

Evolutionary Computation

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Master Artificial Intelligence

Arno Formella

Departamento de Informática
Escola Superior de Enxeñaría Informática
Universidade de Vigo

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Evolutionary methods

- Evolutionary methods work with **populations** of individuals (or only one individual and a certain type of memory).
- There are probabilistic **modification processes** (mutation, reproduction, recombination/crossover) that change the population from one to the next generation.
- The **performance** of the individuals is based on a **fitness** which usually is the objective function (but not necessarily).
- There is a **selection process** to maintain a (more or less) stable state (size) of the population.
- Most of the algorithmic decisions are drawn **probabilistically**.

I will not give details on the history and researchers, please, take a look at the literature/bibliography.

Genetic algorithms (GA)

- We distinguish the **genotype** (codification of the individuals) and the **phenotype** (elements of the search space).
- There should exist a **bijection** between genotype and phenotype.
(mapping of phenotype to genotype can be relaxed)
- The genotype encodes the **free parameters** of an individual.
- The modifications (mutation and recombination/crossover) are carried out over the genotype.
- The fitness is evaluated over the phenotype (our objective function).
- We have to explain: codification (of the genotype), initialization, mutation, recombination/crossover, selection, and stopping.



A genetic algorithm can be summarized in the following principal loop:

```
InitializePopulation()      # initialization
EvaluateIndividuals()       # evaluation
while not Stopping():      # stopping
    DetermineParents()      # selection
    GenerateChildren()      # recombination
    MutateChildren()        # mutation
    EvaluateIndividuals()   # evaluation
    ReestablishPopulation() # selection
```

GA: encoding of the individuals

There are many possibilities how to **encode** the free parameters of an individual to form its genotype:

- use a binary bitstring, e.g., (101101)
- use a sequence of integer values in certain ranges, e.g., $(2, 6, 98, 3) \in [1 : 2] \times [1 : 10] \times [0 : 100] \times [1 : 5]$
- use a sequence of real values in certain ranges, e.g., $(1.23, 34.4, -2.1) \in [-50.0, 50.0]$
- use a permutation
- use a k-dimensional structure
- use a binary tree
- use a general graph
- use whatever you like (recall: do something, be happy...)

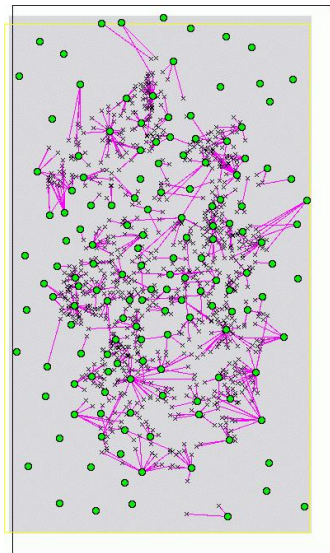
Remember: we need a bijection between genotype and phenotype and we need to implement crossovers and mutations that are able to explore the entire search space (or at least the region of interest).



GA: names taken from biology

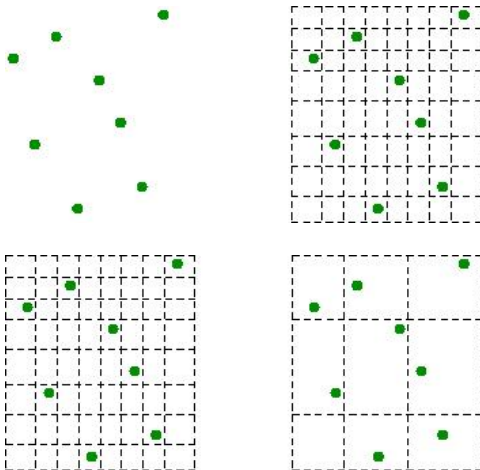
- The individual components of the sequences are called **genes**.
- The possible values of a gene are called **allele**.
- The encoding of an individual is called its **genome** or **chromosome**.

