ARTIFICIAL INTELLIGENCE

Solving search problems

Evolutionary Algorithms

Nature-inspired search

Best method for solving a problem

- Human brain

  Has created the wheel, car, town, etc.
- Mechanism of evolution

  Has created the human brain

Simulation of nature

- By machines' help → the artificial neural networks simulate the brain

  Flying vehicles, DNA computers, membrane-based computers

- By algorithms' help

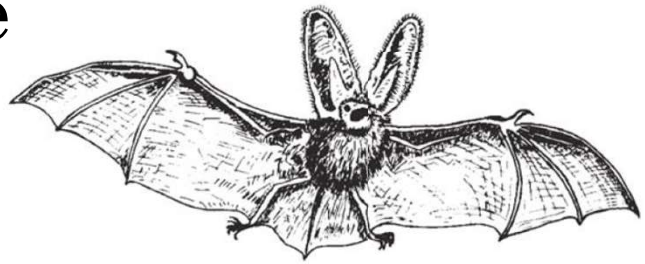
  Evolutionary algorithms simulate the evolution of nature

  Particle Swarm Optimisation simulates the collective and social behaviour

  Ant Colony Optimisation

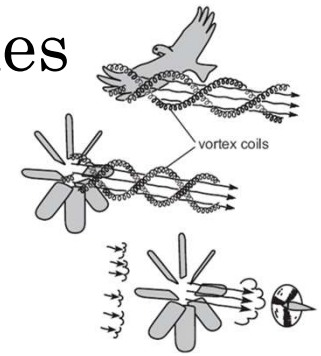
Basic elements

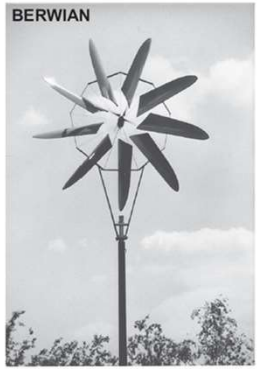
- Simulation of nature
  - Fly of bats



  - Leonardo da Vinci – sketch of a flying machine

  - Flies of birds and planes
  - Flies of birds and wind-turbines





Basic elements

Main characteristics of EAs

- Iterative and parallel processes
- Based on random search
- Bio-inspired – involve mechanisms as:

  Natural selection

  Reproduction

  Recombination

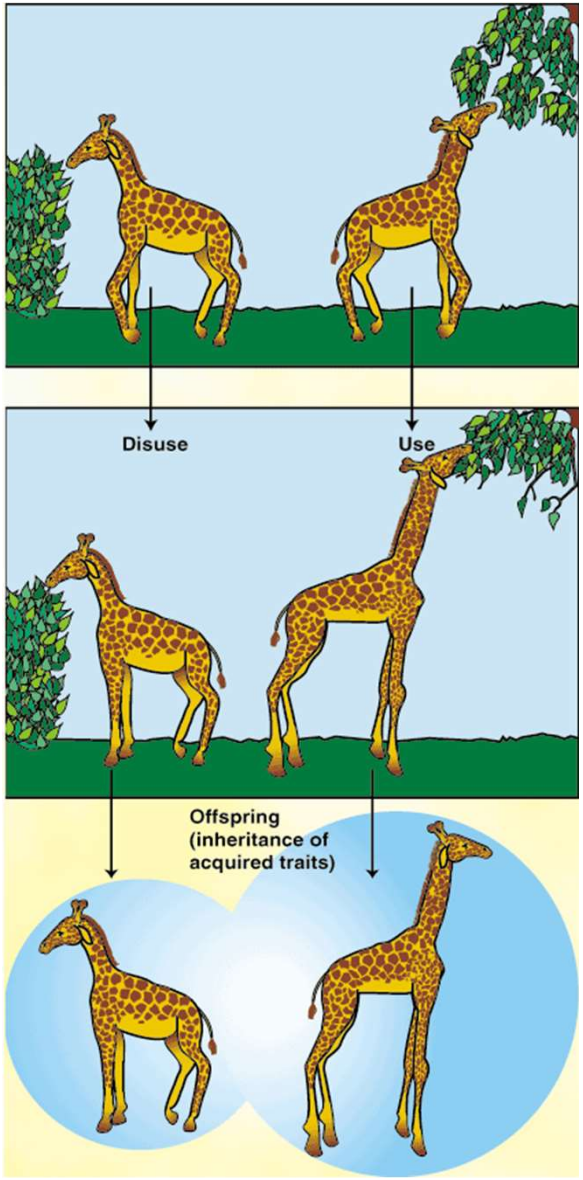
  Mutation

Basic elements

Historical points

- Jean Baptise de Lamark (1744-1829)
  - Has proposed in 1809 an explanation

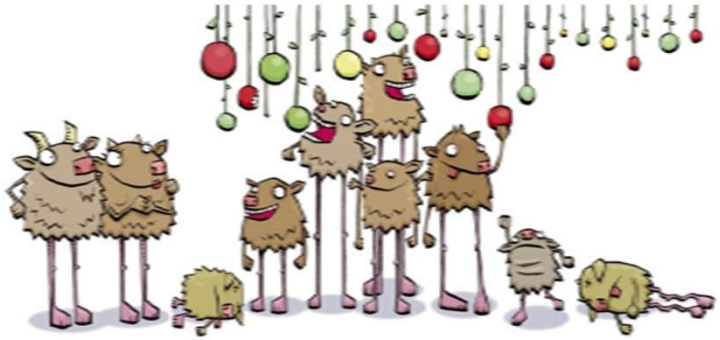
    For origin of species in the book *Zoological Philosophy*:
    - Needs of an organism determine the evolving characteristics
    - Useful characteristics could be transferred to offspring
  - *use and disuse law*



Basic elements

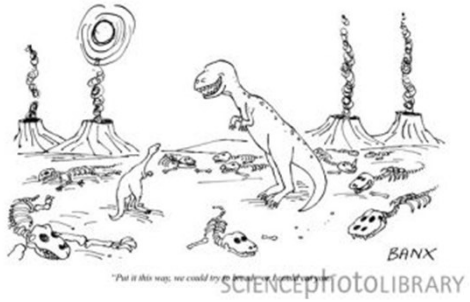
Historical points

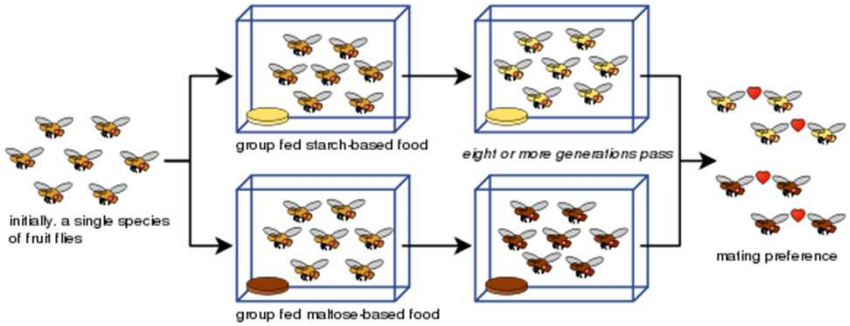
- Charles Darwin (1807-1882)
  - In the book *Origin of Species* he proved that



all the organisms have evolved based on:

- Variation
  - Overproduction of offspring
- Natural selection
  - Competition (generation of constant size)
  - Fitness survival
  - Reproduction
  - Occurrence of new species





Basic elements

Historical points

Modern theory of evolution

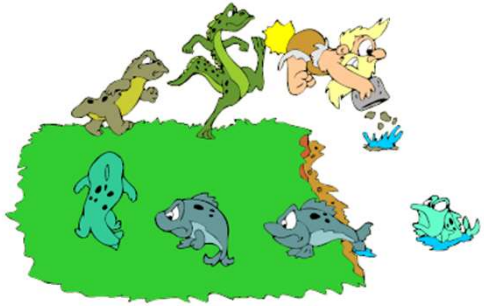
- Darwin's theory is improved by mechanism of genetic ingeritance
- Genetic variance is produced by
  - Mutation and
  - Sexual recombination
- L. Fogel 1962 (San Diego, CA) → *Evolutionary Programming (EP)*
- J. Holland 1962 (Ann Arbor, MI) → *Genetic Algorithms* (GAs)
- I. Rechenberg & H.-P. Schwefel 1965 (Berlin, Germany) → *Evolution Strategies (ESs)*
- J. Koza 1989 (Palo Alto, CA) → *Genetic Programming (GP*)

Basic elements

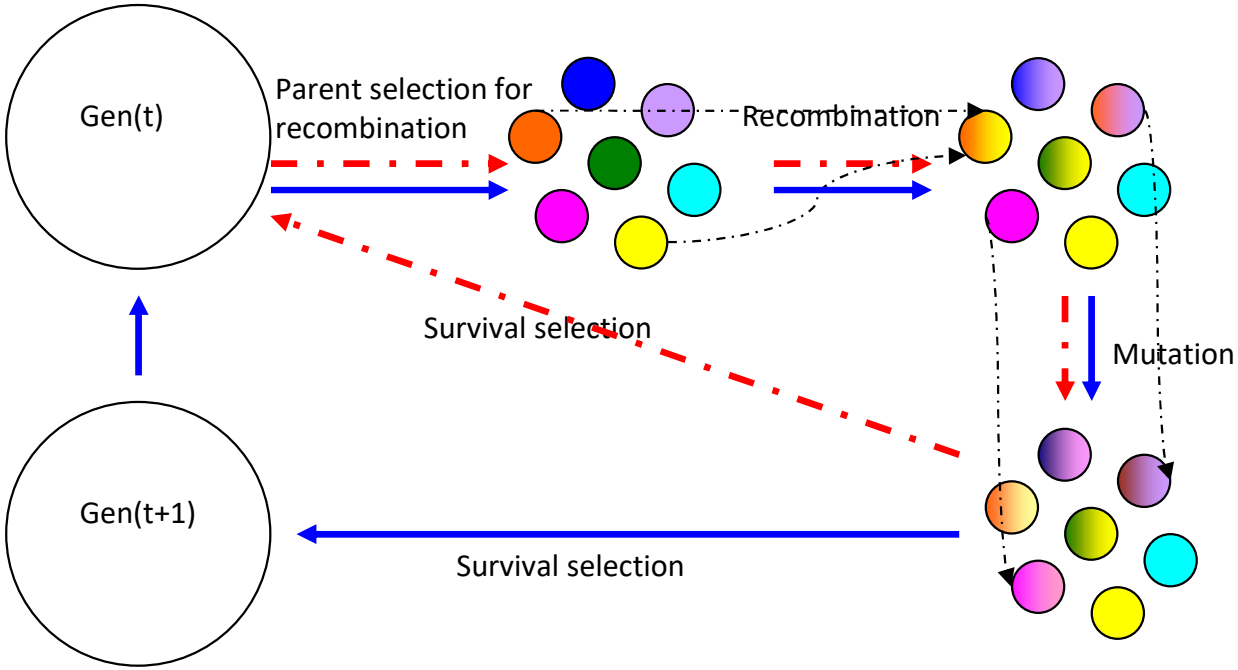
Evolutionary metaphor

Natural evolution		Problem solving
Individual	↔	Possible solution
Population	↔	Set of possible solutions
Chromosome	↔	Coding of a possible solution
Gene	↔	Part of coding
Fitness	↔	Quality
Crossover and Mutation	↔	Search operators
Environment	↔	Problem

