Package ‘GA’

August 29, 2016

Version 3.0.2
Date 2016-06-07
Title Genetic Algorithms

Description An R package for optimisation using genetic algorithms. The package provides a flexible general-purpose set of tools for implementing genetic algorithms search in both the continuous and discrete case, whether constrained or not. Users can easily define their own objective function depending on the problem at hand. Several genetic operators are available and can be combined to explore the best settings for the current task. Furthermore, users can define new genetic operators and easily evaluate their performances. Local search using general-purpose optimisation algorithms can be applied stochastically to exploit interesting regions. GAs can be run sequentially or in parallel, using an explicit master-slave parallelisation or a coarse-grain islands approach.

Depends R (>= 3.0), methods, foreach, iterators
Imports stats, graphics, grDevices, utils
Suggests parallel, doParallel, doRNG (>= 1.6), knitr (>= 1.8)
License GPL (>= 2)
ByteCompile true
LazyLoad yes
VignetteBuilder knitr

URL https://github.com/luca-scr/GA
Repository CRAN

R topics documented:

<table>
<thead>
<tr>
<th>GA-package</th>
<th>binary2decimal</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>3</td>
</tr>
</tbody>
</table>
GA-package

Description

An R package for optimization using genetic algorithms. The package provides a flexible general-purpose set of tools for implementing genetic algorithms search in both the continuous and discrete case, whether constrained or not. Users can easily define their own objective function depending on the problem at hand. Several genetic operators are available and can be combined to explore the best settings for the current task. Furthermore, users can define new genetic operators and easily evaluate their performances. Local search using general-purpose optimisation algorithms can be applied stochastically to exploit interesting regions. GAs can be run sequentially or in parallel, using an explicit master-slave parallelisation or a coarse-grain islands approach.

Details

For a quick intro to GA package see the vignette accompanying the package. Further details are provided in the papers referenced below.
References


Author(s)

Luca Scrucca <luca.scrucca@unipg.it>

---

**binary2decimal**

*Binary encoding of decimal numbers and viceversa.*

**Description**

Functions for computing binary to decimal conversion of numbers and vice versa.

**Usage**

```r
decimal2binary(x, length)
binary2decimal(x)
```

**Arguments**

- `x` input value.
- `length` an optional value giving the length of binary string to return.

**Details**

- `decimal2binary` converts a numerical value (which is forced to be an integer) to a binary representation, i.e. a vector of 0s and 1s. For real numerical values see the example below.
- `binary2binary` converts a binary value, i.e. a vector of 0s and 1s, to a decimal representation.

**Author(s)**

Luca Scrucca

**See Also**

`binary2gray`
Examples

# for integer values
dval <- 12
(bval <- decimal2binary(dval))
binary2decimal(bval)

# for real values
dval <- 12.456
# use
(bval <- decimal2binary(dval*1000))
binary2decimal(bval)/1000

---

binary2gray  Gray encoding for binary strings

Description

Functions for computing Gray encoding from/to binary strings.

Usage

binary2gray(x)
gray2binary(x)

Arguments

x          the string to be evaluated

Details

Gray encoding allows to obtain binary strings not affected by the well-known Hamming cliff problem. With Gray encoding the number of bit differences between any two consecutive values is one, whereas in binary strings this is not always true.

Author(s)

Luca Scrucca

See Also

binary2decimal
Examples

# Consider a five-bit encoding of values 15 and 16 using the standard binary coding
decimal2binary(15, 5)
decimal2binary(16, 5)
# Moving from 15 to 16 (or vice versa) all five bits need to be changed, but using Gray encoding the two binary strings differ by one bit.
binary2gray(decimal2binary(15, 5))
binary2gray(decimal2binary(16, 5))

---

**Genetic Algorithms**

**Description**

Maximization of a fitness function using genetic algorithms (GAs). Local search using general-purpose optimisation algorithms can be applied stochastically to exploit interesting regions. The algorithm can be run sequentially or in parallel using an explicit master-slave parallelisation.

**Usage**

```r
 ga(type = c("binary", "real-valued", "permutation"),
    fitness, ...,
    min, max, nBits,
    population = gaControl(type)$population,
    selection = gaControl(type)$selection,
    crossover = gaControl(type)$crossover,
    mutation = gaControl(type)$mutation,
    popSize = 50,
    pcrossover = 0.8,
    pmutation = 0.1,
    elitism = base::max(1, round(popSize*0.05)),
    updatePop = FALSE,
    postFitness = NULL,
    maxiter = 100,
    run = maxiter,
    maxFitness = Inf,
    names = NULL,
    suggestions = NULL,
    optim = FALSE,
    optimArgs = list(method = "L-BFGS-B",
                     poptim = 0.05,
                     pressel = 0.5,
                     control = list(fnscale = -1, maxit = 100)),
    keepBest = FALSE,
    parallel = FALSE,
    monitor = if(interactive())
```
{ if(is.RStudio()) gaMonitor else gaMonitor2 }
else FALSE,
seed = NULL)

Arguments

type the type of genetic algorithm to be run depending on the nature of decision variables. Possible values are:

"binary" for binary representations of decision variables.
"real-valued" for optimization problems where the decision variables are floating-point representations of real numbers.
"permutation" for problems that involves reordering of a list.

fitness the fitness function, any allowable R function which takes as input an individual string representing a potential solution, and returns a numerical value describing its “fitness”.

