

Genetic Algorithms

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- 1 Introducing genetic algorithms
- 2 The standard genetic algorithm
- 3 Solving a standard GA
- 4 Real-valued encoding

Introducing genetic algorithms

Genetic algorithms

Genetic algorithms are inspired by **evolution**:

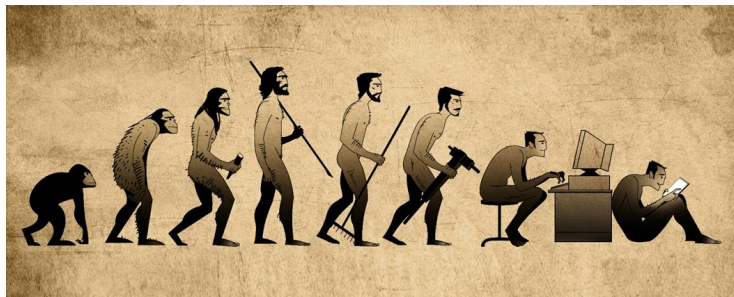


Figure 1: Evolution

Evolution

Evolution is the change of heritable conditions of biological populations over successive generations:

- Heritable conditions are **encoded** in the **genotype**, and are displayed in the **phenotype**.
- Heritable conditions change by **variation** mechanisms: **crossover** of parent's genes and gene **mutation**.
- Only the individuals who fit to the environment are **selected** in the next generation.

Can we use the mechanism of evolution (variation and selection) to solve optimization problems?

Genetic algorithms and evolution

Genetic algorithm is a **metaheuristic** inspired in the process of natural selection and evolution

- Metaheuristic: a template to create an algorithm to solve a specific problem.
- Other metaheuristics: particle swarm optimization, simulated annealing, tabu search. . .

First introduced by John Holland (1975) to simulate evolutionary processes, later used for optimization.

The genetic algorithm flow

- ① Define a **starting population** of candidate solutions
- ② While there is no **convergence**, create a new generation:
 - ▶ Create a new generation member by **crossover** of members of previous generation.
 - ▶ **Mutate** generation members with a probability.
 - ▶ **Select** the members of the new generation, according to its **fitness**.

Frequently the selection process is embedded in crossover: only individuals fit to the environment are allowed to mate.

The elements of a genetic algorithm

What do we need to build a genetic algorithm?

- A way to **encode** a candidate solution: how to obtain the genotype from the phenotype.
- Definition of **crossover**, **mutation** and **selection** operators. These operators work with the genotype of solutions.
- A **fitness function** that help us assess how does a population member fit to the environment.
- A **convergence** criterion to know when the algorithm stops.

The standard genetic algorithm

Binary encoding

A standard implementation of the genetic algorithm metaheuristic:

- A continuous **fitness function** to optimize (maximize or minimize) of p variables, sometimes with **constraints**.
- A **region** to explore with the genetic algorithm, defined by an upper and lower bound of variables (additional constraints).
- A **bit string** representation of each variable:
 - ▶ Phenotype: a real number $x \in \mathcal{R}$.
 - ▶ Genotype: a binary string $\mathbf{b} \in \mathcal{B}^n$.
- Creation of new population with a **crossover** operator:
 - ▶ Uniform, one-point, two-point crossover
- **Proportional selection** of crossover elements:
 - ▶ The probability of selection is higher for elements of good value of fitness function.

Bit string representation

Standard encoding mapping $\mathcal{B}^n \rightarrow [L, U] \subset \mathcal{R}$ of n bits slices a continuous interval into $2^n - 1$ bins:

$$x = L + \frac{U - L}{2^n - 1} \sum_{i=0}^{n-1} b_{n-1-i} 2^i$$

For $n = 3$ bits we have eight marks of the $[-10, 10]$ interval:

| | | | | | | | | | |
|----|-----|--------|-------|-------|-------|------|------|------|-------|
| ## | [1] | -10.00 | -7.14 | -4.29 | -1.43 | 1.43 | 4.29 | 7.14 | 10.00 |
|----|-----|--------|-------|-------|-------|------|------|------|-------|

| | | | | | | | | |
|-----------|-----|-------|-------|-------|------|------|------|-----|
| Genotype | 000 | 001 | 010 | 011 | 100 | 101 | 110 | 111 |
| Phenotype | -10 | -7.14 | -4.29 | -1.43 | 1.43 | 4.29 | 7.14 | 10 |

Bit string representation

The bit string has a precision equal to interval width:

$$\Delta x = \frac{U - L}{2^n - 1}$$

A high precision requires high number of bits, increasing computational cost.