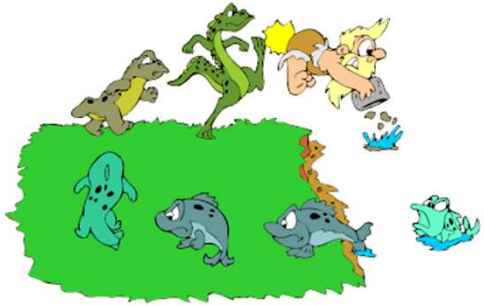
Algorithm



- General sketch of an EA
  - Generational
  - Steady-state



Algorithm

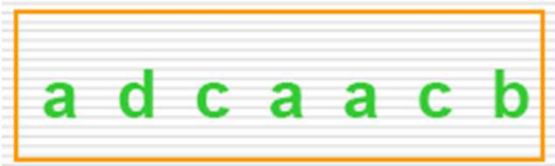


- Design
  - Chromosome representation
  - Population model
  - Fitness function
  - Genetic operators
    - Selection
    - Mutation
    - Crossover
  - Stop condition

Representation

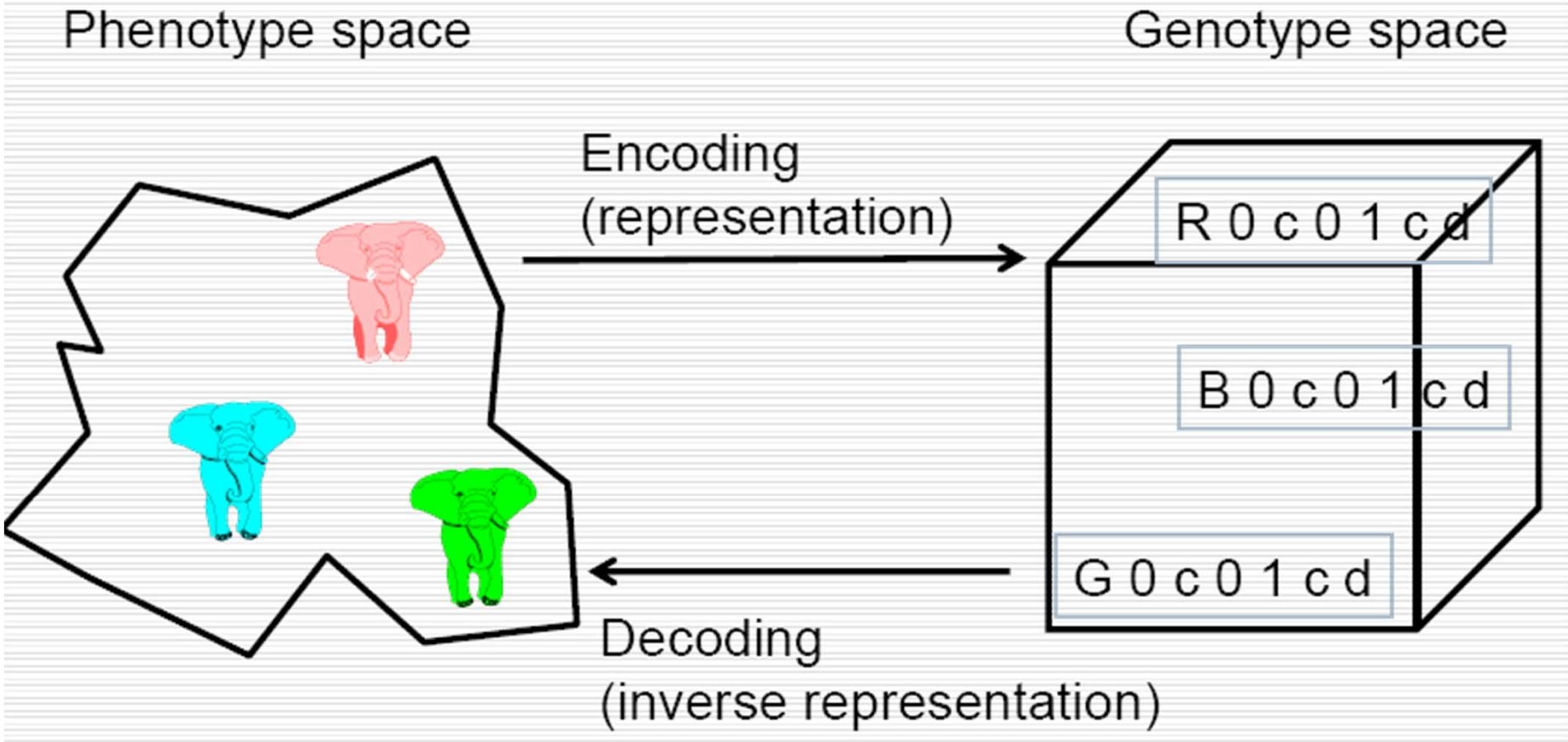
- 2 levels of each possible solution
  - External level → phenotype
    - Individual – original object in the context of the problem
    - The possible solutions are evaluated here
    - Ant, knapsack, elephant, towns, ...

  - Internal level → genotype
    - Chromosome – code associated to an object
      - Composed by genes, located in loci (fix positions) and having some values (alleles)
    - The possible solutions are searched here
    - One-dimensional vector (with numbers, bits, characters), matrix, …



Representation

- Representation must be representative for:
  - Problem
  - Fitness function and
  - Genetic operators



Representation

Linear

- Discrete

  Binary → knapsack problem

  Not-binary

  - Integers
    - Random → image processing
    - Permutation → travelling salesman problem (TSP)
  - Class-based → map colouring problem
- Continuous (real) → function optimization

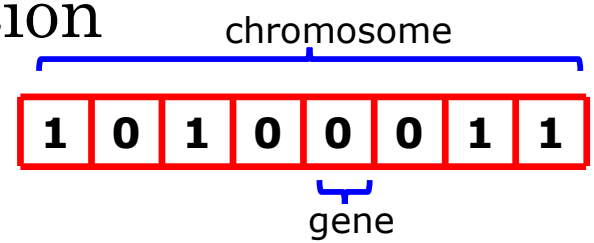
Tree-based → regression problems

Representation

Linear discrete and binary representation

- Genotype

  Bit-strings



Representation

- Linear discrete and binary representation
  - Genotype
    - Bit-strings
  - Phenotype
    - Boolean elements
      - Ex. Knapsack problem – selected objects for the bag

Genotype

1	0	1	0	0	0	1	1

Phenotype

$ob_1+ob_3+ob_7+ob_8$

Objects 1, 3, 7 and 8 are selected

Representation

- Linear discrete and binary representation
  - Genotype
    - Bit-strings
  - Phenotype
    - Boolean elements
      - Ex. Knapsack problem – selected objects for the bag
    - Integers

Genotype Phenotype

1	0	1	0	0	0	1	1

= 163

$1*2^7 + 0*2^6 + 1*2^5 + 0*2^4 + 0*2^3 + 0*2^2 + 1*2^1 + 1*2^0 =$

$128 + 32 + 2 + 1 = 163$

Representation

- Linear discrete and binary representation
  - Genotype
    - Bit-strings
  - Phenotype
    - Boolean elements
      - Ex. Knapsack problem – selected objects for the bag
    - Integers
    - Real numbers from a range (ex. [2.5, 20.5])

Genotype Phenotype

1	0	1	0	0	0	1	1	= 13.9609

$$x = 2.5 + \frac{163}{256}(20.5 - 2.5) = 13.9609$$

Representation

Transformation of real values from binary representation

- Let be $z \in [x,y] \subseteq \mathbb{R}$ represented as $\{a_1, \ldots, a_L\} \in \{0, 1\}^L$
- Function $[x,y] \rightarrow \{0,1\}^L$ must be inversely (a phenotype corresponds to a genotype)
- Function $\mathbf{\Gamma}$: $\{0,1\}^L \rightarrow [x,y]$ defines the representation

$$\Gamma(a_1,\ldots,a_L) = x + \frac{y-x}{2^L - 1} \cdot \left(\sum_{j=0}^{L-1} a_{L-j} \cdot 2^j\right) \in [x,y]$$

- Remarks
  - 2^L values can be represented
  - L – maximum precision of solution
  - For a better precision → long chromosomes → slowly evolution

Representation

Linear discrete non-binary integer random representation

- Genotype

  Vector of integers from a given range

- Phenotype

  Utility of numbers in the problem

- Ex. Pay a sum S by using different n coins

  Genotype → vector of n integers from range [0, S/value of current coin]

  Phenotype → how many coins of each type must be considered

Representation

Linear discrete non-binary integer permutation representation

- Genotype

  Permutation of n elements (n – number of genes)

- Phenotype

  Utility of permutation in problem

- Ex. Traveling Salesman Problem

  Genotype → permutation of n elements

  Phenotype → visiting order of towns (each town has associated a number from $\{1,2,\ldots,n\}$)

Representation

Linear discrete non-binary integer class-based representation

- Similarly to integer one, but labels are used instead numbers

- Genotype

  Vector of labels from a given set

- Phenotype

  Labels' meaning

- Ex. Map colouring problem

  Genotype → vector of n colours (n – number of countries)

  Phenotype → what colour has to be used for each country

Representation

Linear continuous (real) representation

- Genotype

  Vector of real numbers

- Phenotype

  Number meaning

- Ex. Function optimisation $f{:}R^n \rightarrow R$

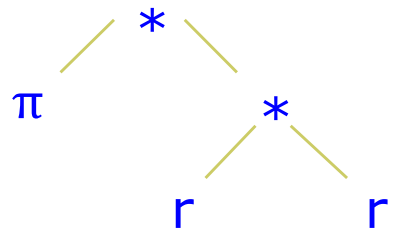
  Genotype → more real numbers $X=[x_1, x_2, \ldots, x_n]$, $x_i \in R$

  Phenotype → values of function f arguments

Representation

- Tree-based representation
  - Genotype
    - Trees than encode S-expressions
    - Internal nodes □functions (F)
      - Mathematical
        - Arithmetic operators
        - Boolean operators
      - Statements
        - Of a given programming language
        - Of other language type
    - Leaf → terminals (T)
      - Real or Boolean values, constants or variables
      - Sub-programs
  - Phenotype
    - Meaning of S-expressions
  - Ex. Computing the circle area

$$\pi * r^2$$



Population

Population – concept

- Aim

  Keeps a collection of possible solutions (candidate solutions)

  - Repetitions are allowed

  Is entirely utilised during selection for recombination

- Properties

  (usually) fixed dimension μ

  Diversity

  - Number of different fitnesses/phenotypes/genotypes

- Remarks

  Represents the basic unit that evolves

  - The entire population evolves, not only the individuals!