... additional arguments to be passed to the fitness function. This allows to write fitness functions that keep some variables fixed during the search.

min a vector of length equal to the decision variables providing the minimum of the search space in case of real-valued or permutation encoded optimizations.

max a vector of length equal to the decision variables providing the maximum of the search space in case of real-valued or permutation encoded optimizations.

nBits a value specifying the number of bits to be used in binary encoded optimizations.

population an R function for randomly generating an initial population. See ga.Population for available functions.

selection an R function performing selection, i.e. a function which generates a new population of individuals from the current population probabilistically according to individual fitness. See ga.Selection for available functions.

crossover an R function performing crossover, i.e. a function which forms offsprings by combining part of the genetic information from their parents. See ga.Crossover for available functions.

mutation an R function performing mutation, i.e. a function which randomly alters the values of some genes in a parent chromosome. See ga.Mutation for available functions.

popSize the population size.

updatePop a logical defaulting to FALSE. If set at TRUE the first attribute attached to the value returned by the user-defined fitness function is used to update the population. Be careful though, this is an experimental feature!

postFitness a user-defined function which, if provided, receives the current ga-class object as input, performs post fitness-evaluation steps, then returns an updated version of the object which is used to update the GA search. Be careful though, this is an experimental feature!

pcrossover the probability of crossover between pairs of chromosomes. Typically this is a large value and by default is set to 0.8.
pmutation

the probability of mutation in a parent chromosome. Usually mutation occurs with a small probability, and by default is set to 0.1.

elitism

the number of best fitness individuals to survive at each generation. By default the top 5% individuals will survive at each iteration.

maxiter

the maximum number of iterations to run before the GA search is halted.

run

the number of consecutive generations without any improvement in the best fitness value before the GA is stopped.

maxFitness

the upper bound on the fitness function after that the GA search is interrupted.

names

a vector of character strings providing the names of decision variables.

suggestions

a matrix of solutions strings to be included in the initial population. If provided the number of columns must match the number of decision variables.

optim

a logical defaulting to FALSE determining whether or not a local search using general-purpose optimisation algorithms should be used. See argument optimArgs for further details and finer control.

optimArgs

a list controlling the local search algorithm with the following components:

method a string specifying the general-purpose optimisation method to be used, by default is set to "L-BFGS-B". Other possible methods are those reported in optim.

poptim a value in the range [0,1] specifying the probability of performing a local search at each iteration of GA (default 0.1).

pressel a value in the range [0,1] specifying the pressure selection (default 0.5). The local search is started from a random solution selected with probability proportional to fitness. High values of pressel tend to select the solutions with the largest fitness, whereas low values of pressel assign quasi-uniform probabilities to any solution.

control a list of control parameters. See 'Details' section in optim.

keepBest a logical argument specifying if best solutions at each iteration should be saved in a slot called bestSol. See ga-class.

parallel a logical argument specifying if parallel computing should be used (TRUE) or not (FALSE, default) for evaluating the fitness function. This argument could also be used to specify the number of cores to employ; by default, this is taken from detectCores. Finally, the functionality of parallelization depends on system OS: on Windows only 'snow' type functionality is available, while on Unix/Linux/Mac OSX both 'snow' and 'multicore' (default) functionalities are available.

monitor a logical or an R function which takes as input the current state of the ga-class object and show the evolution of the search. By default, for interactive sessions, the function gaMonitor or gaMonitor2, depending on whether or not is an RStudio session, prints the average and best fitness values at each iteration. If set to plot these information are plotted on a graphical device. Other functions can be written by the user and supplied as argument. In non interactive sessions, by default monitor = FALSE so any output is suppressed.

seed an integer value containing the random number generator state. This argument can be used to replicate the results of a GA search. Note that if parallel computing is required, the doRNG package must be installed.
Details

Genetic algorithms (GAs) are stochastic search algorithms inspired by the basic principles of biological evolution and natural selection. GAs simulate the evolution of living organisms, where the fittest individuals dominate over the weaker ones, by mimicking the biological mechanisms of evolution, such as selection, crossover and mutation.

The GA package is a collection of general purpose functions that provide a flexible set of tools for applying a wide range of genetic algorithm methods.

The ga function enables the application of GAs to problems where the decision variables are encoded as "binary", "real-valued", or "permutation" strings.

Default genetic operators are set via gaControl. To retrieve the currently set operators:

\[
\begin{align*}
\text{gaControl}(\text{"binary"}) \\
\text{gaControl}(\text{"real-valued"}) \\
\text{gaControl}(\text{"permutation"})
\end{align*}
\]

Value

Returns an object of class ga-class. See ga-class for a description of available slots information.

Author(s)

Luca Scrucca <luca.scrucca@unipg.it>

References


See Also

summaryLgaMmethod, plotLgaMmethod, ga-class, ga_Population, ga_Selection, ga_Crossover, ga_Mutation, gaControl.