GA: genotype an example



- green: base stations
- crosses: mobile users
- magenta: assignment
- **goal:** find the minimal subset of base stations that guarantees an assignment of all mobiles
- Note: computation of the objective function is quite complex (and will not be detailed here).

GA: genotype an example



- initial
8 × 8 grid
- reduced to
3 × 3 grid
- 4 allele
(2-bit strings)
 - unusable
 - used
 - unused
 - fixed

GA: mutation possibilities

gene mutation:

just change randomly one (or more) gen(es) to another permitted allele

gene flip:

interchange the values of two (or more) genes

gene sequence displacement:

cut a sequence/part and insert at another position

gene sequence inversion:

revert the order of a (partial) sequence

what-ever-you-like:

do something, be happy...

- The mutation rate should be, more or less, inversely proportional to the size of the genome.
- For larger populations maybe reduce mutation rate in the on-going optimization process.
- With low diversity in the populations, maybe a larger mutation rate helps.

GA: crossover possibilities

simple crossover:

parents	cut	children
(101101)	(10 1101)	→ (100111)
(010111)	(01 0111)	→ (011101)
(2, 8, 98, 3)	(2, 8, 98, 3)	→ (2, 8, 40, 4)
(1, 9, 40, 4)	(1, 9, 40, 4)	→ (1, 9, 98, 3)

k-point crossover:

cut at k points and interchange the corresponding parts (variation: take k at random)

uniform crossover:

interchange each gene with certain probability

multiple parent mating:

use more than two parents and interchange genes (variation: merge entire parent set)

GA: crossover possibilities (continued)

arithmetic crossover: assign to children **convex combination** of parent genes with some random weight, $\alpha \in [0, 1]$, e.g., with $\alpha = 0.7$ on second gene:

$$34.5 \cdot 0.7 + 13.5 \cdot 0.3 = 28.2$$

$$(1.23, 34.5, -2.1) \longrightarrow (1.23, 28.2, -2.1)$$

$$13.5 \cdot 0.7 + 34.5 \cdot 0.3 = 19.8$$

$$(10.5, 13.5, 23.1) \longrightarrow (10.5, 19.8, 23.1)$$

(again variations: as k -point, or with all genes, or with k at random)

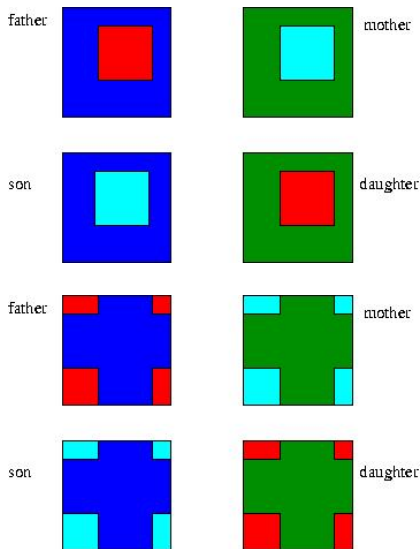
blended crossover: blend two corresponding parent genes with a certain, usually fixed, value $\alpha \in [-0.5, \infty]$ according to the current gene spread

simulated binary crossover: blend two corresponding parent genes according to a suitable probability density function

what-ever-you like: remember, do something, be happy...



GA: crossover example (2-point cyclic crossover)



- select two grid points
- interchange rectangles

A genetic algorithm can be summarized in the following principal loop (parts that are dealt with marked with *DONE*):

```
InitializePopulation()      # initialization
EvaluateIndividuals()      # evaluation      DONE
while not Stopping():      # stopping
    DetermineParents()      # selection
    GenerateChildren()      # recombination  DONE
    MutateChildren()        # mutation      DONE
    EvaluateIndividuals()    # evaluation    DONE
    ReestablishPopulation()  # selection
```