Bit string representation

Hamming distance of two bit strings: number of different bits.

The Hamming distance of 001100 and 100110 is 3: bits 1, 3 and 5 are different.

Problem: contiguous bit string can have high Hamming distance (change of one bit can alter the value of x):

| | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|
| 000 | 001 | 010 | 011 | 100 | 101 | 110 | 111 |
| — | 1 | 2 | 1 | 3 | 1 | 2 | 1 |

Bit string representation

Alternative: reflected binary code or Gray code (after Frank Gray). Can be obtained from standard binary:

$$g_1 = b_1$$

$$g_i = b_i \oplus b_{i-1}, \quad i = 2, \dots, n$$

Gray encoding for $n = 3$

| | | | | | | | | |
|----------|-----|-----|-----|-----|-----|-----|-----|-----|
| b | 000 | 001 | 010 | 011 | 100 | 101 | 110 | 111 |
| g | 000 | 001 | 011 | 010 | 110 | 111 | 101 | 100 |

Two consecutive strings encoded in Gray coding have Hamming distance equal to one.

about Gray encoding

Crossover operators

A crossover operator obtains one offspring from two or more elements of the population. Crossovers for binary strings:

Element 1: 001011101001 Element 2: 110000111000

Uniform crossover with mask (at random): 011000110110, son
01001111001

One-point crossover with cut at $i = 5$: 001010111000

Two-point crossover with cut at $i = 3$ and $i = 10$: 001000111001

Crossover and selection

Usually we give a higher chance to mate to elements with good values of fitness function.

In **proportional selection** probability of mating is proportional to fitness function (in MAX problems)

In **tournament selection** we pick the best-fitting individual from a subset of elements selected at random.

Mutation operators

The offspring obtained from crossover can be mutated with a probability p_m .
Objective: increasing variation and avoid convergence in a local optimum.

In binary encodings consists in negating some elements of the bit string.

Element to mutate: 001010111000

Inorder mutation (e.g., three elements from $i = 3$):

00**101**0111000

00**010**0111000

Random mutation (e.g., three positions):

00**1**010**1**1100**0**

00**0**010**0**110**1**0

Elitism

We want to keep the best result obtained in all previous generations, as it is the output of the algorithm.

Adopting an **elitist strategy** means including this element in the next generation.

Convergence

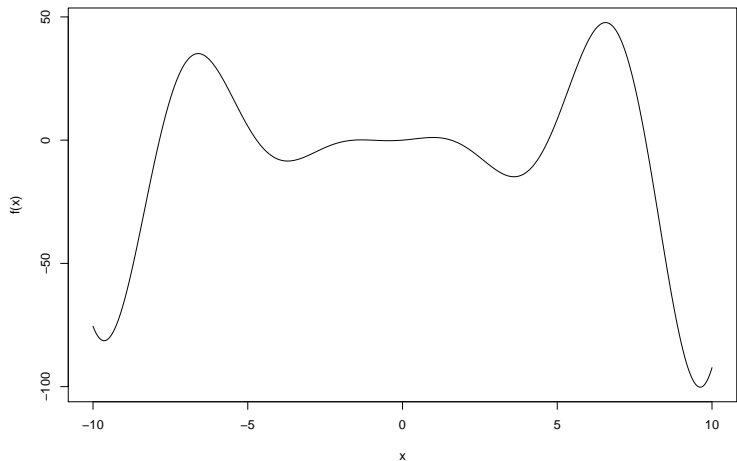
Some criteria for convergence (stopping):

- The algorithm reaches a specified number of generations.
- There is no improvement of the fitness function in a number of iterations.
- There is no variation in the last generation (all elements are equal).

Solving a standard GA

A simple example

We want to obtain the maximum in $-10 \leq x \leq 10$ of $(x^2 - x)\cos(x)$:



Let's use a binary encoding implementation.

The GA R package

We will use the GA package of R, written by Luca Scrucca

Installing R and RStudio on Windows

Installing R and RStudio on mac

Defining the fitness function (binary encoding)

As the genetic algorithm works with binary encoding, we need to provide a fitness function with binary input:

```
bin2real <- function(b, l, u){  
  n <- length(b)  
  s <- 0  
  for(i in 0:(n-1)) s <- s + b[n-i]*2^i  
  s <- l + (u-l)*s/(2^n - 1)  
  return(s)  
}  
  
f.stdbin <- function(b, lbound=-10, ubound=10){  
  x <- bin2real(b, lbound, ubound)  
  return((x^2+x)*cos(x))  
}
```

Applying genetic algorithm (binary encoding)

First time you use this you need to install GA package:

```
install.packages("GA")
```

