

Element	Edges	Element	Edges
1	2,5,4,9	6	2,5+,7
2	1,3,6,8	7	3,6,8+
3	2,4,7,9	8	2,7+, 9
4	1,3,5,9	9	1,3,4,8
5	1,4,6+		

## Permutation Representations: Edge Recombination (2/3)

Informal procedure: once edge table is constructed

1. Pick an initial element, *entry*, at random and put it in the offspring
2. Set the variable *current element* = *entry*
3. Remove all references to *current element* from the table
4. Examine list for current element:
  - If there is a common edge, pick that to be next element
  - Otherwise pick the entry in the list which itself has the shortest list
  - Ties are split at random
5. In the case of reaching an empty list:
  - a new element is chosen at random

# Permutation Representations: Edge Recombination (3/3)

Element	Edges	Element	Edges
1	2,5,4,9	6	2,5+,7
2	1,3,6,8	7	3,6,8+
3	2,4,7,9	8	2,7+, 9
4	1,3,5,9	9	1,3,4,8
5	1,4,6+		

Choices	Element selected	Reason	Partial result
All	1	Random	[1]
2,5,4,9	5	Shortest list	[1 5]
4,6	6	Common edge	[1 5 6]
2,7	2	Random choice (both have two items in list)	[1 5 6 2]
3,8	8	Shortest list	[1 5 6 2 8]
7,9	7	Common edge	[1 5 6 2 8 7]
3	3	Only item in list	[1 5 6 2 8 7 3]
4,9	9	Random choice	[1 5 6 2 8 7 3 9]
4	4	Last element	[1 5 6 2 8 7 3 9 4]

# Permutation Representations:

## Order crossover (1/2)

- Idea is to preserve relative order that elements occur
- Informal procedure:
  - 1. Choose an arbitrary part from the first parent
  - 2. Copy this part to the first child
  - 3. Copy the numbers that are not in the first part, to the first child:
    - starting right from cut point of the copied part,
    - using the **order** of the second parent
    - and wrapping around at the end
  - 4. Analogous for the second child, with parent roles reversed



# Permutation Representations:

## Order crossover (2/2)

- Copy randomly selected set from first parent

1	2	3	4	5	6	7	8	9
---	---	---	---	---	---	---	---	---



			4	5	6	7		
--	--	--	---	---	---	---	--	--

9	3	7	8	2	6	5	1	4
---	---	---	---	---	---	---	---	---

- Copy rest from second parent in order  
1,9,3,8,2

1	2	3	4	5	6	7	8	9
---	---	---	---	---	---	---	---	---



3	8	2	4	5	6	7	1	9
---	---	---	---	---	---	---	---	---

9	3	7	8	2	6	5	1	4
---	---	---	---	---	---	---	---	---

# Permutation Representations:

## Cycle crossover (1/2)

### Basic idea:

Each allele comes from one parent *together with its position*.

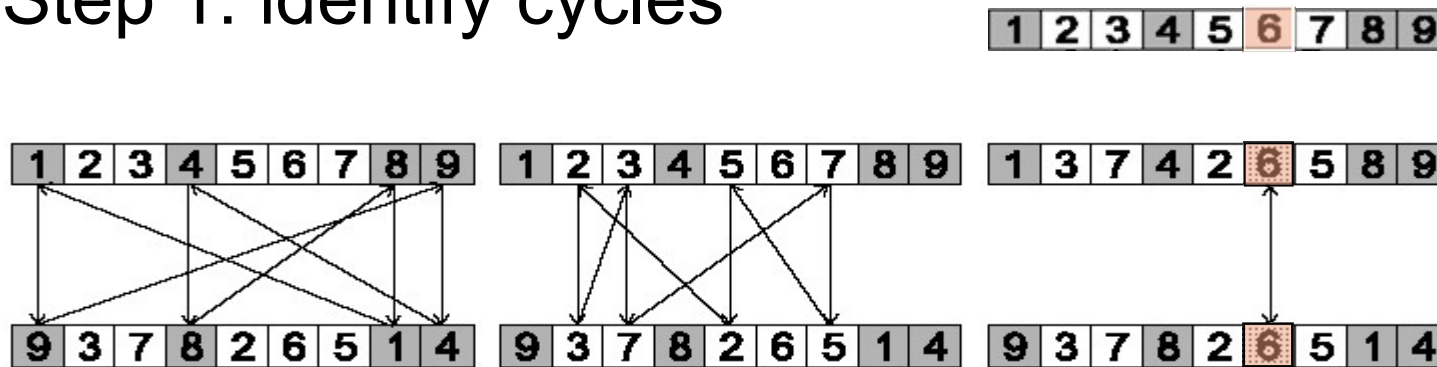
### Informal procedure:

1. Make a cycle of alleles from P1 in the following way.
  - (a) Start with the first allele of P1.
  - (b) Look at the allele at the *same position* in P2.
  - (c) Go to the position with the *same allele* in P1.
  - (d) Add this allele to the cycle.
  - (e) Repeat step b through d until you arrive at the first allele of P1.
2. Put the alleles of the cycle in the first child on the positions they have in the first parent.
3. Take next cycle from second parent

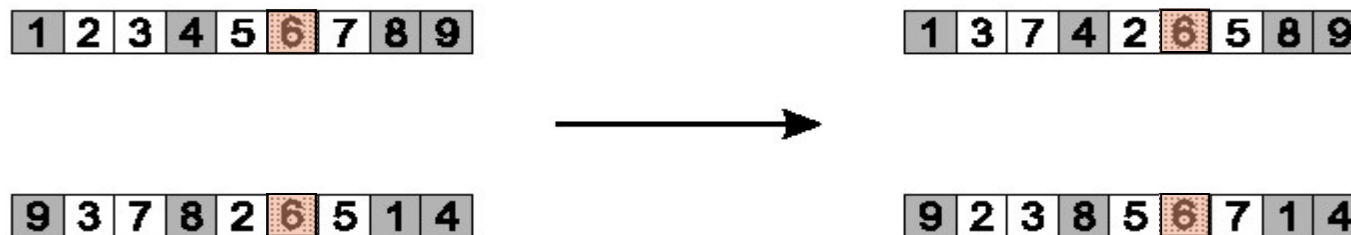
# Permutation Representations:

## Cycle crossover (2/2)

- Step 1: identify cycles



- Step 2: copy **alternate** cycles into offspring

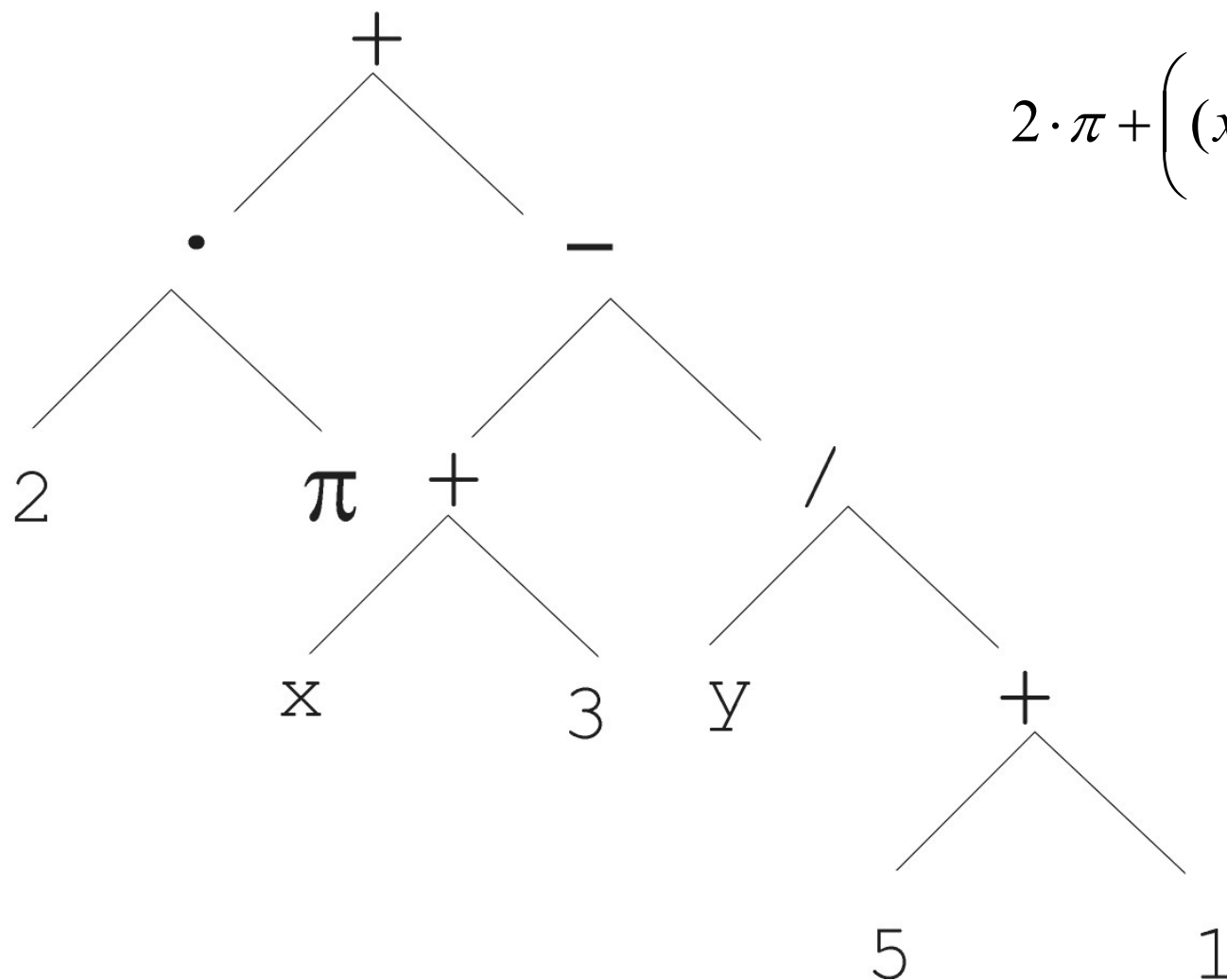


## Tree Representation (1/5)

- Trees are a universal form, e.g. consider
- Arithmetic formula:  $2 \cdot \pi + \left( (x + 3) - \frac{y}{5 + 1} \right)$
- Logical formula:  $(x \wedge \text{true}) \rightarrow ((x \vee y) \vee (z \leftrightarrow (x \wedge y)))$
- Program:

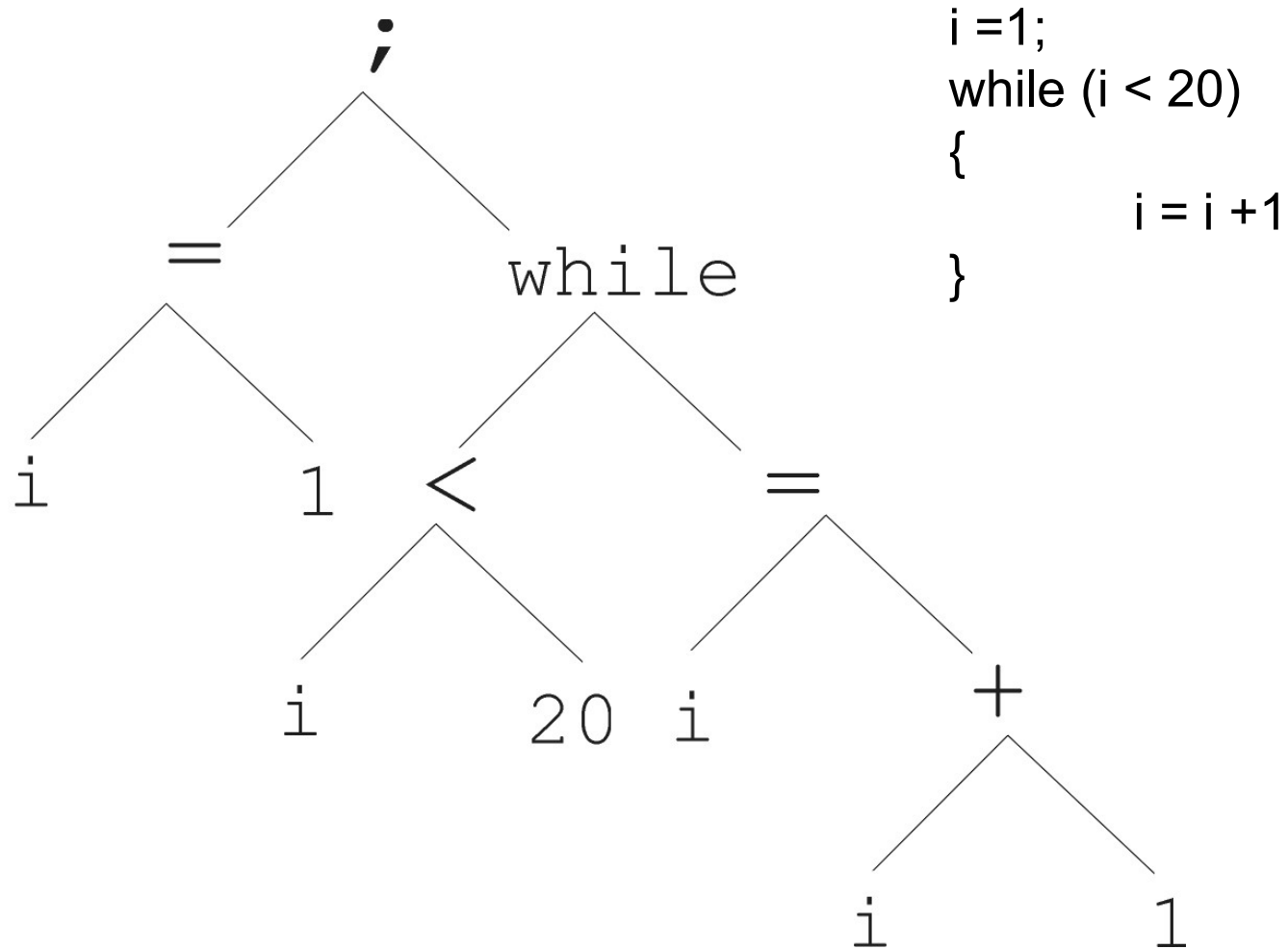
```
i = 1;
while (i < 20)
{
    i = i + 1
}
```