Population

Population - initialisation

- Uniformly distributed in the search space (if it is possible)

Binary strings

- Randomly generation of 0 and 1 with a 0.5 probability (fifty-fifth)

Arrays of real numbers uniformly generated (in a given range)

Permutations

- Generation of identical permutation and making some changes

Population

Population - initialisation

- Uniformly distributed in the search space (if it is possible)

  Trees

  - *Full* method – complete trees
    - Nodes of depth $d < D_{max}$ are randomly initialised by a function from function set F
    - nodes of depth $d = D_{max}$ are randomly initialised by a terminal from the terminal set T
  - *Grow* method – incomplete trees
    - Nodes of depth $d < D_{max}$ are randomly initialised by an element from *F U T*
    - nodes of depth $d = D_{max}$ are randomly initialised by a terminal from the terminal set T
  - *Ramped half and half* method
    - ½ of population is initialised by *Full* methods
    - ½ of population is initialised by *Grow* methods
    - By using different depths

Population

Population model:

- Generational EA
  - Each generation creates μ offspring
  - Each individual survives a generation only
  - Set of parents is totally replaced by set of offspring
- Steady-state EA
  - Each generation creates a single offspring
  - A single parent (the worst one) is replaced by the offspring

Generation Gap

- Proportion of replaced population
- $1 = \mu/\mu$, for generational model
- $1/\mu$, for steady-state model

Fitness function

Aim

- Reflects the adaptation to environment
- Quality function or objective function
- Associates a value to each candidate solution

  Consequences over selection → the more different values, the better

Properties

- Costly stage

  Unchanged individuals could not be re-evaluated

Typology:

- Number of objectives

  One-objective

  Multi-objective → Pareto fronts
- Optimisation direction

  Maximisation

  Minimisation
- Degree of precision

  Deterministic

  Heuristic

Fitness function

Examples

- Knapsack problem

  Representation → linear, discrete and binary

  Fitness → abs(knapsack's capacity – weight of selected objects) → min

- Problem of paying sum s by using different coins

  Representation → linear, discrete and integer

  Fitness → abs(sum to be paid – sum of selected coins) → min

- TSP

  Representation → linear, discrete, integer, permutation

  Fitness → cost of path → min

- Numerical function optimization

  Representation → linear, continuous, real

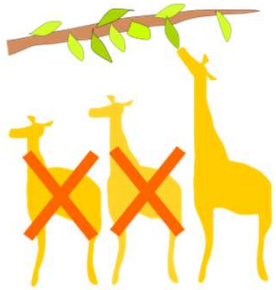
  Fitness → value of function → min/max

- Computing the circle's area

  Representation → tree-based

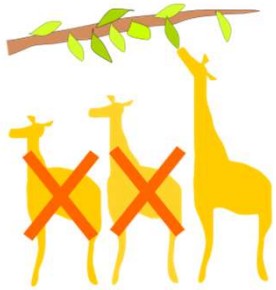
  Fitness → sum of square errors (difference between the real value and the computed value for a given set of examples) → min

Selection



- Aim:
  - Gives more reproduction/survival chances to better individuals
    - Weaker individuals have chances also because they could contain useful genetic material
  - Orients the population to improve its quality
- Properties
  - Works at population-level
  - Is based on fitness only (is independent to representation)
  - Helps to escape from local optima (because its stochastic nature)

Selection



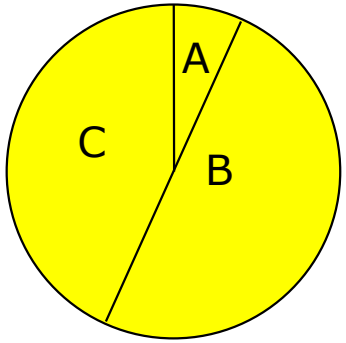
- Aim
  - Parent selection (from current generation) for reproduction
  - Survival selection (from parents and offspring) for next generation
- Winner strategy
  - Deterministic – the best wins
  - Stochastic – the best has more chances to win
- Mechanism
  - Selection for recombination
    - Proportional selection (based on fitness) } Based on entire population
    - Rank-based selection
    - Tournament selection → Based on a part of population
  - Survival selection
    - Age-based selection
    - Fitness-based selection

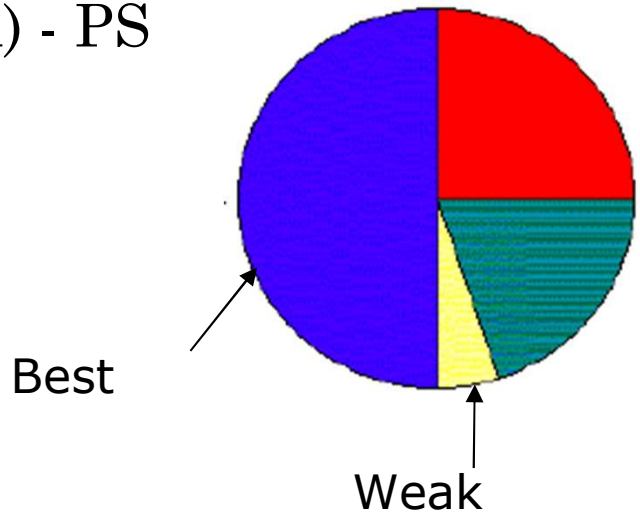
Recombination selection

- Proportional selection (fitness-based selection) - PS
  - Main idea
    - Roulette algorithm for entire population
    - Estimation of the copies # of an individual (selection pressure)

$$E(n_i) = \mu \frac{f(i)}{\langle f \rangle}$$, where:

    - μ = size of population,
    - $f(i)$ = fitness of individual i,
    - $\langle f \rangle$ = mean fitness of population
  - Better individuals
    - Have more space on roulette
    - Have more chances to be selected
  - Ex. A population of μ = 3 individuals



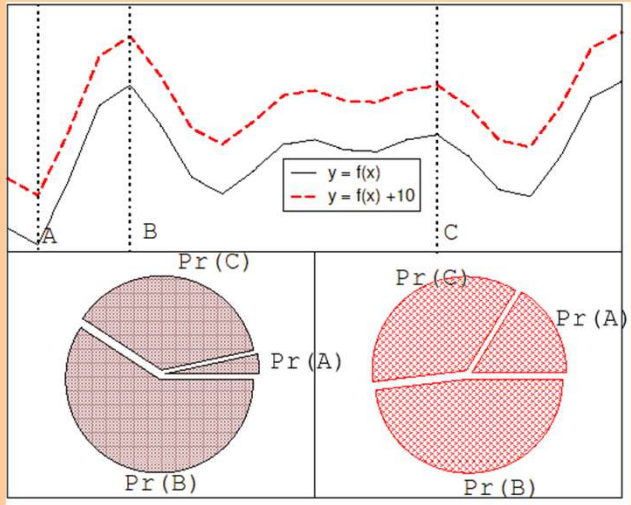


	f(i)	$P_{selPS}(i)$
A	1	1/10=0.1
B	5	5/10=0.5
C	4	4/10=0.4
Sum	10	1

Recombination selection

Proportional selection (fitness-based selection) – PS

- Advantages
  - Simple algorithm
- Disadvantages
  - Premature convergence
    - Best chromosomes predispose to dominate the population
  - Low selection pressure when fitness functions are very similar (at the end of a run)
  - Real results are different to theoretical probabilistic distribution
  - Works at the entire population level
- Solutions
  - Fitness scaling
    - Windowing
      - $f'(i) = f(i) - \beta^t$, where β is a parameter that depends on evolution history
        - eg. β is the fitness of the weakest individual of current population (the tth generation)
    - Sigma scaling (Goldberg type)
      - $f'(i) = \max\{f(i) - (\langle f \rangle - c * \sigma_f), 0.0\}$, where:
        - C – a constant (usually, 2)
        - $\langle f \rangle$ – average fitness of population
        - σ_f – standard deviation of population fitness
    - Normalisation
      - Starts by absolute (initial) fitnesses
      - Standardize these fitnesses such as the fitnesses:
        - Belong to [0,1]
        - Best fitness is the smallest one (equal to 0)
        - Sum of them is 1
  - Another selection mechanism



Selection for recombination

- Ranking selection – RS
  - Main idea
    - Sort the entire population based on fitness
      - Increases the algorithm complexity, but it is negligible related to the fitness evaluation
    - Each individual receives a rank
    - Computes the selection probabilities based on these ranks
      - Best individual has rank μ
      - Worst individual has rank 1
    - Tries to solve the problems of proportional selection by using relative fitness (instead of absolute fitness)

Selection for recombination

- Ranking selection - RS
  - Ranking procedures
    - Linear (LR) $$P_{lin\_rank}(i) = \frac{2-s}{\mu} + \frac{2i(s-1)}{\mu(\mu-1)}$$
      - s – selection pressure
        - Measures the advantages of the best individual
        - $1.0 < s \leq 2.0$
        - In the generational algorithm s represents the copies number of an individual
      - Ex. For a population of $\mu = 3$ individuals

	f(i)	$P_{selPS}(i)$	Rank	$P_{selLR}(i)$ for s=2	$P_{selRL}(i)$ for s=1.5
A	1	1/10=0.1	1	0.33	0.33
B	5	5/10=0.5	3	1.00	0.33
C	4	4/10=0.4	2	0.67	0.33
Sum	10	1			

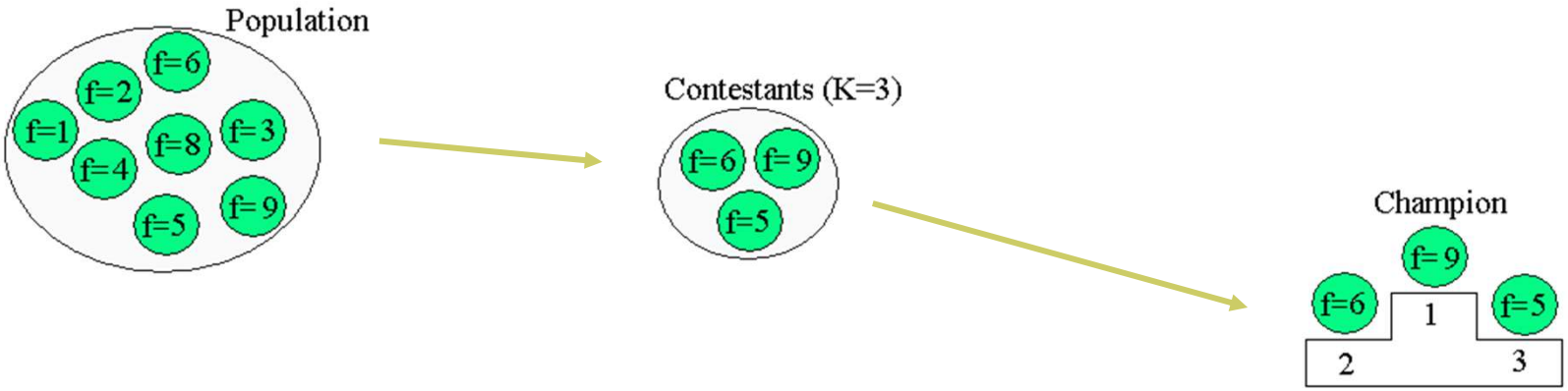
    - Exponential (ER) $$P_{\exp\_rank}(i) = \frac{1-e^{-i}}{c}$$
      - Best individual can have more than 2 copies
      - C – normalisation factor
        - Depends on the population size (μ)
        - Must be choose such as the sum of selection probabilities to be 1

Selection for recombination

- Ranking selection - RS
  - Advantages
    - Keep the selection pressure constant
  - Disadvantages
    - Works with the entire population
  - Solutions
    - Another selection procedure

Selection for recombination

- Tournament selection
  - Main idea
    - Chooses k individuals → sample of k individuals (k – tournament size)
    - Selects the best individual of the sample
    - Probability of sample selection depends on
      - Rank of individual
      - Sample size (k)
        - The larger k is, the greater selection pressure is
      - Choosing manner – with replacement (steady-state model) or without replacement
        - Selection without replacement increases the selection pressure
      - For k =2 the time required by the best individual to dominate the population is the same to that from linear ranking selection with s = 2 * *p*, *p* – selection probability of the best individual from population



Selection for recombination

- Tournament selection
  - Advantages
    - Does not work with the entire population
    - Easy to implement
    - Easy to control the selection pressure by using parameter k
  - Disadvantages
    - The real results of this selection are different to theoretical distribution (similarly to roulette selection)

Survival selection

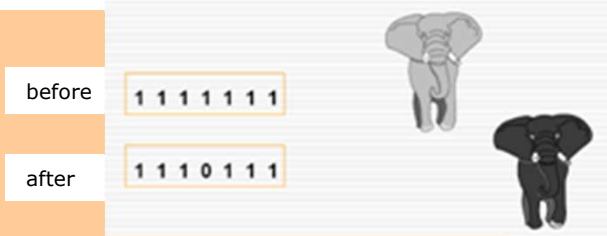
- Survival selection (selection for replacement)
  - Based on age
    - Eliminates the oldest individuals
  - Based on fitness
    - Proportional selection
    - Ranking selection
    - Tournament selection
    - Elitism
      - Keep the best individuals from a generation to the next one (if the offspring are weaker than parents, then keep the parents)
    - GENITOR (replaces the worst individual)
      - Elimination of the worst λ individuals

Variation operators

- Aim :
  - Generation of new possible solutions
- Properties
  - Works at individual level
  - Is based on individual representation (fitness independent)
  - Helps the exploration and exploitation of the search space
  - Must produce valid individuals
- Typology
  - Arity criterion
    - Arity 1 → mutation operators
    - Arity > 1 → recombination/crossover operators

Mutation

- Aim
  - Reintroduces in population the lost genetic material
  - Unary search operator (continuous space)
  - Introduces the diversity in population (discrete space)
- Properties
  - Works at genotype level
  - Based on random elements



  - Responsible to the exploration of promising regions of the search space
  - Responsible to escape from local optima
  - Must introduce small and stochastic changes for an individual
  - Size of mutation must be controllable
  - Can probabilistic take place (by a given probability p_m) at the gene level

Mutation

- Binary representation
  - Strong mutation – bit-flipping
  - Weak mutation
- Integer representation
  - Random resetting
  - Creep mutation
- Permutation representation
  - Insertion mutation
  - Swap mutation
  - Inverse mutation
  - scramble mutation
  - K-opt mutation
- Real representation
  - Uniform mutation
  - Non-uniform mutation
    - Gaussian mutation
    - Cauchy mutation
    - Laplace mutation
- Tree-based representation → future lecture
  - Grow mutation
  - Shrink mutation
  - Switch mutation
  - Cycle mutation
  - Koza mutation
  - Mutation for numerical terminals

Mutation (binary representation)

- A chromosome $c = (g_1, g_2, \ldots, g_L)$ becomes $c' = (g_1', g_2', \ldots, g_L')$, where $g_i, g_i' \in \{0,1\}$, for $i = 1, 2, \ldots, L$.