GA: selection

- In the principal loop, there are **two selection** processes:
 - How to **select the parents** to generate the off-springs? and
 - How to rearrange the **final population** or next generation?
- We use the following notation:
 - μ stands for the number of individuals in the population
 - λ stands for the number of children being generated
- We distinguish **two main** strategies:
 - **$(\mu + \lambda)$ -strategy**
 - from the μ individuals of the current generation select the parents and generate λ children
 - from the $\mu + \lambda$ individuals choose the μ best ones as new generation
 - **(μ, λ) -strategy**
 - from the μ individuals of the current generation select the parents and generate $\lambda \geq \mu$ children
 - from the λ children choose the μ best ones as new generation

The second question from above is answered.



GA: selection options

To **select** the parents being allowed **to have off-springs**, there exists a bunch of suggestions:

roulette wheel: assign to each individual a fraction of the wheel according to its relative fitness and spin the wheel (variation: smooth, weight, or normalize the fitness somehow, e.g., use log of objective function, or use z-score)

rank based: order the individuals according to fitness and select with a probability weighted by the rank (variation: compute selection probability with linear function of rank, so the least ranked still gets certain probability to get selected)

GA: selection options (continued)

tournament based: draw a certain number of random individuals, select the best one as parent
(variation: select directly the best two as parents)

truncation selection: only the individuals with highest fitness values will be parents

what-ever-you like: remember, do something, be happy...

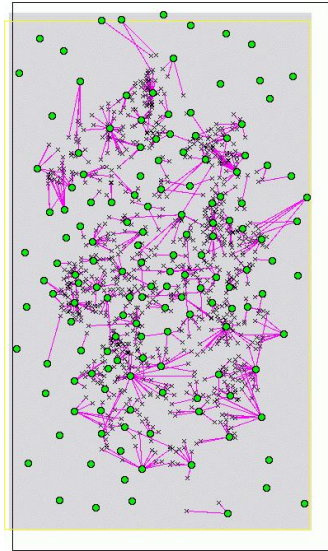
The first question (from two slides earlier) is answered.

- generate the initial population with **random genomes**
 - take into account that the distribution according to genotype not necessarily is similar to the distribution in phenotype
 - maybe there are many individuals with very low fitness
 - the initial convergence rate might be slow
- generate the initial population with individuals from another **heuristic algorithm** or various such algorithms
 - the population might be biased into a certain region of the search space
 - the diversity of the population might be low
 - the convergence rate might be trapped early in a local optimum
- recommendation: use a **mixture of both**

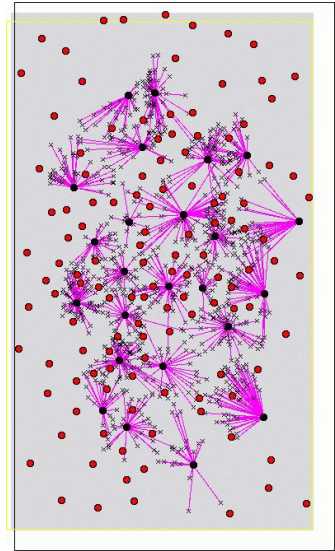
There are many possibilities **when to stop** the iteration of a genetic algorithm:

- once the **first solution** has been found
- once a **sufficiently good** solution has been found
- once the **optimum** has been found
- once a certain **number of iterations** has been executed
- once the **diversity** of the population is below a certain threshold
- once the **convergence rate** of the improvement is below a certain threshold
- once a certain amount of **runtime** has been spent
- once the iteration is stopped by **user interruption**
- recommendation: use an **OR-mixture of all**

GA: results for the example (2007)



119 of 149 nodes used



24 of 149 nodes used

GA: use for antenna design (small satellites)

Horny, AlGlobus, Linden, Lohn: Automated Antenna Design with Evolutionary Algorithms (2012)

<https://arc.aiaa.org/doi/10.2514/6.2006-7242> or https://www.researchgate.net/publication/228909002_Automated_Antenna_Design_with_Evolutionary_Algorithms