## Tree Representation (2/5)



$$2 \cdot \pi + \left( (x + 3) - \frac{y}{5 + 1} \right)$$

## Tree Representation (4/5)

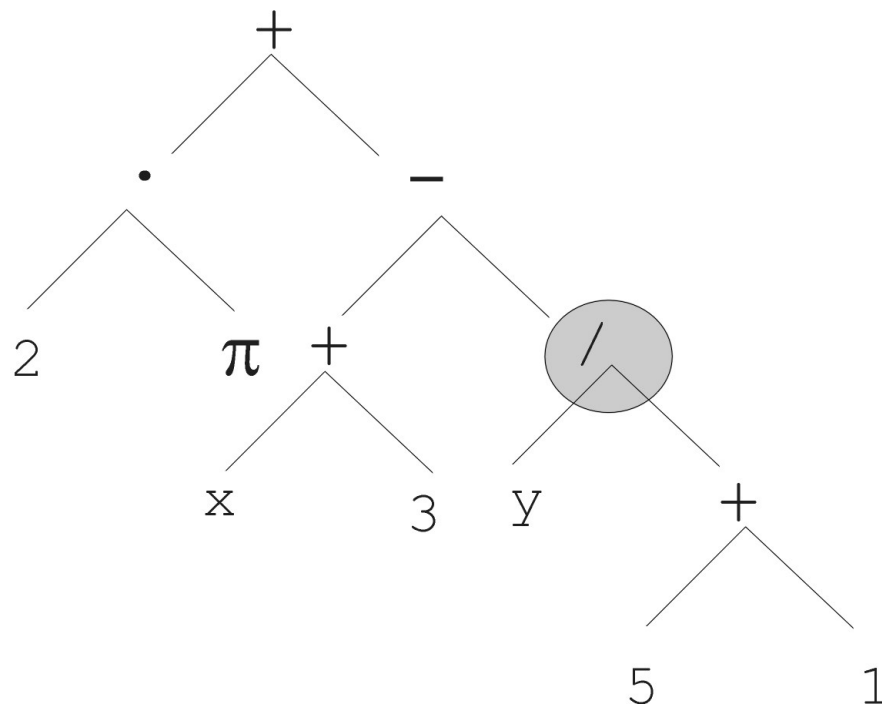


## Tree Representation (5/5)

- In GA, ES, EP chromosomes are linear structures (bit strings, integer string, real-valued vectors, permutations)
- Tree shaped chromosomes are non-linear structures
- In GA, ES, EP the size of the chromosomes is fixed
- Trees in GP (Genetic Programming) may vary in depth and width

## Tree Representation: Mutation (1/2)

- Most common mutation: replace randomly chosen subtree by randomly generated tree