- Strong mutation – *bit flipping*
  - Main idea
    - Changes by probability p_m (mutation rate) all the genes in their complement
      - $1 \rightarrow 0$
      - $0 \rightarrow 1$
    - Ex. A chromosome of $L = 8$ genes, $p_m = 0.1$

1	0	1	0	0	0	1	1

$\longrightarrow$

1	1	1	0	0	0	0	1

Mutation (binary representation)

- A chromosome $c = (g_1, g_2, \ldots, g_L)$ becomes
  $c' = (g_1', g_2', \ldots, g_L')$,
  where $g_i, g_i' \in \{0,1\}$, for $i = 1, 2, \ldots, L$

- Weak mutation
  - Main idea
    - Changes by probability p_m (mutation rate) some of the genes in 0 or 1
      - 1 → 0/1
      - 0 → 1/0
    - Eg. A chromosome of $L = 8$ genes, $p_m = 0.1$

1	0	1	0	0	0	1	1

→

1	1	1	0	0	0	0	1

Mutation (integer representation)

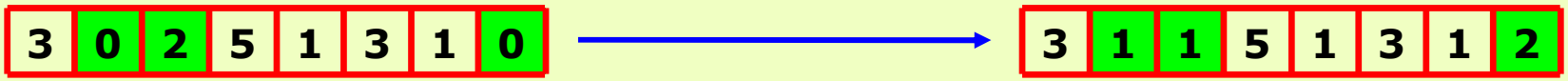
- A chromosome $c = (g_1, g_2, \ldots, g_L)$ becomes $c' = (g_1', g_2', \ldots, g_L')$, where $g_i, g_i' \in \{val_1, val_2, \ldots, val_k\}$ for $i = 1, 2, \ldots, L$.

- Random resetting mutation
  - Main idea
    - The value of a gene is changed (by probability p_m) into another value (from the definition domain)

Mutation (integer representation)

- A chromosome $c = (g_1, g_2, \ldots, g_L)$ becomes $c' = (g_1', g_2', \ldots, g_L')$, where $g_i, g_i' \in \{val_1, val_2, \ldots, val_k\}$, for $i = 1, 2, \ldots, L$.

- *Creep* mutation
  - Main idea
    - The value of a gene is changed (by probability p_m) by adding a positive/negative value
      - New value follows a 0 symmetric distribution
      - The performed change is very small



Mutation (permutation representation)

- A chromosome $c = (g_1, g_2, \ldots, g_L)$ with $g_i \neq g_j$ for all $i \neq j$ becomes

  $c' = (g_1', g_2', \ldots, g_L')$, where $g_i, g_i' \in \{val_1, val_2, \ldots, val_L\}$,

  for $i = 1, 2, \ldots, L$ s. a. $g_i' \neq g_j'$ for all $i \neq j$.

- *Swap mutation*
  - Main idea
    - Randomly choose 2 genes and swap their values

Mutation (permutation representation)

- A chromosome $c = (g_1, g_2, \ldots, g_L)$ with $g_i \neq g_j$ for all $i \neq j$ becomes

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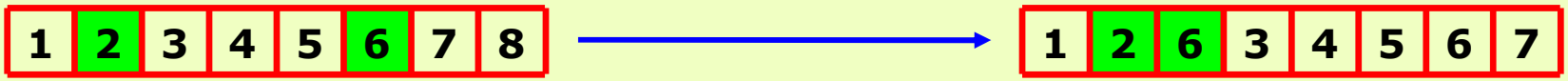
  for $i = 1, 2, \ldots, L$ s. a. $g_i' \neq g_j'$ for all $i \neq j$.

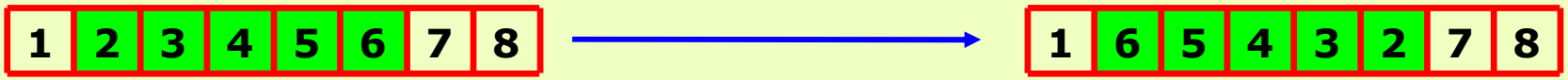
- Insertion mutation
  - Main idea
    - Randomly choose *2* genes g_i and g_j with $j > i$
    - Insert gene g_j after gene g_i s.a. $g_i' = g_i$, $g_{i+1}' = g_j$, $g_{k+2}' = g_{k+1}$, for $k = i, i+1, i+2, \ldots$



Mutation (permutation representation)

- A chromosome $c = (g_1, g_2, \ldots, g_L)$ with $g_i \neq g_j$ for all $i \neq j$ becomes
  $c' = (g_1', g_2', \ldots, g_L')$, where $g_i, g_i' \in \{val_1, val_2, \ldots, val_L\}$,
  for $i = 1, 2, \ldots, L$ s.a. $g_i' \neq g_j'$ for all $i \neq j$.

- Inversion mutation
  - Main idea
    - Randomly choose 2 genes and inverse the order of genes between them (sub-string of genes)



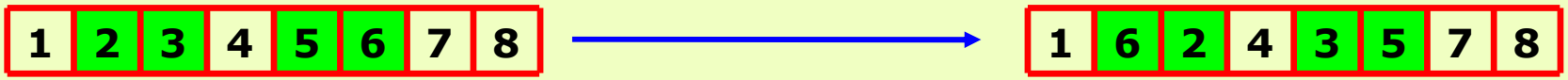
Mutation (permutation representation)

- A chromosome $c = (g_1, g_2, \ldots, g_L)$ with $g_i \neq g_j$ for all $i \neq j$ becomes

  $c' = (g_1', g_2', \ldots, g_L')$, where $g_i, g_i' \in \{val_1, val_2, \ldots, val_L\}$,

  for $i = 1, 2, \ldots, L$ s.a. $g_i' \neq g_j'$ for all $i \neq j$.

- *scramble mutation*
  - Main idea
    - Randomly choose a (continuous or discontinuous) sub-array of genes and re-organise that genes



Mutation (permutation representation)

- A chromosome $c = (g_1, g_2, \ldots, g_L)$ with $g_i \neq g_j$ for all $i \neq j$ becomes

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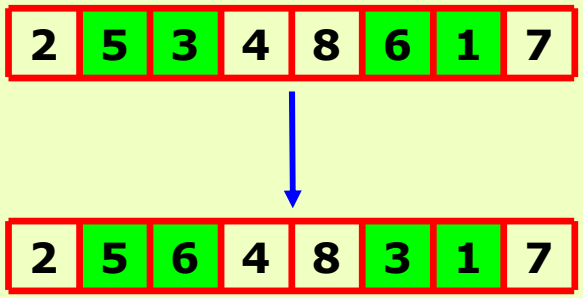
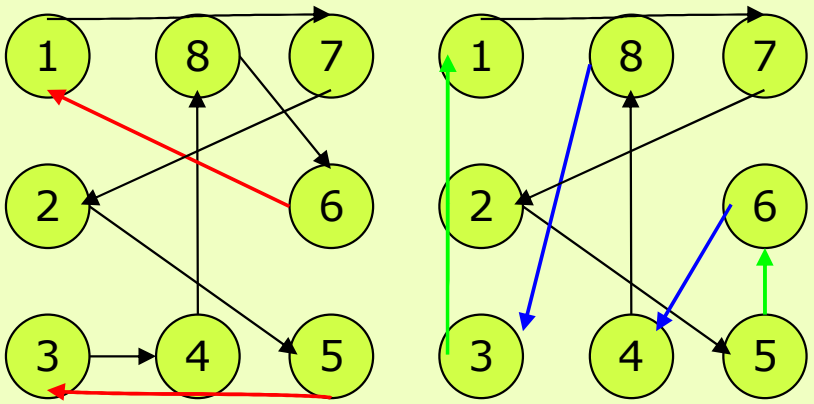
  for $i = 1, 2, \ldots, L$ s.a. $g_i' \neq g_j'$ for all $i \neq j$.

- K-opt mutation
  - Main idea
    - Choose 2 disjoint sub-strings of length k
    - Interchange 2 elements of these sub-strings

k=2





Mutation (real representation)

- A chromosome $c = (g_1, g_2, \ldots, g_L)$ becomes $c' = (g_1', g_2', \ldots, g_L')$, where $g_i, g_i' \in [a_i, b_i]$, for $i=1, 2, \ldots, L$.

- Uniform mutation
  - Main idea
    - g_i' is changed by probability p_m into a new value that is randomly uniform generated in $[a_i, b_i]$ range

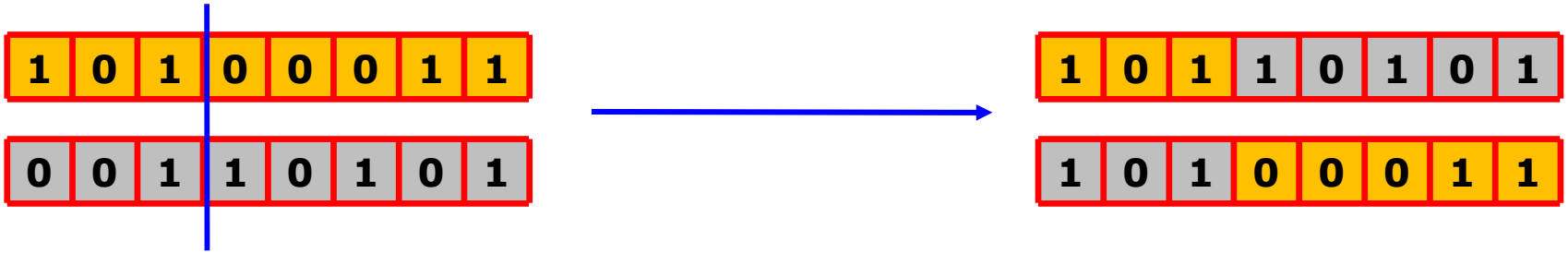
Mutation (real representation)