Perform GA and store results in g01.stdbinary variable:

```
library(GA)
g01.stdbinary <- ga(type = "binary", fitness = f.stdbin,
maxiter=50, lbound=-10, ubound=10, nBits=32, seed=1313)
```


Results (binary encoding)

```
summary(g01.stdbinary)
```

```
## -- Genetic Algorithm -----
```

```
##
```

```
## GA settings:
```

```
## Type = binary
```

```
## Population size = 50
```

```
## Number of generations = 50
```

```
## Elitism = 2
```

```
## Crossover probability = 0.8
```

```
## Mutation probability = 0.1
```

```
##
```

```
## GA results:
```

```
## Iterations = 50
```

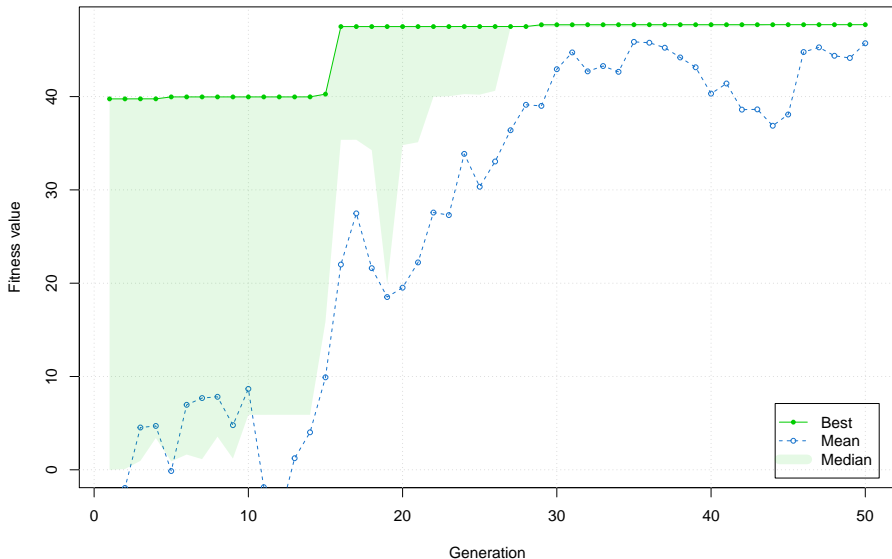
```
## Fitness function value = 47.70562
```

```
## Solution =
```

```
##      x1 x2 x3 x4 x5 x6 x7 x8 x9 x10 ... x31 x32
```

Performance (binary encoding)

```
plot(g01.stdbinary)
```



Define fitness function (Gray encoding)

We need an additional function to convert from Grey to binary:

```
Gray2bin <- function(g){  
  n <- length(g)  
  b <- logical(n)  
  b[1] <- g[1]  
  for(i in 2:n) b[i] <- ifelse(g[i]==0, b[i-1], !b[i-1])  
  return(b)  
}  
  
f.gray <- function(g, lbound=-10, ubound=10){  
  b <- Gray2bin(g)  
  x <- bin2real(b, lbound, ubound)  
  return((x^2+x)*cos(x))  
}
```

Genetic algorithm (Gray encoding)

```
g01.gray <- ga(type = "binary", fitness = f.gray,  
maxiter=50, lbound=-10, ubound=10, nBits=32, seed=1313)
```

Results (Gray encoding)

```
summary(g01.gray)
```

```
## -- Genetic Algorithm -----
```

```
##
```

```
## GA settings:
```

```
## Type = binary
```

```
## Population size = 50
```

```
## Number of generations = 50
```

```
## Elitism = 2
```

```
## Crossover probability = 0.8
```

```
## Mutation probability = 0.1
```

```
##
```

```
## GA results:
```

```
## Iterations = 50
```

