# Genetic Algorithms

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- Introducing genetic algorithms
- 2 The standard genetic algorithm
- Solving a standard GA
- Real-valued encoding
- 5 Using MATLAB for genetic algorithms
- 6 Constrained optimisation
- Influence of parameters on performance
- 8 Genetic algorithm extensions

Jose M Sallan Genetic Algorithms 7/3/2019

2/70

Introducing genetic algorithms

## Genetic algorithms

#### Genetic algorithms are inspired by **evolution**:

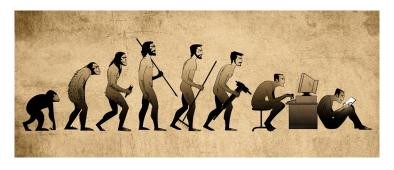


Figure 1: Evolution

#### **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 optimisation problems?

## Genetic algorithms and evolution

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

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

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

## The genetic algorithm flow

- 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.

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

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

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

Jose M Sallan Genetic Algorithms 7/3/2019 11 / 70

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.

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):

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

$$g_1 = b_1$$
  

$$g_n = b_n \oplus b_{n-1}, i = 2, \dots, n$$

Gray encoding for n = 3

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 010011111001

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

000100111000

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

001010111000

000010011010

#### **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.

Jose M Sallan Genetic Algorithms 7/3/2019 18 / 70

### Convergence

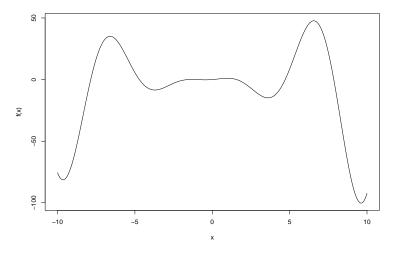
Some criteria for convergence (stopping):

- 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  $-10 \le x \le 10$  of  $(x^2 + x)\cos(x)$ :



Let's use a binary encoding implementation.

Jose M Sallan Genetic Algorithms 7/3/2019 21/70

## 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 < -1 + (u-1)*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)</pre>
```

# Results (binary encodign)

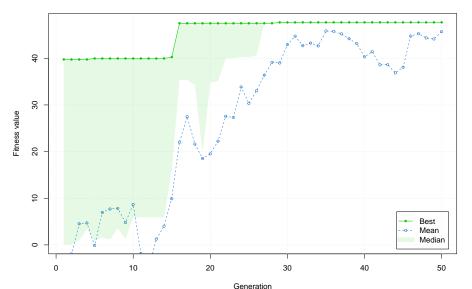
```
summary(g01.stdbinary)
```

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

 Jose M Sallan
 Genetic Algorithms
 7/3/2019
 25 / 70

# Performance (binary encoding)

plot(g01.stdbinary)



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# Define fitness function (Gray encoding)

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

```
Gray2bin <- function(g){</pre>
  n <- length(g)
  b <- logical(n)
  b[1] \leftarrow g[1]
  for(i in 2:n) b[i] \leftarrow 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)</pre>
```

 Jose M Sallan
 Genetic Algorithms
 7/3/2019
 28 / 70

# Results (Gray encoding)

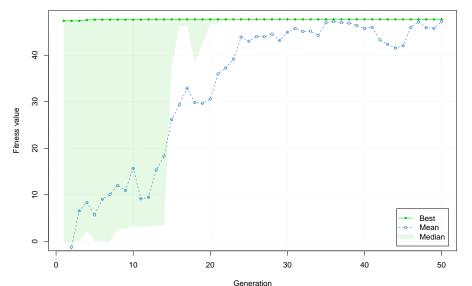
#### summary(g01.gray)

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

Jose M Sallan 7/3/2019 29 / 70

# Performance (Gray encoding)

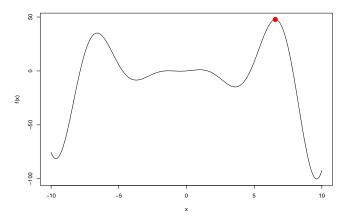
plot(g01.gray)



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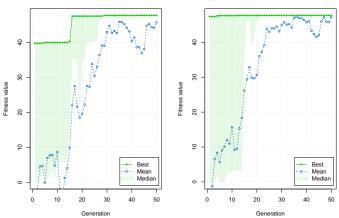
## Conclusions of binary vs Gray comparison

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:

$$[x_i^1 - \alpha(x_i^2 - x_i^1), x_2^1 + \alpha(x_i^2 - x_i^1)]$$
  
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.

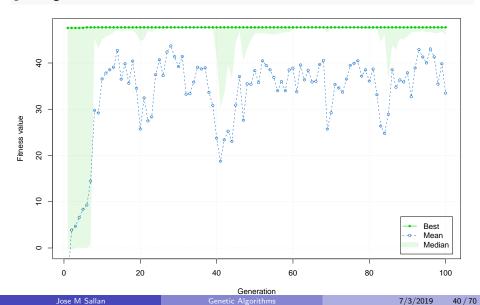
## Genetic algorithm (real-valued encoding)