Examples

# 1) one-dimensional function
f <- function(x) abs(x)+cos(x)
curve(f, -20, 20)
fitness <- function(x) -f(x)
GA <- ga(type = "real-valued", fitness = fitness, min = -20, max = 20)
summary(GA)
plot(GA)
curve(f, -20, 20)
abline(v = GA@solution, lty = 3)

# 2) one-dimensional function
f <- function(x) (x^2+x)*cos(x) # -10 < x < 10
curve(f, -10, 10)

# write your own tracing function
monitor <- function(obj)
{
  curve(f, -10, 10, main = paste("iteration =", obj@iter))
  points(obj@population, obj@fitness, pch = 20, col = 2)
  rug(obj@population, col = 2)
  Sys.sleep(0.2)
}
## Not run:
GA <- ga(type = "real-valued", fitness = f, min = -10, max = 10, monitor = monitor)

## End(Not run)
# or if you want to suppress the tracing
GA <- ga(type = "real-valued", fitness = f, min = -10, max = 10, monitor = NULL)
summary(GA)

monitor(GA)
abline(v = GA@solution, lty = 3)

# 3) two-dimensional Rastrigin function
Rastrigin <- function(x1, x2)
{

20 + x1\^2 + x2\^2 - 10*(\cos(2*\pi*x1) + \cos(2*\pi*x2))
}
x1 <- x2 <- seq(-5.12, 5.12, by = 0.1)
f <- outer(x1, x2, Rastrigin)
persp3D(x1, x2, f, theta = 50, phi = 20)
filled.contour(x1, x2, f, color.palette = jet.colors)

GA <- ga(type = "real-valued", fitness = function(x) -Rastrigin(x[1], x[2]),
          min = c(-5.12, -5.12), max = c(5.12, 5.12),
          popSize = 50, maxiter = 100)
summary(GA)
plot(GA)

# 4) Parallel GA
# Simple example of an expensive fitness function obtained artificially by
# introducing a pause statement.
## Not run:
Rastrigin <- function(x1, x2)
{
  Sys.sleep(0.1)
  20 + x1^2 + x2^2 - 10*(\cos(2*\pi*x1) + \cos(2*\pi*x2))
}

system.time(GA1 <- ga(type = "real-valued",
                       fitness = function(x) -Rastrigin(x[1], x[2]),
                       min = c(-5.12, -5.12), max = c(5.12, 5.12),
                       popSize = 50, maxiter = 100, monitor = FALSE,
                       seed = 12345))

system.time(GA2 <- ga(type = "real-valued",
                       fitness = function(x) -Rastrigin(x[1], x[2]),
                       min = c(-5.12, -5.12), max = c(5.12, 5.12),
                       popSize = 50, maxiter = 100, monitor = FALSE,
                       seed = 12345, parallel = TRUE))

## End(Not run)

# 5) Hybrid GA
# Example of GA with local search

Rastrigin <- function(x1, x2)
{
  20 + x1^2 + x2^2 - 10*(\cos(2*\pi*x1) + \cos(2*\pi*x2))
}

GA <- ga(type = "real-valued",
          fitness = function(x) -Rastrigin(x[1], x[2]),
          min = c(-5.12, -5.12), max = c(5.12, 5.12),
          popSize = 50, maxiter = 100,
          optim = TRUE)
summary(GA)
Description

An S4 class for genetic algorithms

Objects from the Class

Objects can be created by calls to the `ga` function.

Slots

call an object of class "call" representing the matched call;
type a character string specifying the type of genetic algorithm used;
min a vector providing for each decision variable the minimum of the search space in case of real-valued or permutation encoded optimizations;
max a vector providing for each decision variable the maximum of the search space in case of real-valued or permutation encoded optimizations;
nBits a value specifying the number of bits to be used in binary encoded optimizations;
names a vector of character strings providing the names of decision variables (optional);
popSize the population size;
iter the actual (or final) iteration of GA search;
runt the number of consecutive generations without any improvement in the best fitness value before the GA is stopped;
maxiter the maximum number of iterations to run before the GA search is halted;
suggestions a matrix of user provided solutions and included in the initial population;
population the current (or final) population;
elitism the number of best fitness individuals to survive at each generation;
crossover the crossover probability;
mutation the mutation probability;
fitness the values of fitness function for the current (or final) population;
summary a matrix of summary statistics for fitness values at each iteration (along the rows);
bestSol if keepBest = TRUE, the best solutions at each iteration;
fitnessValue the best fitness value at the final iteration;
solution the value(s) of the decision variables giving the best fitness at the final iteration.

Author(s)

Luca Scrucca

See Also

For examples of usage see `ga`. 
Description

Default settings for genetic operators used in the GA package.

Usage

gaControl(...)

Arguments

... no arguments, a single character vector, or a named list with components.

Details

If the function is called with no arguments returns the current default settings, i.e., a list with the following default components:

- "binary"
  - population = "gabin_Population"
  - selection = "gabin_lrSelection"
  - crossover = "gabin_spCrossover"
  - mutation = "gabin_raMutation"
- "real-valued"
  - population = "gareal_Population"
  - selection = "gareal_lsSelection"
  - crossover = "gareal_laCrossover"
  - mutation = "gareal_raMutation"
- "permutation"
  - population = "gaperm_Population"
  - selection = "gaperm_lrSelection"
  - crossover = "gaperm_oxCrossover"
  - mutation = "gaperm_simMutation"
- "eps" = the tolerance value used by the package functions. By default set at sqrt(.Machine$double eps).

The function may be called with a single string specifying the name of the component. In this case the function returns the current default settings.