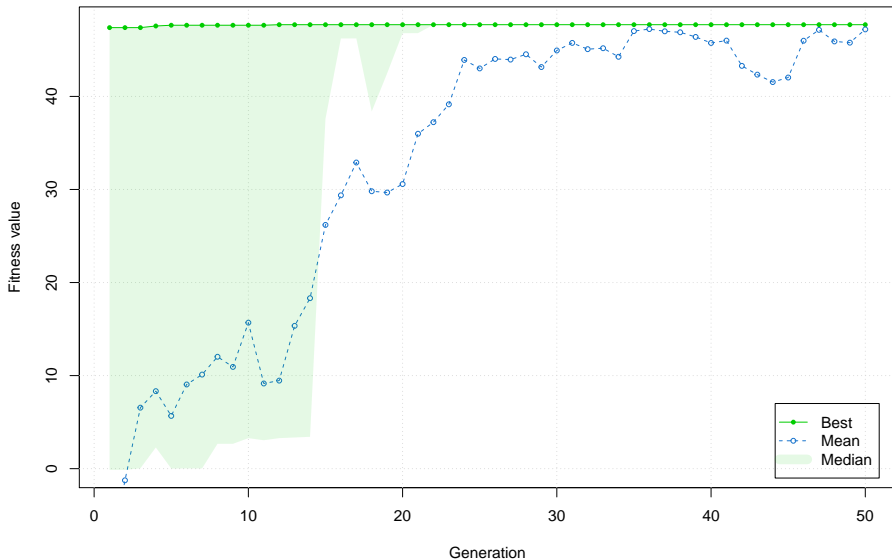
```
## Fitness function value = 47.70562
```

```
## Solution =
```

```
##      x1 x2 x3 x4 x5 x6 x7 x8 x9 x10 ... x31 x32
```

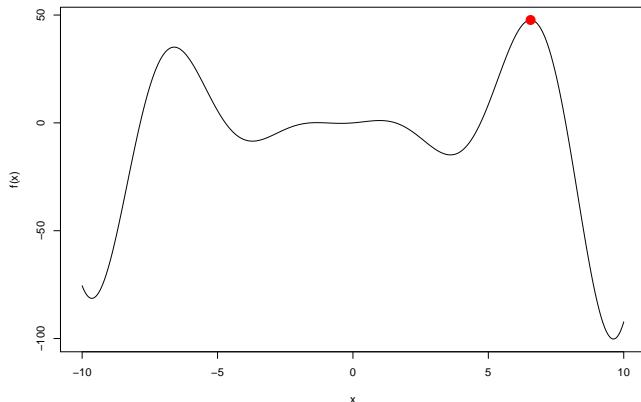
Performance (Gray encoding)

```
plot(g01.gray)
```



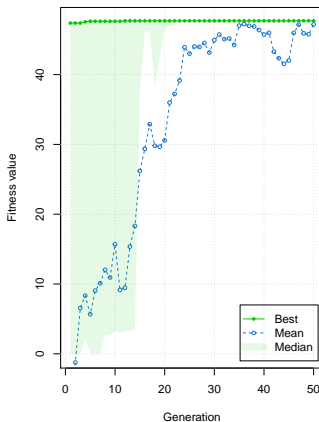
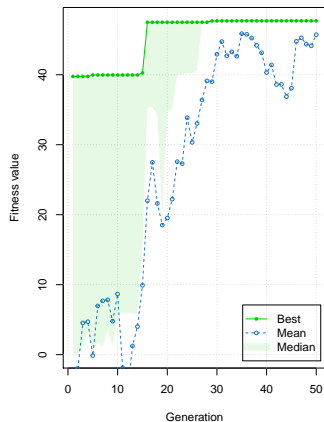
Conclusions of binary vs Gray comparison

Both algorithms reach optimum. . .



Conclusions of binary vs Gray comparison

... but Gray (right) is faster than standard binary (left)



Real-valued encoding

Real-valued encoding

For problems having decision variables $\mathbf{x} \in \mathcal{R}^n$, the most natural encoding is the floating-point or real-valued encoding.

In this encoding, the genotype is simply the phenotype (that is, the vector itself).

Crossover operators

The most used crossover operators are:

- Vector-level:
 - ▶ Whole arithmetic crossover
- Variable-level:
 - ▶ Local arithmetic crossover
 - ▶ Blend crossover
 - ▶ Uniform crossover

Crossover operators

Whole arithmetic crossover: from two parents \mathbf{x}^1 and \mathbf{x}^2 we can obtain two offspring:

$$\alpha \mathbf{x}^1 + (1 - \alpha) \mathbf{x}^2$$

$$(1 - \alpha) \mathbf{x}^1 + \alpha \mathbf{x}^2$$

with $\alpha \in [0, 1]$

Local arithmetic crossover: we perform a similar crossover at the variable level.

$$\alpha x_i^1 + (1 - \alpha) x_i^2$$

$$(1 - \alpha) x_i^1 + \alpha x_i^2$$

again with $\alpha \in [0, 1]$

Crossover operators

Blend crossover: we construct the offspring selecting each variable randomly from the interval:

$$[x_i^1 - \alpha(x_i^2 - x_i^1), x_i^1 + \alpha(x_i^2 - x_i^1)]$$

with $x_i^2 > x_i^1$.

Usually $\alpha = 0.5$ yields good results. If necessary, variables of offspring should be adjusted to upper or lower bounds.