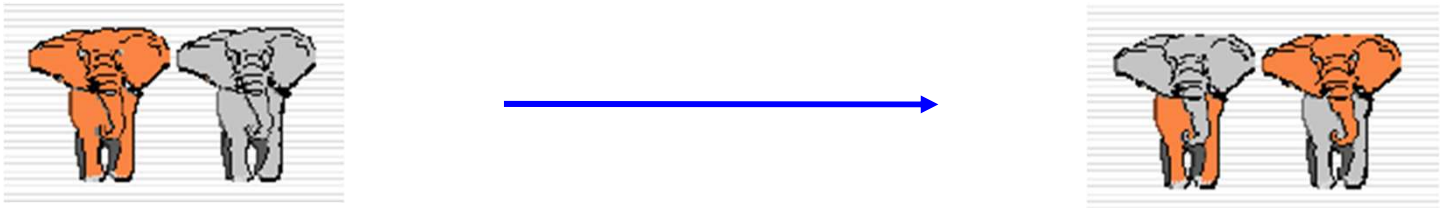
- A chromosome $c = (g_1, g_2, \ldots, g_L)$ becomes $c' = (g_1', g_2', \ldots, g_L')$, where $g_i, g_i' \in [a_i, b_i]$, for $i = 1, 2, \ldots, L$.
- Non-uniform mutation
  - Main idea
    - The value of a gene is probabilistically (p_m) changed by adding a positive/negative value
      - The added value belongs to a distribution of type
        - $N(\mu, \sigma)$ (Gaussian) with $\mu = 0$
        - Cauchy (x_0, γ)
        - Laplace (μ, b)
      - And it is re-introduced in $[a_i, b_i]$ range (if it is necessary) – *clamping*

Recombination

- Aim
  - Mix the parents' information

- Properties
  - The offspring has to inherit something from both parents
    - Selection of mixed information is randomly performed
  - Operator for exploitation of already discover possible solutions
  - The offspring can be better, the same or weaker than their parents
  - Its effects are reducing while the search converges





Recombination

- Types
  - Binary and integer representation
    - With cutting points
    - Uniforme
  - Permutation representation
    - Order crossover (version 1 and version 2)
    - Partially Mapped Crossover
    - Cycle crossover
    - Edge-based crossover
  - Real representation
    - Discrete
    - Arithmetic
      - Singular
      - Simple
      - Complete
    - Geometric
    - Shuffle crossover
    - Simulated binary crossover
  - Tree-based representation
    - Sub-tree based crossover → future lecture

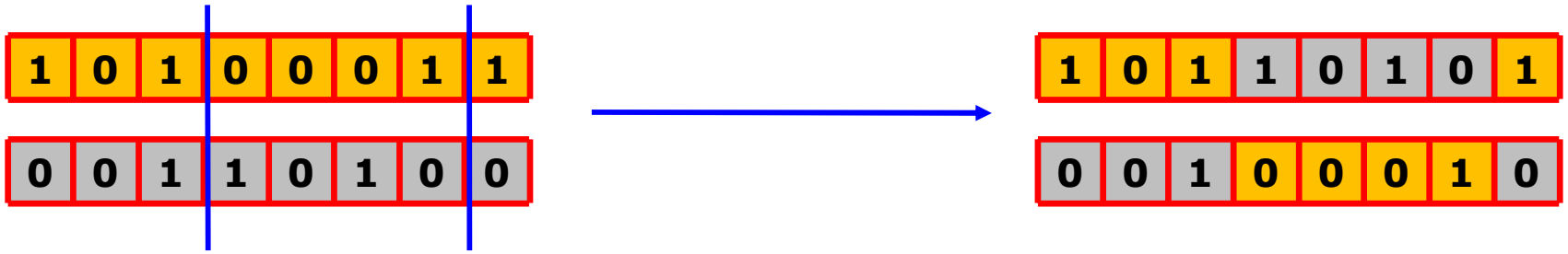
Recombination (binary and integer representation)

- From 2 parent chromosomes
  - $p_1 = (g_1^1, g_2^1, \ldots, g_L^1)$ and $p_2 = (g_1^2, g_2^2, \ldots, g_L^2)$
- 2 offspring are obtained
  - $c_1 = (g_1', g_2', \ldots, g_L')$ and $c_2 = (g_1'', g_2'', \ldots, g_L'')$,
  - where $g_i^1, g_i^2, g_i', g_i'' \in \{0, 1\} / \{val_1, val_2, \ldots, val_k\}$, for $i = 1, 2, \ldots, L$

N-cutting point crossover

- Main idea
  - Choose n cutting-points ($n < L$)
  - Cut the parents through these points
  - Put together the resulted parts, by alternating the parents

n=2



Recombination (binary and integer representation)

- N cutting point crossover
  - Properties
    - Average of values encoded by parents = average of values encoded by offspring
      - Eg binary representation on *4* bits of integer numbers – XO with $n = 1$ after second bit
        - $p_1 = (1, 0, 1, 0)$, $p_2 = (1, 1, 0, 1)$
        - $c_1 = (1, 0, 0, 1)$, $c_2 = (1, 1, 1, 0)$
        - $val(p_1) = 10$, $val(p_2) = (13)$ ➔ $(val(p_1) + val(p_2)) / 2 = 23 / 2 = 11.5$
        - $val(c_1) = 9$, $val(c_2) = (14)$ ➔ $(val(c_1) + val(c_2)) / 2 = 23 / 2 = 11.5$
      - Eg. Binary representation on *4* bits for knapsack problem ($K=10$, *4* items of weight and value: *(2,7), (1,8), (3,1), (2,3)*)
        - $p_1 = (1, 0, 1, 0)$, $p_2 = (1, 1, 0, 1)$
        - $c_1 = (1, 0, 0, 1)$, $c_2 = (1, 1, 1, 0)$
        - $val(p_1) = 8$, $val(p_2) = 18$ ➔ $(val(p_1) + val(p_2)) / 2 = 26 / 2 = 13$
        - $val(c_1) = 10$, $val(c_2) = 16$ ➔ $(val(c_1) + val(c_2)) / 2 = 26 / 2 = 13$
    - Probability of $\beta \approx 1$ is the largest one

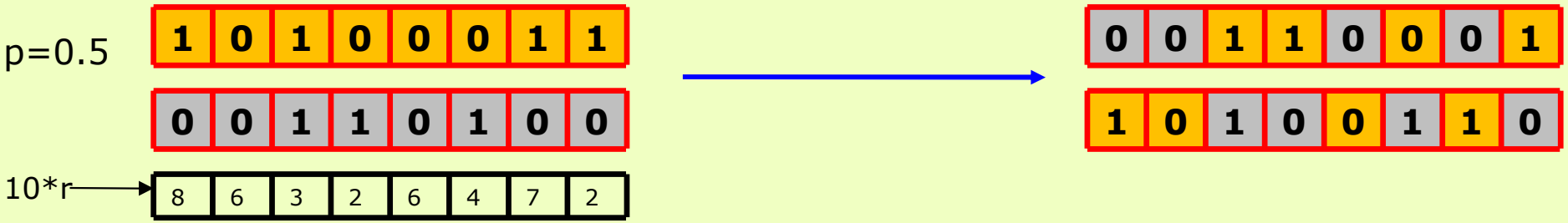
$$\beta = \left| \frac{val(d_1) - val(d_2)}{val(p_1) - val(p_2)} \right|$$

      - Contracting crossover $\beta < 1$
        - Offspring values are between parent values
      - Expanding crossover $\beta > 1$
        - Parent values are between offspring values
      - Stationary crossover $\beta = 1$
        - Offspring values are equal to parent values

Recombination (binary and integer representation)

- From 2 parent chromosomes
  - $p_1 = (g_1^1, g_2^1, \ldots, g_L^1)$ and $p_2 = (g_1^2, g_2^2, \ldots, g_L^2)$
- 2 offspring are obtained
  - $c_1 = (g_1', g_2', \ldots, g_L')$ and $c_2 = (g_1'', g_2'', \ldots, g_L'')$,
  - where $g_i^1, g_i^2, g_i', g_i'' \in \{0, 1\} / \{val_1, val_2, \ldots, val_k\}$, for $i = 1, 2, \ldots, L$

- Uniform crossover
  - Main idea
    - Each gene of an offspring comes from a randomly and uniform selected parent:
      - For each gene a uniform random number r is generated
      - If $r < probability\ p$ (usually, $p=0.5$), c_1 will inherit that gene from p_1 and c_2 from p_2,
      - otherwise, c_1 will inherit p_2 and c_2 will inherit p_1



Recombination (permutation representation)

- From 2 parent chromosomes
  - $p_1 = (g_1^1, g_2^1, \ldots, g_L^1)$ and $p_2 = (g_1^2, g_2^2, \ldots, g_L^2)$
- 2 offspring are obtained
  - $c_1 = (g_1', g_2', \ldots, g_L')$ and $c_2 = (g_1'', g_2'', \ldots, g_L'')$,
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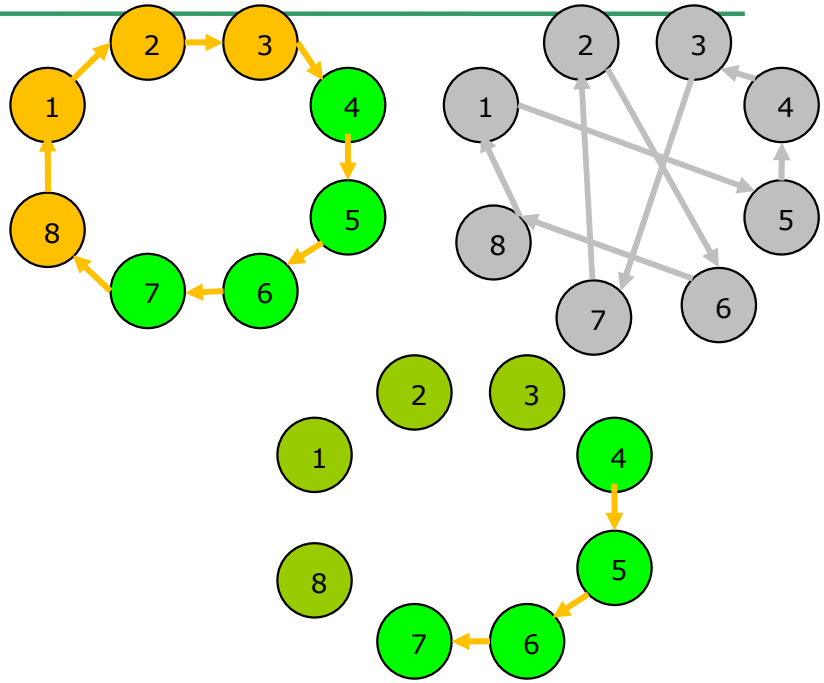
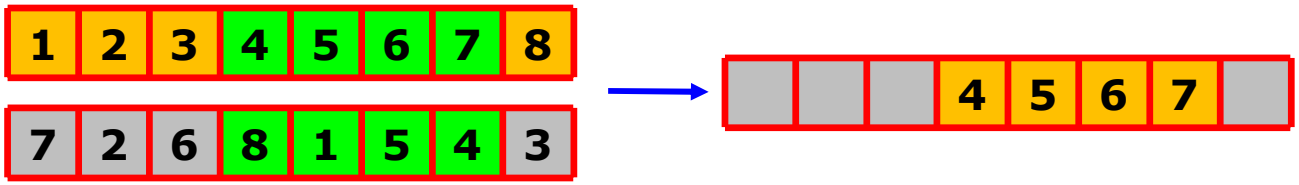


- Order crossover
  - Main idea
    - Offspring keep the order of genes from parents
    - Choose a substring of genes from the parent p_1
    - Copy the substring from p_1 into offspring d_1 (on corresponding positions)



Recombination (permutation representation)