To change the default values, a named component must be followed by a single value (in case of "eps") or a list of component(s) specifying the name of the function for a genetic operator. See the Examples section.
Value

If the argument list is empty the function returns the current list of values. If the argument list is not empty, the returned list is invisible.

Note

The parameter values set via a call to this function will remain in effect for the rest of the session, affecting the subsequent behaviour of the functions for which the given parameters are relevant.

Author(s)

Luca Scrucca

See Also

ga

Examples

# get and save defaults
defaultControl <- gaControl()
print(defaultControl)
# get current defaults only for binary search
gaControl("binary")
# set defaults for selection operator of binary search
.gaControl("binary" = list(selection = "gabin_tourSelection"))
# set defaults for selection and crossover operators of binary search
.gaControl("binary" = list(selection = "ga_rwSelection",
.crossover = "gabin_uCrossover"))
gaControl("binary")
# restore defaults
gaControl(defaultControl)
gaControl()
Usage

gaisl(type = c("binary", "real-valued", "permutation"),
    fitness, ..., 
    min, max, nBits,
    population = gaControl(type)$population,
    selection = gaControl(type)$selection,
    crossover = gaControl(type)$crossover,
    mutation = gaControl(type)$mutation,
    popSize = 100,
    numIslands = 4,
    migrationRate = 0.1,
    migrationInterval = 10,
    pcrossover = 0.8,
    pmutation = 0.1,
    elitism = base::max(1, round(popSize/numIslands*0.05)),
    updatePop = FALSE,
    postFitness = NULL,
    maxiter = 1000,
    run = maxiter,
    maxFitness = Inf,
    names = NULL,
    suggestions = NULL,
    optim = FALSE,
    optimArgs = list(method = "L-BFGS-B",
                     poptim = 0.05,
                     pressel = 0.5,
                     control = list(fnscale = -1, maxit = 100)),
    parallel = TRUE,
    monitor = if(interactive())
            { if(is.RStudio()) gaislMonitor else gaislMonitor2 }
            else FALSE,
    seed = NULL)

Arguments

type the type of genetic algorithm to be run depending on the nature of decision
variables. Possible values are:

"binary" for binary representations of decision variables.
"real-valued" for optimization problems where the decision variables are floating-point representations of real numbers.
"permutation" for problems that involves reordering of a list.

fitness the fitness function, any allowable R function which takes as input an individual
string representing a potential solution, and returns a numerical value describing its “fitness”.

... additional arguments to be passed to the fitness function. This allows to write
fitness functions that keep some variables fixed during the search.

min a vector of length equal to the decision variables providing the minimum of the
search space in case of real-valued or permutation encoded optimizations.

max  a vector of length equal to the decision variables providing the maximum of the search space in case of real-valued or permutation encoded optimizations.

nBits  a value specifying the number of bits to be used in binary encoded optimizations.

population  an R function for randomly generating an initial population. See `ga_Population` for available functions.

numIslands  an integer value specifying the number of islands to be used in a ring topology, in which each island is connected unidirectionally with another island, hence forming a single continuous pathway.

migrationRate  a value in the range $[0,1]$ providing the proportion of individuals that should migrate between the islands.

migrationInterval  an integer value specifying the number of iterations at which exchange of individuals takes place.

selection  an R function performing selection, i.e. a function which generates a new population of individuals from the current population probabilistically according to individual fitness. See `ga_Selection` for available functions.

crossover  an R function performing crossover, i.e. a function which forms offsprings by combining part of the genetic information from their parents. See `ga_Crossover` for available functions.

mutation  an R function performing mutation, i.e. a function which randomly alters the values of some genes in a parent chromosome. See `ga_Mutation` for available functions.

popSize  the population size.

updatePop  a logical defaulting to FALSE. If set at TRUE the first attribute attached to the value returned by the user-defined fitness function is used to update the population. Be careful though, this is an experimental feature!

postFitness  a user-defined function which, if provided, receives the current `gaMclass` object as input, performs post fitness-evaluation steps, then returns an updated version of the object which is used to update the GA search. Be careful though, this is an experimental feature!

crossover  the probability of crossover between pairs of chromosomes. Typically this is a large value and by default is set to 0.8.

pmutation  the probability of mutation in a parent chromosome. Usually mutation occurs with a small probability, and by default is set to 0.1.

elitism  the number of best fitness individuals to survive at each generation. By default the top 5% individuals in each island will survive at each iteration.

maxiter  the maximum number of iterations to run before the GA search is halted.

run  the number of consecutive generations without any improvement in the best fitness value before the GA is stopped.

maxFitness  the upper bound on the fitness function after that the GA search is interrupted.

names  a vector of character strings providing the names of decision variables.
suggestions a matrix of solutions strings to be included in the initial population. If provided
the number of columns must match the number of decision variables.

optim a logical defaulting to FALSE determining whether or not a local search using
general-purpose optimisation algorithms should be used. See argument
optimArgs for further details and finer control.

optimArgs a list controlling the local search algorithm with the following components:

method a string specifying the general-purpose optimisation method to be used,
by default is set to "L-BFGS-B". Other possible methods are those reported
in optim.

poptim a value in the range [0,1] specifying the probability of performing a
local search at each iteration of GA (default 0.1).