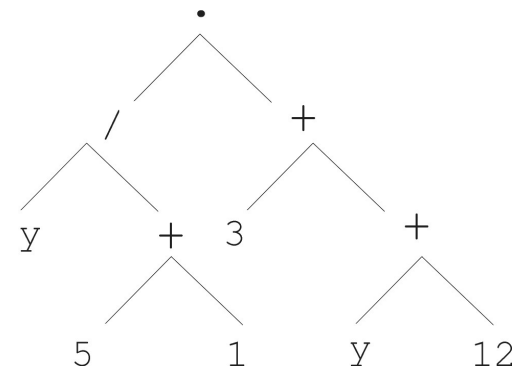
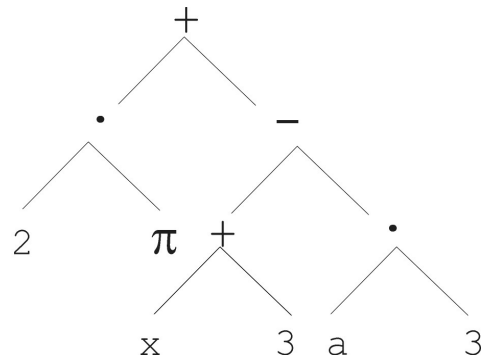
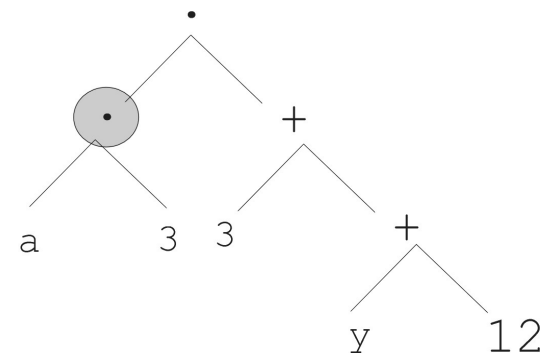
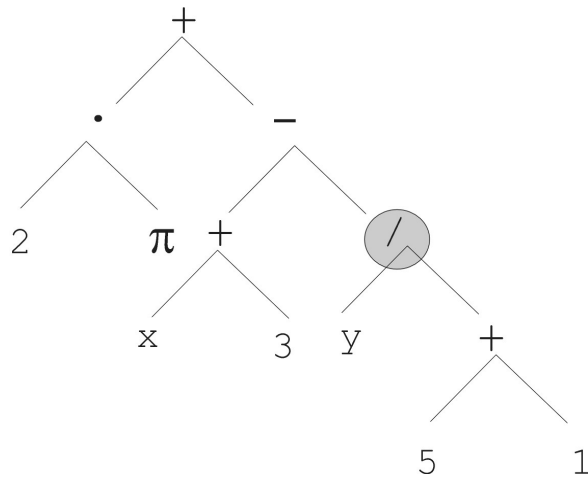
## Tree Representation: Mutation (2/2)

- Mutation has two parameters:
  - Probability  $p_m$  to choose mutation
  - Probability to choose an internal point as the root of the subtree to be replaced
- Remarkably  $p_m$  is advised to be 0 (Koza'92) or very small, like 0.05 (Banzhaf et al. '98)
- The size of the child can exceed the size of the parent