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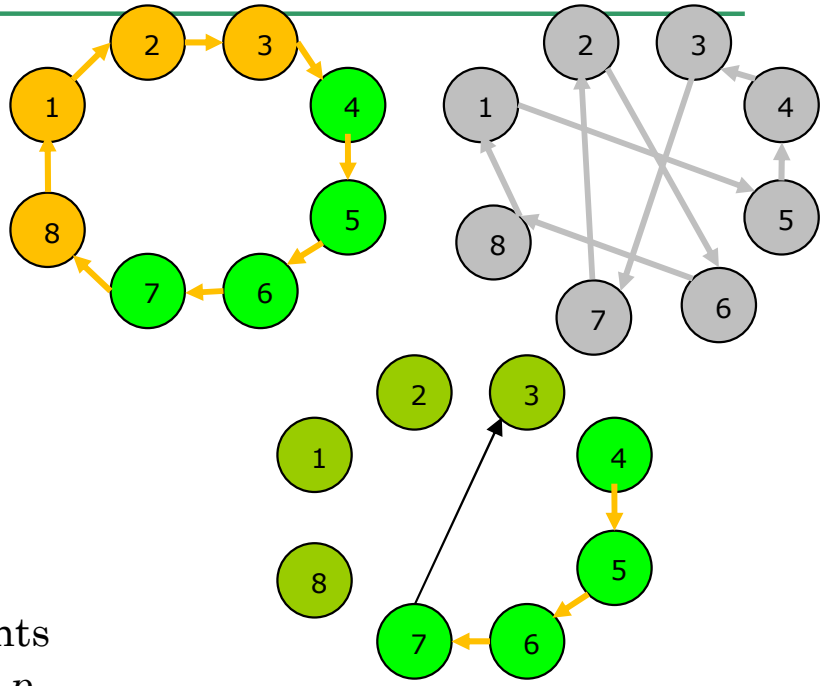

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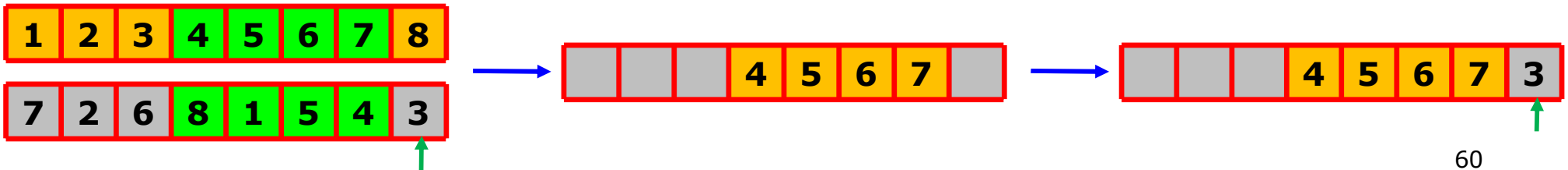
    - Copy the genes of p_2 in offspring d_1:
      - Starting with the first position after sub-string
      - Respecting gene's order from p_2 and
      - Re-loading the genes from start (if the end of chromosome is reached)



Recombination (permutation representation)

- From 2 parent chromosomes
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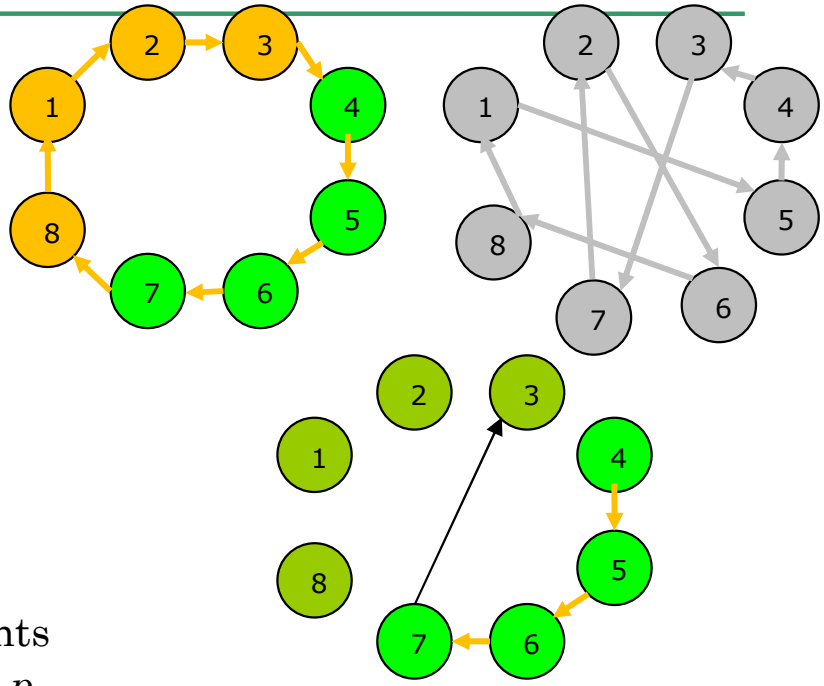

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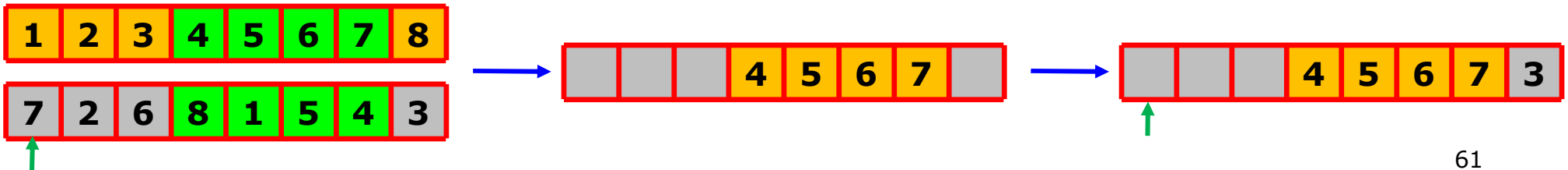

Recombination (permutation representation)

- From 2 parent chromosomes
  - $p_1 = (g_1^1, g_2^1, \ldots, g_L^1)$ and $p_2 = (g_1^2, g_2^2, \ldots, g_L^2)$
- 2 offspring are obtained
  - $c_1 = (g_1', g_2', \ldots, g_L')$ and $c_2 = (g_1'', g_2'', \ldots, g_L'')$,
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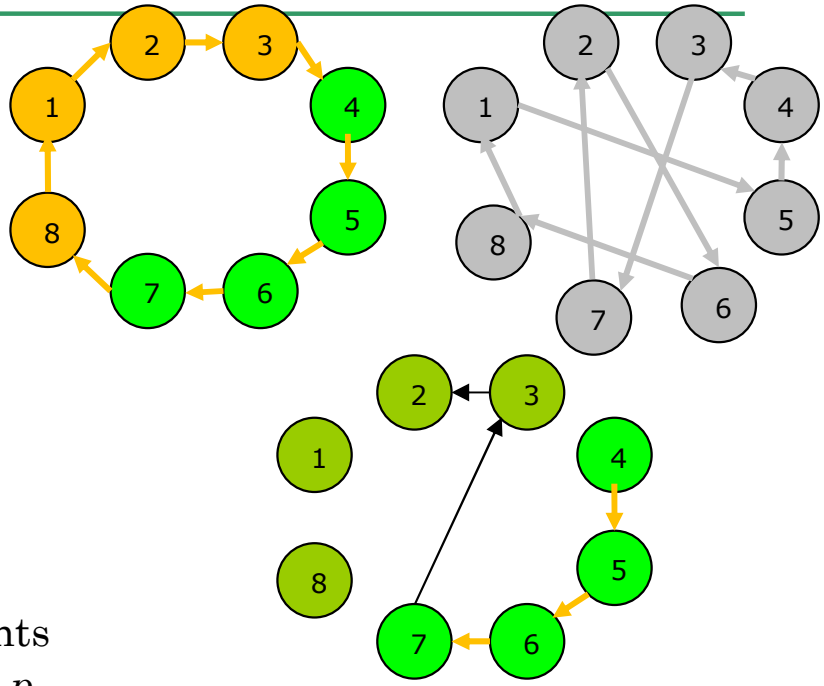

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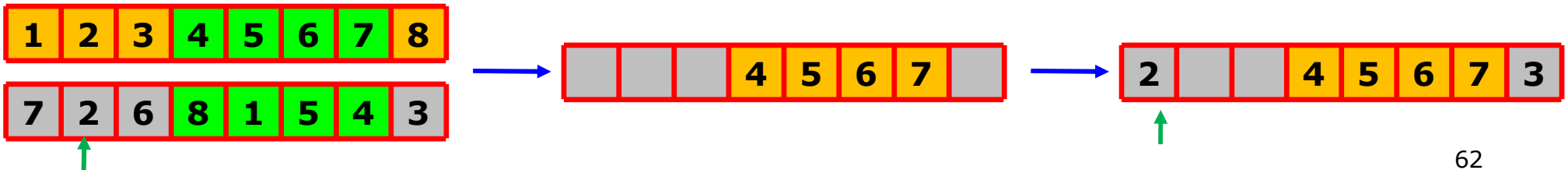

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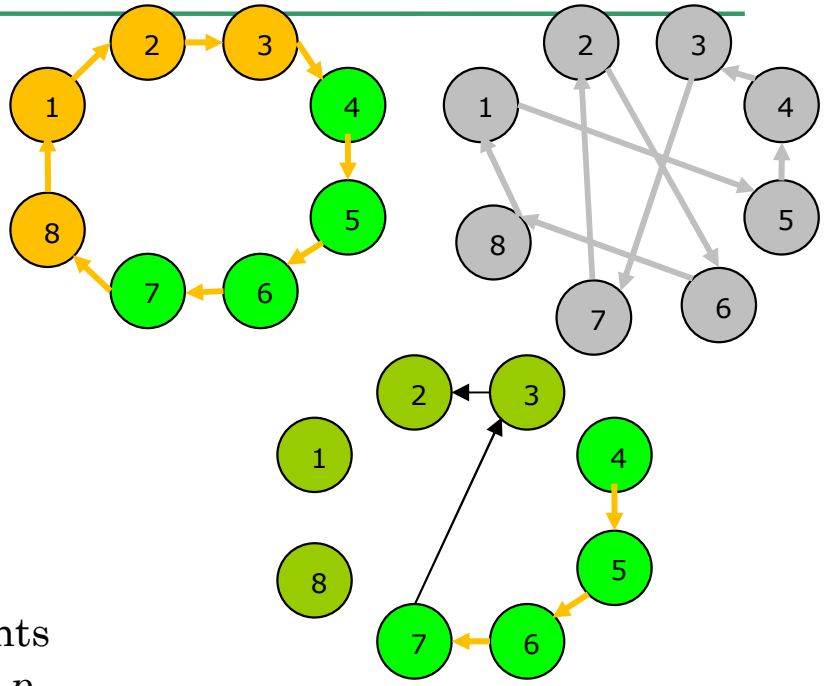

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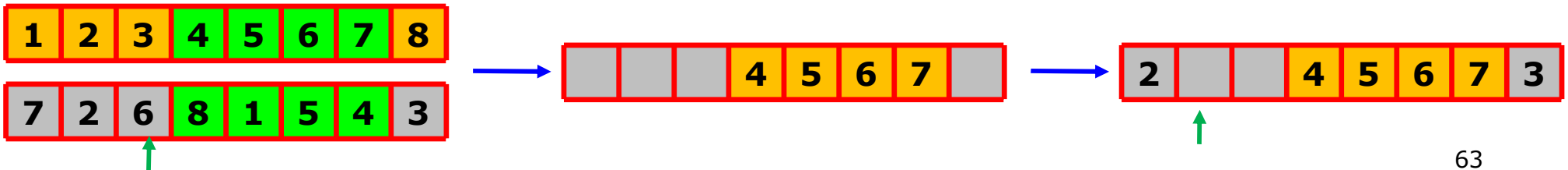