pressel a value in the range [0,1] specifying the pressure selection (default
0.5). The local search is started from a random solution selected with prob-
ability proportional to fitness. High values of pressel tend to select the
solutions with the largest fitness, whereas low values of pressel assign
quasi-uniform probabilities to any solution.

control a list of control parameters. See 'Details' section in optim.

parallel a logical argument specifying if GAs evolution should be performed in paral-
lel (TRUE, default) or sequentially (FALSE). This argument could also be used to
specify the number of cores to employ; by default, this is taken from detectCores.
Note that it is possible to specify a number of islands larger than the number of
available cores. In such a case, the parallel algorithm will be run using blocks of
islands, with the block size depending on the maximal number of cores available
or the number of processors as specified by the user. Finally, the functionality of
parallelization depends on system OS: on Windows only 'snow' type func-
tionality is available, while on Unix/Linux/Mac OSX both 'snow' and 'multicore'
(default) functionalities are available.

monitor a logical or an R function which takes as input the current state of the gaisl-class
object and show the evolution of the search in different epochs. By default, for
interactive sessions, the function gaislMonitor or gaislMonitor2, depend-
ing on whether or not is an RStudio session, prints the average and best fitness
values at each epoch for each island. In non interactive sessions, by default
monitor = FALSE so any output is suppressed.

seed an integer value containing the random number generator state. This argument
can be used to replicate the results of a ISLGA search. Note that if parallel
computing is required, the doRNG package must be installed.

Details

Genetic algorithms (GAs) are stochastic search algorithms inspired by the basic principles of bi-
ological evolution and natural selection. GAs simulate the evolution of living organisms, where
the fittest individuals dominate over the weaker ones, by mimicking the biological mechanisms of
evolution, such as selection, crossover and mutation.

The gaisl function implements the islands GAs approach, where the population is partitioned into
several subpopulations and assigned to separated islands. Independent GAs are executed in each
island, and only occasionally sparse exchanges of individuals are performed among the islands. The
algorithm can be run in parallel or sequentially. For more information on GAs see ga.
Value

Returns an object of class gaisl-class. See gaisl-class for a description of available slots information.

Author(s)

Luca Scrucca <luca.scrucca@unipg.it>

References


See Also

summaryLgaislMmethod, plotLgaislMmethod, gaislMclass, ga

Examples

```r
## Not run:
# two-dimensional Rastrigin function
Rastrigin <- function(x1, x2)
{  
  20 + x1^2 + x2^2 - 10*(cos(2*pi*x1) + cos(2*pi*x2))
}

x1 <- x2 <- seq(-5.12, 5.12, by = 0.1)
f <- outer(x1, x2, Rastrigin)
persp3D(x1, x2, f, theta = 50, phi = 20)
filled.contour(x1, x2, f, color.palette = jet.colors)

GA <- gaisl(type = "real-valued",
            fitness = function(x) -Rastrigin(x[1], x[2]),
            min = c(-5.12, -5.12), max = c(5.12, 5.12),
            popSize = 80, maxiter = 500,
            numIslands = 4, migrationInterval = 50)

summary(GA)
plot(GA)

## End(Not run)
```
Description

An S4 class for islands genetic algorithms (ISLGAs)

Objects from the Class

Objects can be created by calls to the `gaisl` function.

Slots

- `call` an object of class "call" representing the matched call;
- `type` a character string specifying the type of genetic algorithm used;
- `min` a vector providing for each decision variable the minimum of the search space in case of real-valued or permutation encoded optimizations;
- `max` a vector providing for each decision variable the maximum of the search space in case of real-valued or permutation encoded optimizations;
- `nBits` a value specifying the number of bits to be used in binary encoded optimizations;
- `names` a vector of character strings providing the names of decision variables (optional);
- `popSize` the population size;
- `numIslands` the number of islands;
- `migrationRate` the migration rate;
- `migrationInterval` the migration interval;
- `maxIter` the maximum number of ISLGA iterations before the search is halted;
- `run` the number of consecutive generations without any improvement in the best fitness value before the ISLGA is stopped;
- `maxIter` the maximum number of iterations to run before the GA search is halted;
- `suggestions` a matrix of user provided solutions and included in the initial population;
- `elitism` the number of best fitness individuals to survive at each generation;
- `pcrossover` the crossover probability;
- `pmutation` the mutation probability;
- `islands` a list containing the "ga" objects corresponding to each island GA evolution;
- `summary` a list of matrices of summary statistics for fitness values at each iteration (along the rows).
  - Each element of the list corresponds to the evolution of an island;
- `fitnessValues` a list of best fitness values found in each island at the final iteration;
- `solutions` a list of matrices, one for each island, containing the values of the decision variables giving the best fitness at the final iteration;
- `fitnessValue` the best fitness value at the final iteration;
- `solution` a matrix containing the values of the decision variables giving the best fitness at the final iteration.
gaMonitor

Author(s)
Luca Scrucca

See Also
For examples of usage see gaisl.