If $\alpha = 0$ we have **uniform crossover**.

Mutation operators

The most usual mutation operator is to pick a value within a given radius of the population member.

It is frequent to reduce the radius as generations go (nonuniform mutation), similarly to genetic algorithm.

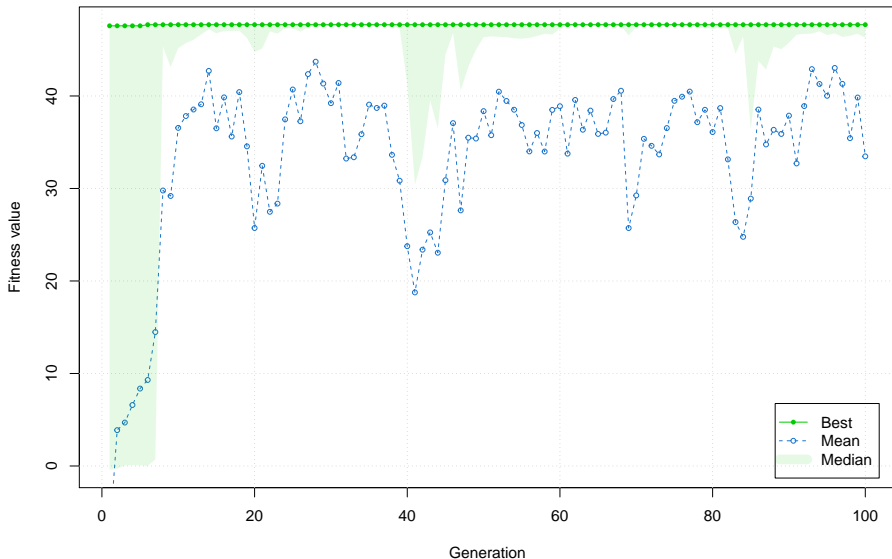
Genetic algorithm (real-valued encoding)

```
f <- function(x) (x^2+x)*cos(x)
lbound <- -10; ubound <- 10
g01.real <- ga(type = "real-valued", fitness = f, lower = lbound, upper = ubound)
```

This implementation also finds the optimum.

Performance (real-valued encoding)

```
plot(g01.real)
```



The Rastrigin function

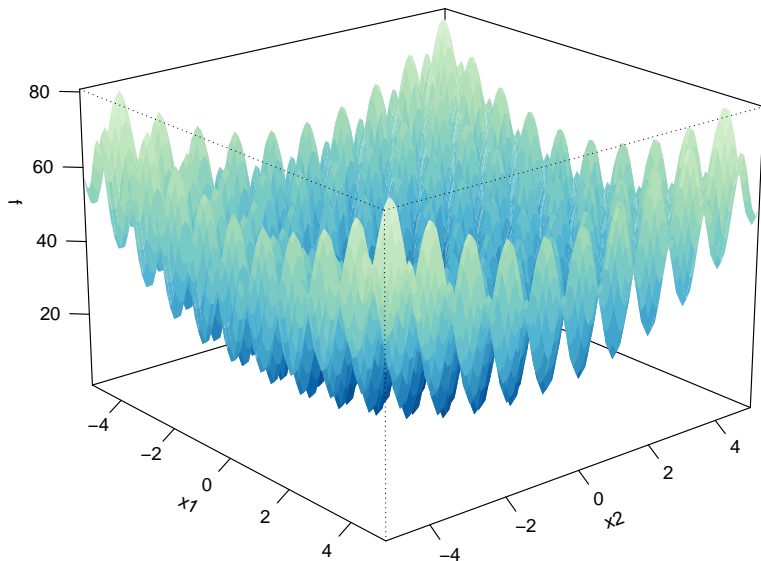
The Rastrigin function is a performance test for optimization algorithms, as it has a large search space and many local minima. For two variables:

$$f = 20 + x_1^2 + x_2^2 - 10(\cos 2\pi x_1 + \cos 2\pi x_2)$$

with $x_i \in [-5.12, 5.12]$

Note that this is a minimization problem, so we must use $-f$ as fitness function.

The Rastrigin function



Solving the Rastrigin problem

```
ga.rastrigin <- ga(type = "real-valued",  
  fitness = function(x) -Rastrigin(x[1], x[2]),  
  lower = c(-5.12, -5.12), upper = c(5.12, 5.12),  
  popSize = 50, maxiter = 1000, run = 100, seed=1313)
```

Set two convergence criteria: maximum number of generations (1000) and maximum number of runs without improvement (100).

The GA finds the optimum (0,0).

Performance (Rastrigin problem)