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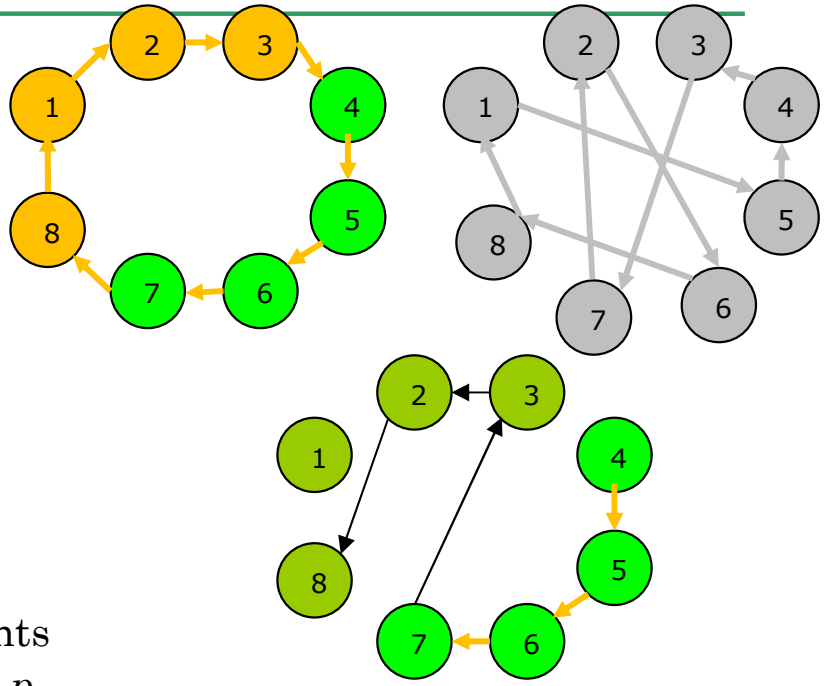

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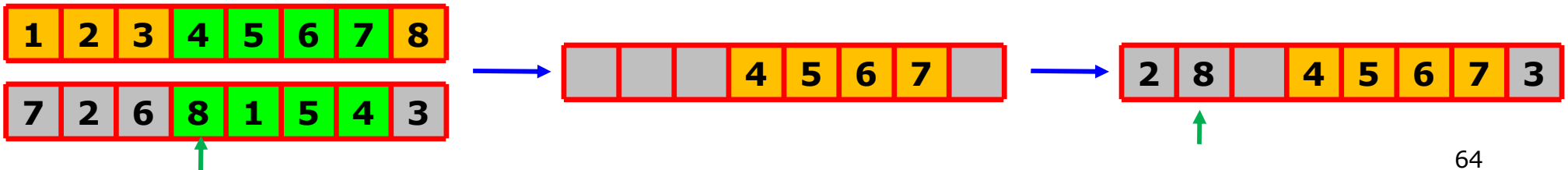

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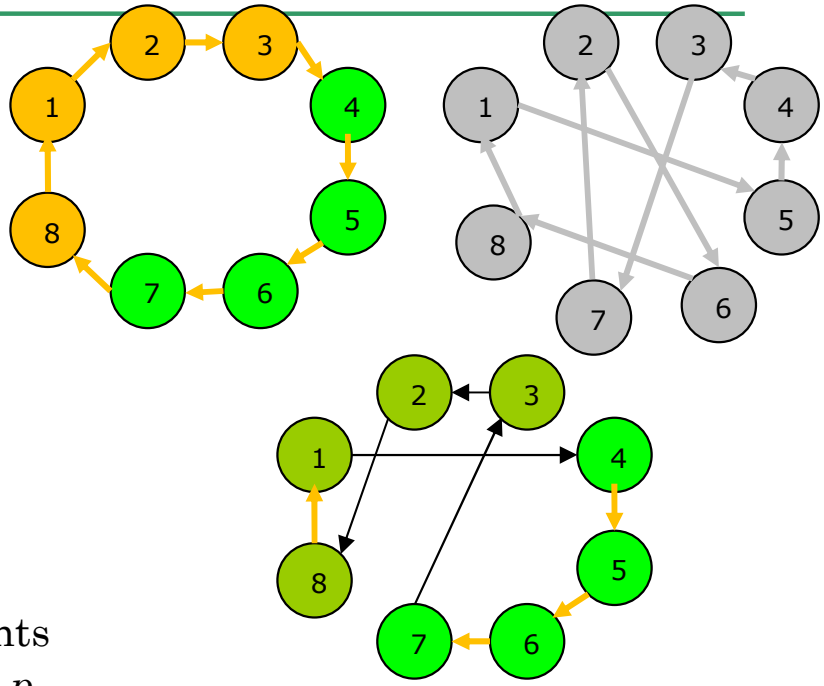

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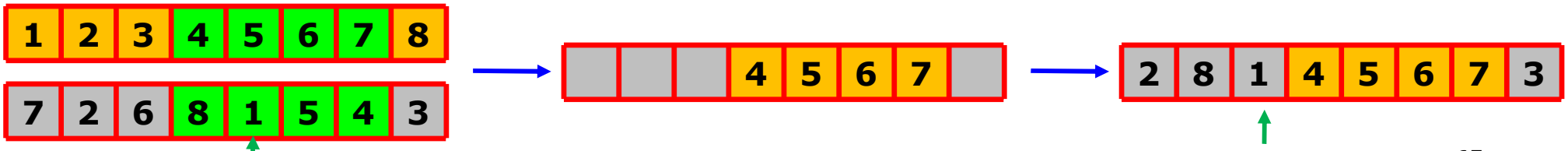
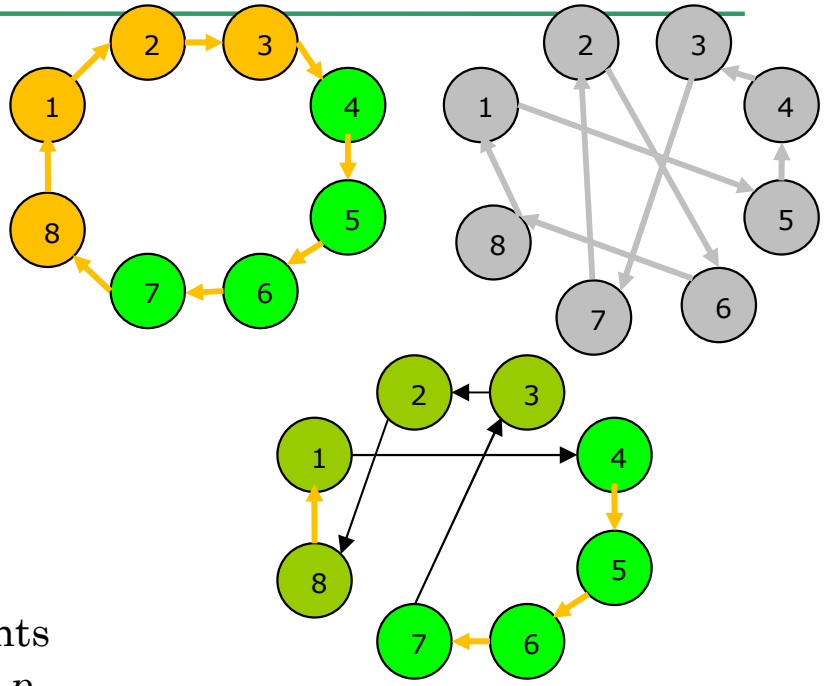
      - Starting with the first position after sub-string
      - Respecting gene's order from p_2 and
      - Re-loading the genes from start (if the end of chromosome is reached)

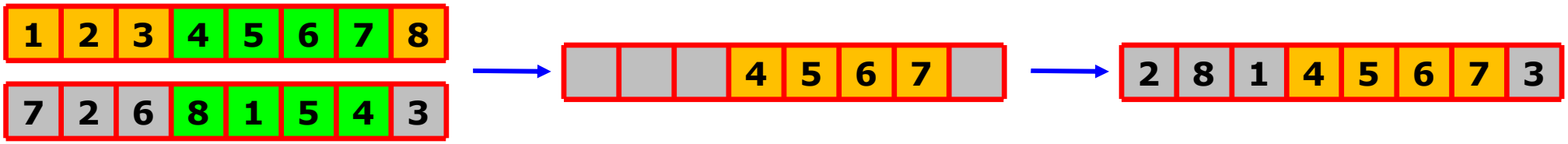


Recombination (permutation representation)

- From 2 parent chromosomes
  - $p_1 = (g_1^1, g_2^1, \ldots, g_L^1)$ and $p_2 = (g_1^2, g_2^2, \ldots, g_L^2)$
- 2 offspring are obtained
  - $c_1 = (g_1', g_2', \ldots, g_L')$ and $c_2 = (g_1'', g_2'', \ldots, g_L'')$,
  - Where $g_i^1, g_i^2, g_i', g_i'' \in [1, L] \cap \mathbb{Z}$, for $i = 1, 2, \ldots, L$.



- Order crossover
  - Main idea
    - Offspring keep the order of genes from parents
    - Choose a substring of genes from the parent p_1
    - Copy the substring from p_1 into offspring d_1 (on corresponding positions)
    - Copy the genes of p_2 in offspring d_1:
      - Starting with the first position after sub-string
      - Respecting gene's order from p_2 and
      - Re-loading the genes from start (if the end of chromosome is reached)



Recombination (real representation)

- From 2 parent chromosomes
  - $p_1 = (g_1^1, g_2^1, \ldots, g_L^1)$ and $p_2 = (g_1^2, g_2^2, \ldots, g_L^2)$
- 2 offspring are obtained
  - $c_1 = (g_1', g_2', \ldots, g_L')$ and $c_2 = (g_1'', g_2'', \ldots, g_L'')$,
  - Where $g_i^1, g_i^2, g_i', g_i'' \in [a_i, b_i]$, for $i = 1, 2, \ldots, L$

- Discrete crossover
  - Main idea
    - Each gene offspring is taken (by the same probability, $p = 0.5$) from one of the parents
    - Similarly to uniform crossover for binary/integer representation
    - The absolute values of genes are not changed (no new information is created)

p=0.5

0.3	-1.5	3.2	2.4	-1.1	0.6	2.0	-1.7
-2.1	1.3	0.2	-1.4	1.1	-0.3	1.0	1.7

10*r

8	6	3	2	6	4	7	2

-2.1	1.3	3.2	2.4	1.1	0.6	1.0	-1.7
0.3	-1.5	0.2	-1.4	-1.1	-0.3	2.0	1.7

Recombination (real representation)

- From 2 parent chromosomes
  - $p_1 = (g_1^1, g_2^1, \ldots, g_L^1)$ and $p_2 = (g_1^2, g_2^2, \ldots, g_L^2)$
- 2 offspring are obtained
  - $c_1 = (g_1', g_2', \ldots, g_L')$ and $c_2 = (g_1'', g_2'', \ldots, g_L'')$,
  - Where $g_i^1, g_i^2, g_i', g_i'' \in [a_i, b_i]$, for $i = 1, 2, \ldots, L$

- Arithmetic crossover
  - Main idea
    - Create offspring between parents → arithmetic crossover
      - $z_i = \alpha\, x_i + (1 - \alpha)\, y_i$ where $0 \leq \alpha \leq 1$.
    - Parameter α can be:
      - Constant → uniform arithmetic crossover
      - Variable → eg. Depends on the age of population
      - Random → generated for each new XO that is performed
    - New values of a gene can appear

- Types:
  - Singular arithmetic crossover
  - Simple arithmetic crossover
  - Complete arithmetic crossover

Recombination (real representation)

- From 2 parent chromosomes
  - $p_1 = (g_1^1, g_2^1, \ldots, g_L^1)$ and $p_2 = (g_1^2, g_2^2, \ldots, g_L^2)$
- 2 offspring are obtained
  - $c_1 = (g_1', g_2', \ldots, g_L')$ and $c_2 = (g_1'', g_2'', \ldots, g_L'')$,
  - Where $g_i^1, g_i^2, g_i', g_i'' \in [a_i, b_i]$, for $i = 1, 2, \ldots, L$