---

**gaMonitor**  
Monitor genetic algorithm evolution

**Description**
Functions to print summary statistics of fitness values at each iteration of a GA search.

**Usage**

```r
gaMonitor(object, digits =getOption("digits"), ...)
gamonitor2(object, digits =getOption("digits"), ...)
gaislMonitor(object, digits =getOption("digits"), ...)
gaislMonitor2(object, digits =getOption("digits"), ...)
```

**Arguments**

- **object**: an object of class `ga-class` or `gaisl-class`, usually resulting from a call to function `ga` or `gaisl`, respectively.
- **digits**: minimal number of significant digits.
- **...**: further arguments passed to or from other methods.

**Value**
These functions print a summary of current GA step on the console.
By default, `gaMonitor` is called in interactive sessions by `ga`. The old monitoring function, used as the default until version 2.2 of `GA` package, is provided in `gamonitor2`.
By default, `gaislMonitor` is called in interactive sessions by `gaisl`.

**Author(s)**
Luca Scrucca
ga_Summary

Summarize genetic algorithm evolution

Description

A function which returns fitness summary statistics at each iteration of GA search.

Usage

gaSummary(x, ...)

Arguments

x  a vector of fitness values for which summary statistics should be computed.
... further arguments passed to or from other methods.

Details

This function computes summary statistics for a vector of fitness values at current iteration of GA search.

Value

A vector with the following values: (max, mean, median, min)

Author(s)

Luca Scrucca

See Also

ga

----------

ga_Crossover

Crossover operators in genetic algorithms

Description

Functions implementing crossover genetic operator.
Usage

`ga_spCrossover(object, parents, ...)`
`gabin_spCrossover(object, parents, ...)`
`gabin_uCrossover(object, parents, ...)`
`gareal_spCrossover(object, parents, ...)`
`gareal_waCrossover(object, parents, ...)`
`gareal_laCrossover(object, parents, ...)`
`gareal_blxCrossover(object, parents, ...)`
`gareal_laplaceCrossover(object, parents, a = 0, b = 0.35, ...)`
`gaperm_cxCrossover(object, parents, ...)`
`gaperm_pmxCrossover(object, parents, ...)`
`gaperm_oxCrossover(object, parents, ...)`
`gaperm_pbxCrossover(object, parents, ...)`

Arguments

- `object`: An object of class "ga", usually resulting from a call to function `ga`.
- `parents`: A two-rows matrix of values indexing the parents from the current population.
- `...`: Further arguments passed to or from other methods.
- `a, b`: Parameters of genetic operators.

Value

Return a list with two elements:

- `children`: a matrix of dimension 2 times the number of decision variables containing the generated offsprings;
- `fitness`: a vector of length 2 containing the fitness values for the offsprings. A value `NA` is returned if an offspring is different (which is usually the case) from the two parents.

Author(s)

Luca Scrucca

See Also

`ga`
**ga_Mutation**  
*Mutation operators in genetic algorithms*

**Description**

Functions implementing mutation genetic operator.

**Usage**

```r
# Functions implementing mutation genetic operator.
gabin_raMutation(object, parent, ...)
gareal_raMutation(object, parent, ...)
gareal_nraMutation(object, parent, ...)
gareal_rsmutation(object, parent, ...)
gareal_powMutation(object, parent, pow = 4, ...)
gaperm_simMutation(object, parent, ...)
gaperm_ismMutation(object, parent, ...)
gaperm_swMutation(object, parent, ...)
gaperm_dmMutation(object, parent, ...)
gaperm_scrMutation(object, parent, ...)
```

**Arguments**

- `object`: An object of class "ga", usually resulting from a call to function `ga`.
- `parent`: A vector of values for the parent from the current population where mutation should occur.
- `...`: Further arguments passed to or from other methods.
- `pow`: Parameters of genetic operators.

**Value**

Return a vector of values containing the mutated string.

**Author(s)**

Luca Scrucca
**ga_pmutation**  
*Variable mutation probability in genetic algorithms*

**Description**

A function which calculates the mutation probability for the current iteration. This enables to use GAs with variable mutation rate (see examples).

**Usage**

```r
ga_pmutation(object, p0 = 0.5, p = 0.01, T = round(object@maxiter/2), ...)
```

**Arguments**

- `object`: An object of class "ga", usually resulting from a call to function `ga`.
- `p0`: initial probability of mutation.
- `p`: limiting probability of mutation.
- `T`: maximum iteration after which it should converges to `p`.
- `...`: Further arguments passed to or from other methods.

**Value**

Return a numeric value in the range (0,1).

**Author(s)**

Luca Scrucca

**See Also**

`ga`, `ga_Mutation`

**Examples**

```r
## Not run:
Rastrigin <- function(x1, x2)
  {  
    20 + x1^2 + x2^2 - 10*(cos(2*pi*x1) + cos(2*pi*x2)) 
  }

GA <- ga(type = "real-valued",
         fitness = function(x) -Rastrigin(x[1], x[2]),
         min = c(-5.12, -5.12), max = c(5.12, 5.12),
         popSize = 50, maxiter = 500, run = 100,
         pmutation = ga_pmutation)
plot(GA)

GA <- ga(type = "real-valued",
```
fitness = function(x) -Rastrigin(x[1], x[2]),
min = c(-5.12, -5.12), max = c(5.12, 5.12),
popSize = 50, maxiter = 500, run = 100,
pmutation = function(...) ga_pmutation(..., p0 = 0.1))
plot(GA)

## End(Not run)

gaperm_Population object, ...

gaperm_Population object, ...