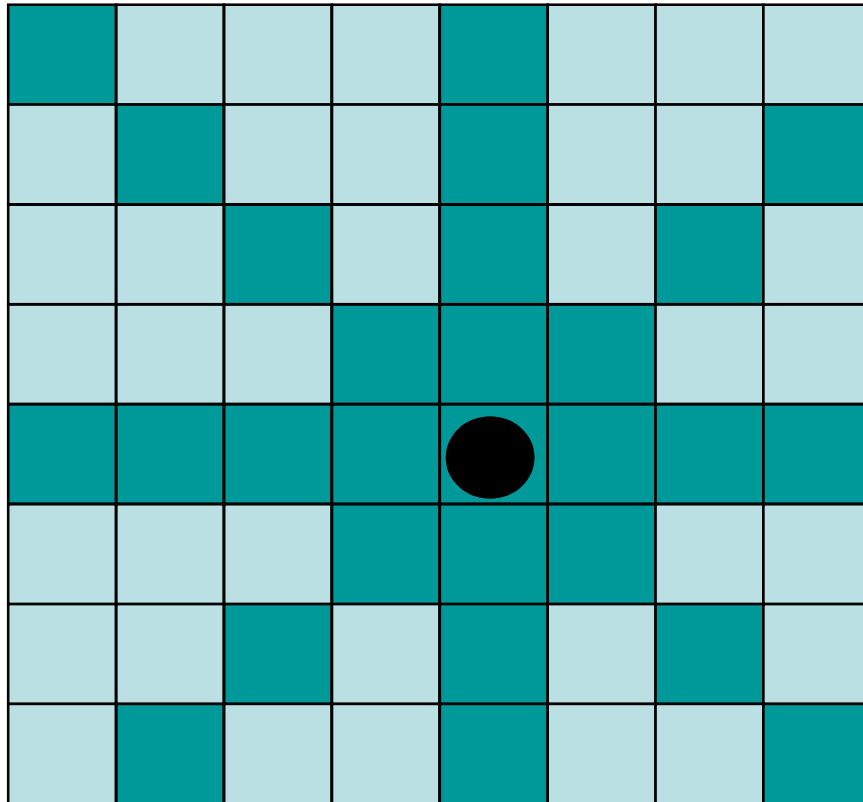
## Tree Representation: Recombination (1/2)

- Most common recombination: exchange two randomly chosen subtrees among the parents
- Recombination has two parameters:
  - Probability  $p_c$  to choose recombination
  - Probability to choose an internal point within each parent as crossover point
- The size of offspring can exceed that of the parents

# Tree Representation: Recombination (2/2)



## Example: The 8-queens problem

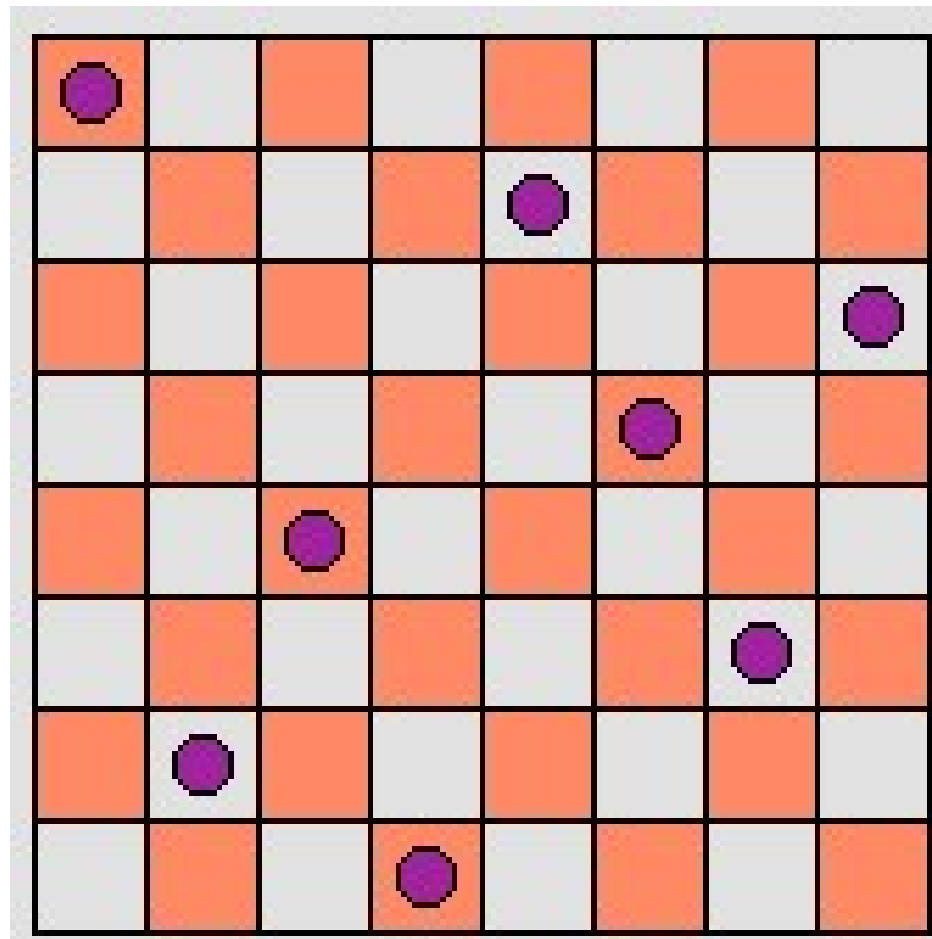


- Representation?
- Fitness function?
- Variation operators?
- Selection operators?