```
f <- function(x) (x^2+x)*cos(x)
lbound <- -10; ubound <- 10
g01.real <- ga(type = "real-valued", fitness = f,
lower = lbound, upper = ubound, seed=1313)</pre>
```

This implementation also finds the optimum.

# Performance (real-valued encoding)

plot(g01.real)



### The Rastrigin function

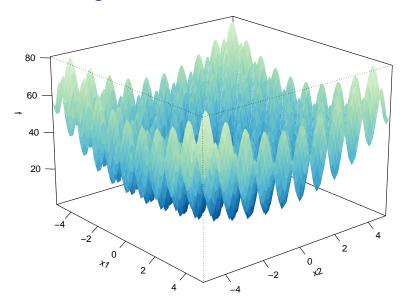
The **Rastrigin function** is a performance test for optimisation algorithms, as it has a large search space and many local minima. For two variables:

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

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

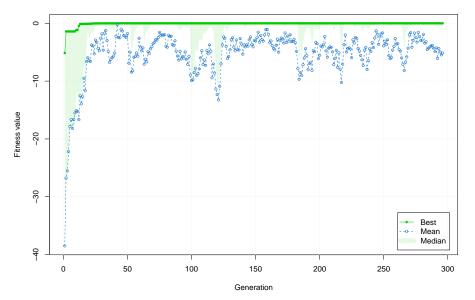


### Solving the Rastrigin problem

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)



## Using MATLAB for genetic algorithms

You can use MATLAB to solve optimisation (minimisation) problems with genetic algorithm using the **ga** solver.

To use the **ga** solver, you need to install the **Global optimisation Toolbox**, an extension of the Optimisation Toolbox.

The generic structure of the **ga** function in MATLAB is:

```
x = ga(fun,nvars,A,b,Aeq,beq,lb,ub,nonlcon,options)
```

#### with:

- fun: function to minimize (required).
- nvars: number of variables (required).
- **A, b:** linear inequalities  $Ax \leq b$ .
- Aeq, beq: linear equalities Ax = b.
- **Ib**, **ub**: low and upper bounds.
- **nonlcon:** function returning nonlinear constraints, being  $c(x) \le 0$  or ceq(x) = 0.
- options: a set of options for the ga created with optimoptions.

The output of the **ga** can be of the form:

```
[x,fval,exitflag,output,population,scores] = ga(...)
```

#### with:

- x: value of the solution.
- **fval**: value of the function to optimize.
- exitflag: identifier of the reason the algorithm stopped.
- output: information about algorithm performance.
- **population, scores:** matrix with the final population and scores vecctor of that final population.

To create the **options** variable we use the **optimoptions** function:

To change population size:

```
options = optimoptions('ga', 'PopulationSize', 100)
```

To get an interactive plot of algorithm evolution:

```
options = optimoptions('ga', 'PlotFcn', 'gaplotbestf')
```

You can find reference of genetic algorithms in MATLAB in the following links:

ga function

options

#### Minimising the Rastrigin function with MATLAB

In MATLAB we can access the Rastrigin function with **@rastriginsfcn** 

**Exercise:** find the (unrestricted) minimum of the Rastrigin function with genetic algorithm in MATLAB with the following parameters:

- Maximum number of generations: 1000.
- Maximum number of runs without improvement (stalls): 300.
- Plot the evolution of best value and mean value of generation gaplotbestf.

## Solving a maximisation problem

Reconsider the problem of maximising  $(x^2 + x)\cos(x)$  in the interval  $-10 \le x \le 10$ .

Write a script with the fitness function and other script with the specification of the **ga** function, which plots algorithm evolution.

Jose M Sallan Genetic Algorithms 7/3/2019 52 / 70

We want to minimise the function:

$$f = 100(x_1^2 - x_2)^2 + (1 - x_1)^2$$

subject to the following constraints and bounds:

$$x_1x_2 + x_1 - x_2 + 1.5 \le 0$$

$$10-x_1x_2\leq 0$$

$$0 \le x_1 \le 1$$

$$0 \le x_2 \le 13$$

Crossover and mutation operators may generate population members that do not satisfy constraints (although in general they discard solutions out of variable bounds).

The way to discard these solutions is to generate a **fitness function with penalties**: solutions that do not satisfy constraints have bad values of fitness function.

Note that fitness function != objective function.

The fitness function to our problem will be (both constraints are  $\leq$  inequalities) minimising:

$$F = f + Mf_1 + Mf_2$$

Where:

$$f_1 = MAX(x_1x_2 + x_1 - x_2 + 1.5, 0)$$

$$f_2 = MAX(10 - x_1x_2, 0)$$

#### Solving constrained optimisation with MATLAB

We need to create two scripts with files representing objective function and constraints:

```
function y = cam_function (x)

y = 100*(x(1)^2 - x(2))^2 + (1 - x(1))^2;
```

```
function [c, ceq]=cam_constraints (x)
c(1) = x(1)*x(2) + x(1) - x(2) + 1.5;
c(2) = 10 - x(1)*x(2);
ceq = [];
end
```

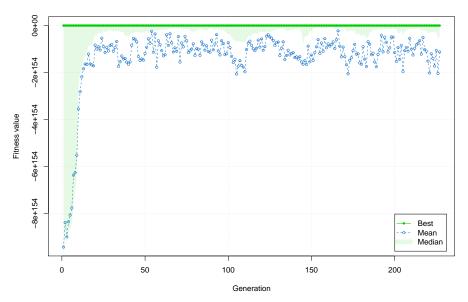
### Solving constrained optimisation with MATLAB

Then we solve the problem doing:

```
lb = [0; 0];
ub = [1; 13];
nonlcon = @cam_constraints;
fun = @cam_function;
options = optimoptions('ga',
   'ConstraintTolerance', 1e-6, 'PlotFcn', 'gaplotbestf')
[x, fval, exitflag, output] =
ga(fun, 2, [],[],[],[], lb, ub, nonlcon, options)
```

You will find the scripts in the cam folder in the examples folder.

## Performance of the R implementation



Influence of parameters on performance

#### Influece of parameters on performance

If the default settings do not work well, we can try to improve performance modifying genetic algorithm parameters:

- Fitness function
- Population parameters: starting population, size
- Mutation and probability of performing mutation

#### Fitness function

The most important element for a genetic algorithm.

Most of the computational cost is computing the fitness function to each element of the population.

Fitness function quantifies the quality of a population member (how close is to optimum):

- penalties for constraints.
- adapt to maximisation / minimisation.

#### Population

The population helps to exploration of candidate solutions:

- Small population: small search space, low time complexity, may need more generations to converge.
- Large population: widens search space, high time complexity, may need less generations to converge.

Seeding of initial population: including good solutions (e.g., obtained by local search).

#### Mutation

Mutation operator increases exploration: if we only perform crossover the genetic algorithm converges fast.

We can test variations on the probability of applying mutation  $p_{mut}$ :

- Raise  $p_{mut}$  in small population sizes.
- Define a  $p_{mut}$  for each population member: individuals with bad fitness function should have higher probability of mutation.
- Reduce  $p_{mut}$  as number of generations increases. This is how the standard MATLAB mutation function **@mutationgaussian** works.

Evaluation of operators can be performed with **experimental design**: see vignette **KPwithGApackage**. Some of this implementations are not supported by stanadard R or MATLAB functions.

#### Practice: Schwebel function

Consider the **Schwebel function**, defined in:

 $\{ https://www.sfu.ca/\sim ssurjano/schwef.html \}$ 

Perform a genetic algorithm implementation with the standard options, and try to improve the result setting new values to parameters and operators.

Genetic algorithm extensions

## Hybrid genetic algorithms

Consist of combining a genetic algorithm with a local search optimization algorithm-

Receives several names in literature:

- Hybrid genetic algorithms
- Memetic algorithms
- Genetic local search
- Cultural algorithms

## Hybrid genetic algorithms implementation

The local search to use may depend on the function to optimize:

- Quasi Newton: **@fminunc** function in MATLAB.
- Simulated annealing.
- Tabu search.

SA and TS are available for binary encoding and permutative representations (e.g., flowshop or tabu search problems).

## Hybrid genetic algorithms implementation

There are several ways of combining genetic algorithm and local search:

- The MATLAB way: the local search function runs after the genetic algorithm termination.
- Performing a local search optimization to all the population every fixed number of generations.
- Performing local search with a probability that can depend on fitness (optimize the best individuals).

Some implementations can be too time consuming.

### Hybrid genetic algorithms in MATLAB

Let's consider the Rastrigin function with 30 variables.

Compare results with and without hybrid GA: scripts **rastrigin30.m** and **rastrigin30\_hybrid.m**