Arguments

object An object of class "ga", usually resulting from a call to function ga.

Details

gabin_Population generates a random population of object@nBits binary values;
gareal_Population generates a random (uniform) population of real values in the range [object@min, object@max];
gaperm_Population generates a random (uniform) population of integer values in the range [object@min, object@max].

Value

Return a matrix of dimension object@popSize times the number of decision variables.

Author(s)

Luca Scrucca

See Also
ga
**Selection operators in genetic algorithms**

**Description**

Functions implementing selection genetic operator.

**Usage**

\[
\text{ga\_lrSelection}(\text{object, } r = 2/(\text{object@popSize} \times (\text{object@popSize} - 1)), \\
q = 2/\text{object@popSize}, ...)
\]

\[
\text{ga\_nlrSelection}(\text{object, } q = 0.25, ...)
\]

\[
\text{ga\_rwSelection}(\text{object, } ...)
\]

\[
\text{ga\_tourSelection}(\text{object, } k = 3, ...)
\]

\[
\text{gabin\_lrSelection}(\text{object, } r = 2/(\text{object@popSize} \times (\text{object@popSize} - 1)), \\
q = 2/\text{object@popSize}, ...)
\]

\[
\text{gabin\_nlrSelection}(\text{object, } q = 0.25, ...)
\]

\[
\text{gabin\_rwSelection}(\text{object, } ...)
\]

\[
\text{gabin\_tourSelection}(\text{object, } k = 3, ...)
\]

\[
\text{gareal\_lrSelection}(\text{object, } r = 2/(\text{object@popSize} \times (\text{object@popSize} - 1)), \\
q = 2/\text{object@popSize}, ...)
\]

\[
\text{gareal\_nlrSelection}(\text{object, } q = 0.25, ...)
\]

\[
\text{gareal\_rwSelection}(\text{object, } ...)
\]

\[
\text{gareal\_tourSelection}(\text{object, } k = 3, ...)
\]

\[
\text{gareal\_lssSelection}(\text{object, } ...)
\]

\[
\text{gareal\_sigmaSelection}(\text{object, } ...)
\]

\[
\text{gaperm\_lrSelection}(\text{object, } r = 2/(\text{object@popSize} \times (\text{object@popSize} - 1)), \\
q = 2/\text{object@popSize}, ...)
\]

\[
\text{gaperm\_nlrSelection}(\text{object, } q = 0.25, ...)
\]

\[
\text{gaperm\_rwSelection}(\text{object, } ...)
\]

\[
\text{gaperm\_tourSelection}(\text{object, } k = 3, ...)
\]

**Arguments**

- **object** An object of class "ga", usually resulting from a call to function `ga`.
- **r** A tuning parameter for the specific selection operator.
- **q** A tuning parameter for the specific selection operator.
- **k** A tuning parameter for the specific selection operator.
- **...** Further arguments passed to or from other methods.
palettes

Value

Return a list with two elements:

- `population`: a matrix of dimension `object@popSize` times the number of decision variables containing the selected individuals or strings;
- `fitness`: a vector of length `object@popSize` containing the fitness values for the selected individuals.

Author(s)

Luca Scrucca

See Also

ga

numericOrNA-class

Virtual Class "numericOrNA" - Simple Class for subassignment Values

Description

The class "numericOrNA" is a simple class union (`setClassUnion`) of "numeric" and "logical".

Objects from the Class

Since it is a virtual Class, no objects may be created from it.

Examples

`showClass("numericOrNA")`

palettes

Colors palettes

Description

Functions for creating a vector of colors from pre-specified palettes.

Usage

- `jet.colors(n)`
- `spectral.colors(n)`
- `bl2gr.colors(n)`
Arguments

n  a numerical value specifying the number of colors in the palette.

Details

jet.colors() creates a palette of colors which tend to have high brightness and not uniform luminance. Furthermore, the brightest colors, yellow and cyan, are used for intermediate data values, and this has the effect of emphasizing uninteresting (and arbitrary) values while demphasizing the extremes. For these reasons this popular palette is not recommended.
spectral.colors() creates a palette based on ColorBrewer http://colorbrewer2.org, so the resulting colors have a much uniform luminance.
The bl2gr.colors() palette returns a palette of colors from blue to green.

Value

Returns a character vector of colors encoded in hexadecimal values.

See Also

colors, rgb.

Examples

jet.colors(9)
spectral.colors(9)
bl2gr.colors(9)

par(mfrow = c(3,1), mar = c(1,1,1,1))
n = 21
image(1:21, 1, as.matrix(1:21), col = jet.colors(21),
ylab = "", xlab = "", xaxt = "n", yaxt = "n", bty = "n")
image(1:21, 1, as.matrix(1:21), col = spectral.colors(21),
ylab = "", xlab = "", xaxt = "n", yaxt = "n", bty = "n")
image(1:21, 1, as.matrix(1:21), col = bl2gr.colors(21),
ylab = "", xlab = "", xaxt = "n", yaxt = "n", bty = "n")
Usage

parNames(object, ...)
## S4 method for signature 'ga'
parNames(object, ...)

Arguments

object An object of class "ga", usually resulting from a call to function ga.
...
Further arguments, currently not used.

Value

A list of character values providing the names of parameters or decision variables.

Author(s)

Luca Scrucca

See Also

ga

description

This function draws a perspective plot of a surface with different levels in different colors.