Place 8 queens on an 8x8 chessboard in such a way that they cannot check each other

# Example:

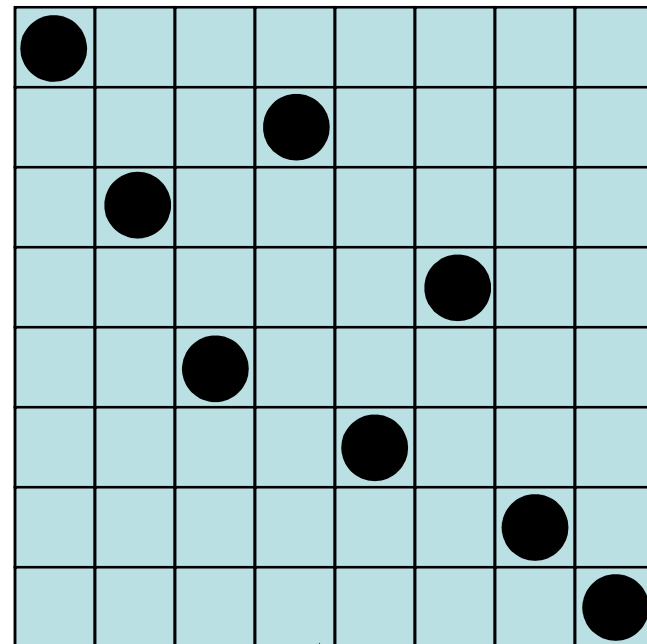
## The 8-queens problem – one solution



# The 8-queens problem: Representation

**Phenotype:**  
a board configuration

**Genotype:**  
a permutation of  
the numbers 1–8



Possible mapping

1	3	5	2	6	4	7	8
---	---	---	---	---	---	---	---

# The 8-queens problem:

## Fitness evaluation

- **Penalty** of one queen: the number of queens she can check
- Penalty of a configuration: the sum of penalties of all queens
- Note: penalty is to be minimized
- **Fitness** of a configuration: inverse penalty to be maximized

# The 8-queens problem: How can we mutate a permutation?

Small variation in one permutation, e.g.:

- swapping values of two randomly chosen positions,



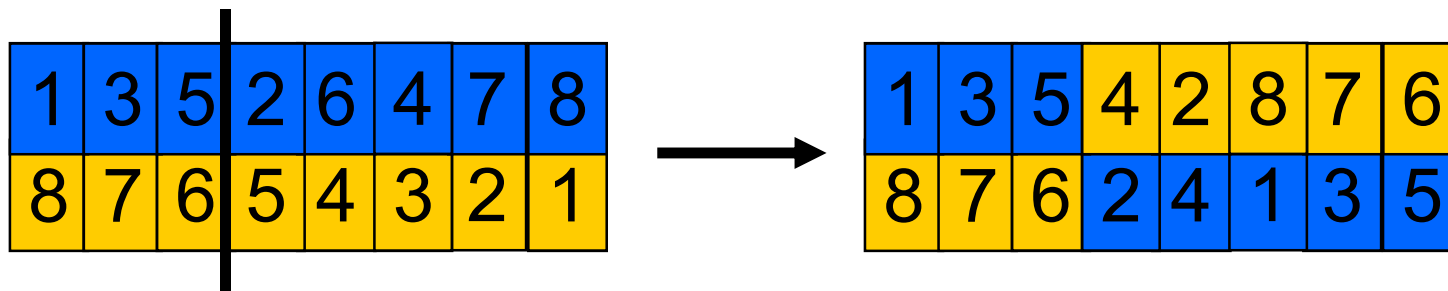


# The 8-queens problem:

## How can we recombine permutations?

Combining two permutations into two new permutations:

- choose random crossover point
- copy first parts into children
- create second part by inserting values from other parent:
  - in the order they appear there
  - beginning after crossover point
  - skipping values already in child



# The 8-queens problem:

## Selection

- Parent selection:
  - Pick 5 random parents and take best 2 to undergo crossover
- Survivor selection (replacement)
  - Merge old (parents) and new (offspring) population
  - Throw out the 2 worst solutions