- Singular arithmetic crossover
  - Choose one gene from two parents (of the same position k) and combine them
    - $g_k' = \alpha\, g_k^1 + (1 - \alpha)\, g_k^2$
    - $g_k'' = (1 - \alpha)\, g_k^1 + \alpha\, g_k^2$
  - The rest of genes are unchanged
    - $g_i' = g_i^1$
    - $g_i'' = g_i^2$, for $i = 1,2,\ldots,L$ and $i \neq k$

$[a, b] = [-2.5, +3]$
$k = 3$
$\alpha = 0.6$

0.6*3.2+(1-0.6)*0.2=2.0

(1-0.6)*3.2+0.6*0.2=1.4

0.3	-1.5	3.2	2.4	-1.1	0.6	2.0	-1.7
-2.1	1.3	0.2	-1.4	1.1	-0.3	1.0	1.7

0.3	-1.5	2.0	2.4	-1.1	0.6	2.0	-1.7
-2.1	1.3	1.4	-1.4	1.1	-0.3	1.0	1.7

Recombination (real representation)

- From 2 parent chromosomes
  - $p_1 = (g_1^1, g_2^1, \ldots, g_L^1)$ and $p_2 = (g_1^2, g_2^2, \ldots, g_L^2)$
- 2 offspring are obtained
  - $c_1 = (g_1', g_2', \ldots, g_L')$ and $c_2 = (g_1'', g_2'', \ldots, g_L'')$,
  - Where $g_i^1, g_i^2, g_i', g_i'' \in [a_i, b_i]$, for $i = 1, 2, \ldots, L$

- Simple arithmetic crossover
  - Select a position k and combine all the genes after that position
    - $g_i' = \alpha\, g_i^1 + (1 - \alpha)\, g_i^2$
    - $g_i'' = (1 - \alpha)\, g_i^1 + \alpha\, g_i^2$, for $i = k, k + 1, \ldots, L$
  - Genes from positions < k rest unchanged
    - $g_i' = g_i^1$
    - $g_i'' = g_i^2$, for $i = 1, 2, \ldots, k - 1$

0.6*0.6+(1-0.6)*(-0.3)=0.24

(1-0.6)*0.6+0.6*(-0.3)=0.06

[a,b] = [-2.5, +3]
k = 6
α = 0.6

0.3	-1.5	3.2	2.4	-1.1	0.6	2.0	-1.7
-2.1	1.3	0.2	-1.4	1.1	-0.3	1.0	1.7

→

0.3	-1.5	3.2	2.4	-1.1	0.24	1.6	-0.34
-2.1	1.3	0.2	-1.4	1.1	0.06	1.4	0.34

Recombination (real representation)

- From 2 parent chromosomes
  - $p_1 = (g_1^1, g_2^1, \ldots, g_L^1)$ and $p_2 = (g_1^2, g_2^2, \ldots, g_L^2)$
- 2 offspring are obtained
  - $c_1 = (g_1', g_2', \ldots, g_L')$ and $c_2 = (g_1'', g_2'', \ldots, g_L'')$,
  - Where $g_i^1, g_i^2, g_i', g_i'' \in [a_i, b_i]$, for $i = 1, 2, \ldots, L$

Complete arithmetic crossover

- All of the genes are combined
  - $g_i' = \alpha\, g_i^1 + (1 - \alpha)\, g_i^2$
  - $g_i'' = (1 - \alpha)\, g_i^1 + \alpha\, g_i^2$, for $i = 1, 2, \ldots, L$

0.6*0.3+(1-0.6)*(-2.1)=-0.66

(1-0.6)*0.3+0.6*(-2.1)=-1.14

$[a, b] = [-2.5, +3]$
$\alpha = 0.6$

0.3	-1.5	3.2	2.4	-1.1	0.6	2.0	-1.7
-2.1	1.3	0.2	-1.4	1.1	-0.3	1.0	1.7

-0.66	4.3	2.0	0.48	-0.22	0.24	1.6	-0.34
-1.14	0.18	1.4	0.12	0.22	0.06	1.4	0.34

Recombination (real representation)

- From 2 parent chromosomes
  - $p_1 = (g_1^1, g_2^1, \ldots, g_L^1)$ and $p_2 = (g_1^2, g_2^2, \ldots, g_L^2)$
- 2 offspring are obtained
  - $c_1 = (g_1', g_2', \ldots, g_L')$ and $c_2 = (g_1'', g_2'', \ldots, g_L'')$,
  - Where $g_i^1, g_i^2, g_i', g_i'' \in [a_i, b_i]$, for $i = 1, 2, \ldots, L$

- Geometric crossover
  - Main idea
    - Each gene of an offspring represents the product between parent's genes, each of them by a given exponent ω and $1-\omega$, respectively (where ω is a real positive number <= 1)
    - $g_i' = (g_i^1)^{\omega} (g_i^2)^{1-\omega}$
    - $g_i'' = (g_i^1)^{1-\omega} (g_i^2)^{\omega}$

$0.3^{0.7}+2.1^{1-0.7}=1.68$

$0.3^{1-0.7}+2.1^{0.7}=2.38$

$[a,b] = [-2.5, +3]$
$\omega = 0.7$

0.3	1.5	3.2	2.4	1.1	0.6	2.0	1.7
2.1	1.3	0.2	1.4	1.1	0.3	1.0	1.7

1.68	2.41	2.87	2.95	2.10	1.40	2.62	2.62
2.38	2.33	1.74	2.57	2.10	1.29	2.23	2.62

Recombination (real representation)

- From 2 parent chromosomes
  - $p_1 = (g_1^1, g_2^1, \ldots, g_L^1)$ and $p_2 = (g_1^2, g_2^2, \ldots, g_L^2)$
- 2 offspring are obtained
  - $c_1 = (g_1', g_2', \ldots, g_L')$ and $c_2 = (g_1'', g_2'', \ldots, g_L'')$,
  - Where $g_i^1, g_i^2, g_i', g_i'' \in [a_i, b_i]$, for $i = 1, 2, \ldots, L$

- *Blend crossover – BLX*
  - Main idea
    - A single offspring is created
    - Offspring's genes are randomly generated from $[Min_i - I * a, Max_i + I * a]$ range, where:
      - $Min_i = min\{g_i^1, g_i^2\}$, $Max_i = max\{g_i^1, g_i^2\}$
      - $I = Max - Min$, a – parameter from $[0, 1]$

[a,b] = [-2.5, +3]
a = 0.7

0.3	1.5	3.2	2.4	1.1	0.6	2.0	1.7
2.1	1.3	0.2	1.4	1.1	0.3	1.0	1.7

1.25	1.45	-1.11	2.37	1.10	0.11	0.70	1.70

Min	0.3	1.3	0.2	1.4	1.1	0.3	1.0	1.7
Max	2.1	1.5	3.2	2.4	1.1	0.6	2.0	1.7
I	0.8	0.2	3.0	1.0	0	0.3	1.0	0.0

Min-Ia	-0.26	1.16	-1.90	0.70	1.10	0.09	0.30	1.70
Max+Ia	2.66	1.50	3.20	2.40	1.10	0.60	2.00	1.70

Recombination or mutation?

- Intense debates
  - Questions:
    - Which is the best operator?
    - Which is the most necessary operator?
    - Which is the most important operator?
  - Answers:
    - Depend on problem, but,
    - In general, is better to use both operators
    - Each of them having another role (purpose).
    - EAs with mutation only are possible, but EAs with crossover only are not possible
- Search aspects:
  - Exploration → discovering promising regions in the search space (accumulating useful information about the problem)
  - Exploitation → optimising in a promising region of the search space (by using the existent information)
  - Cooperation and competition mut exist between these 2 aspects
- Recombination
  - Exploitation operator → performs a large jump into a region somewhere between the regions associated to parents
    - Effects of exploitation decrease while AE is converging
  - Binary/n-ary operator that can combine information from 2/more parents
  - Operator that does not change the frequency of values from chromosome at the population level
- Mutation
  - Exploration operator → performs small random diversions, remaining in a neighbourhood of parent
    - Local optima escape
  - Operator that can introduce new genetic information
  - Operator that change the frequency of values from chromosome at the population level

Stop condition

- Choosing a stop condition
  - An optimal solution was found
  - The physical resources were ended
    - A given number of fitness evaluation has been performed
  - The user resources (time, patience) were ended
    - Several generation without improvements have been born

Evaluation

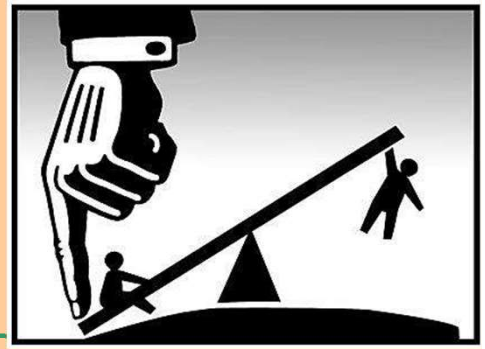
- Performance evaluation of an EA
  - After more runs
    - Statistical measures are computed
      - Average of solutions
      - Median of solutions
      - Best solution
      - Worst solution
      - Standard deviation of solutions – for comparisons
  - The number of independent runs must be large enough

EAs

Analyse of complexity

- The most costly part → fitness evaluation

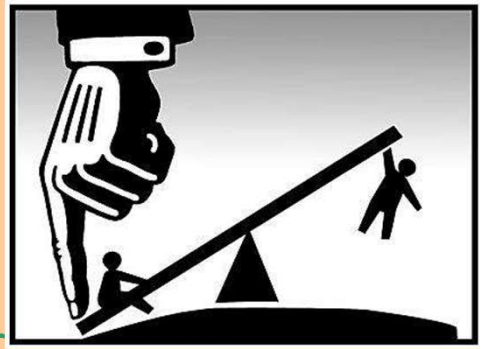
EAs



Advantages

- AEs have a general sketch for all the problems
  - Only
    - representation
    - fitness function
  - are changed
- AEs are able to give better results than classical optimisation methods because
  - They do not require linearization
  - They are not based on some presumptions
  - They do not ignore some possible solutions
- AEs are able to explore more possible solutions than human can

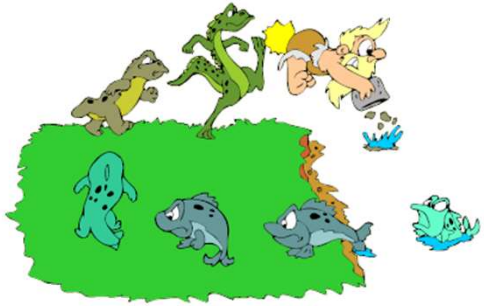
AEs



Disadvantages

- Large running time

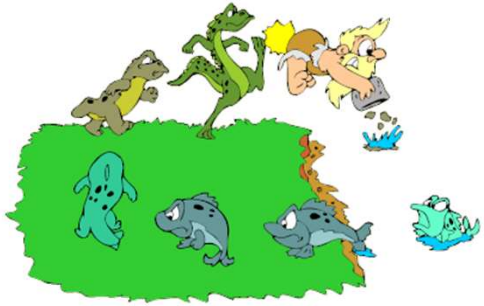
AEs



Applications

- Vehicle design
  - Material composition
  - Vehicle shape
- Engineering design
  - Structural and organisational optimisation of constructions (buildings, robots, satellites, turbines)
- Robotics
  - Design and components optimisation
- Hardware evolution
  - Digital circuits optimisation
- Telecommunication optimisation
- Cross-word game generation
- Biometric inventions (inspired by natural architectures)
- Traffic and transportation routing
- PC games
- Cryptography
- Genetics
- Chemical analysis of kinematics
- Financial and marketing strategies

AEs



Types

- Evolutionary strategies
- Evolutionary programming
- Genetic algorithms
- Genetic programming

Thank you for your attention!