Usage

persp3D(x, y, z, theta = 30, phi = 20, d = 5, expand = 2/3,
xlim = range(x, finite = TRUE), ylim = range(y, finite = TRUE),
zlim = range(z, finite = TRUE), levels = pretty(zlim, nlevels),
nlevels = 20, color.palette = jet.colors, border = NA,
ticktype = "detailed", xlab = NULL, ylab = NULL, zlab = NULL,
...)

Arguments

x, y locations of grid lines at which the values in z are measured. These must be in
ascending order. By default, equally spaced values from 0 to 1 are used. If x is
a list, its components x$x and x$y are used for x and y, respectively.

z a matrix containing the values to be plotted (NAs are allowed).

theta, phi angles defining the viewing direction. theta gives the azimuthal direction and
phi the colatitude.
persp3D

- d: a value which can be used to vary the strength of the perspective transformation.
- expand: a expansion factor applied to the z coordinates.
- xlim, ylim, zlim: x-, y- and z-limits for the axes.
- levels: a vector of values specifying the levels to be used for plotting the surface with different colors.
- nlevels: a value specifying the number of levels to be used for plotting. This value is used if levels argument is not specified.
- color.palette: the color palette used for plotting.
- border: the color of the line drawn around the surface facets. By default is set to NA so no borders are drawn.
- ticktype: a character specifying the type of axes tickmarks. By default "detailed" ticks are drawn.
- xlab, ylab, zlab: character strings specifying the titles for the axes.

Further arguments passed to the function persp.

Details
This function enhances the default perspective plot for drawing 3-dimensional surfaces.

Value
Return a list with the following elements:
- persp: the viewing transformation matrix (see link{persp});
- levels: a vector of values giving the levels used for plotting the surface;
- colors: a vector of strings giving the color used for plotting the surface.

Author(s)
Luca Scrucca

See Also
link{persp}

Examples
```
y <- x <- seq(-10, 10, length=60)
f <- function(x,y) { r <- sqrt(x^2+y^2); 10 * sin(r)/r }
z <- outer(x, y, f)
persp3D(x, y, z, theta = 30, phi = 30, expand = 0.5)
persp3D(x, y, z, color.palette = heat.colors, phi = 30, theta = 225,
       box = TRUE, border = NA, shade = .4)
x1 = seq(-3,3,length=50)
x2 = seq(-3,3,length=50)
```

y = function(x1, x2) sin(x1)+cos(x2)
persp3D(x1, x2, outer(x1,x2,y), zlab="y", theta = 150, phi = 20, expand = 0.6)

plot.ga-method  

Plot of Genetic Algorithm search path

Description

The plot method for ga-class objects gives a plot of best and average fitness values found during the iterations of the GA search.

Usage

## S4 method for signature 'ga'
plot(x, y, ylim, cex.points = 0.7, 
col = c("green3", "dodgerblue3", adjustcolor("green3", alpha.f = 0.1)), 
pch = c(16, 1), lty = c(1,2), legend = TRUE, grid = graphics:::grid, ...)

Arguments

- **x**: An object of class "ga".
- **y**: Not used.
- **ylim**: A vector of two values specifying the limits on the y-axis.
- **cex.points**: The magnification to be used for points.
- **col**: The colors to be used for best and average fitness values.
- **pch**: The type of points to be used for best and average fitness values.
- **lty**: The type of lines to be used for best and average fitness values.
- **legend**: A logical specifying if a legend should be included.
- **grid**: A function for grid drawing of NULL to avoid drawing one.
- **...**: Further arguments, currently not used.

Details

Plot best and average fitness values at each iteration of GA search.

Value

The method invisibly return a data.frame with the iterations and summary statistics for the fitness function evaluated at each iteration.

Author(s)

Luca Scrucca
plot.gaisl-method

See Also
gaisl-class.

Examples

# See examples in help(ga)

# The following code shows how to obtain graphs using the
# ggplot2 plotting system
## Not run:
GA <- ga(...)
out <- plot(GA)
library(reshape2)
df <- melt(out[,c(1:3,5)], id.var = "iter")
library(ggplot2)
ggplot(df, aes(x = iter, y = value, group = variable, colour = variable)) +
  xlab("Generation") + ylab("Fitness values") +
  geom_point(aes(shape = variable)) +
  geom_line(aes(lty = variable)) +
  scale_colour_brewer(palette = "Set1") +
  theme_bw() +
  theme(legend.title = element_blank())

## End(Not run)

Description

The plot method for gaisl-class objects gives a plot of best fitness values found in each island during the GA iterations.

Usage

## S4 method for signature 'gaisl'
plot(x, y, ...)

Arguments

x An object of class "gaisl".

y Not used.

... Further arguments passed to plot.default, such as ylim, ylab, etc., or to matplot, such as col, lty, and lwd.

Details

Plot best fitness values found in each island during the GA iterations.
Value
The method invisibly return a list with the following components:

- `iter`: a vector of values specifying the interation.
- `summary`: a matrix of best fitness values for each island along the columns.

Author(s)
Luca Scrucca

See Also
`gaisl`, `gaisl-class`.

Examples
```
# See examples in help(gaisl)

# The following code shows how to obtain graphs using the
# ggplot2 plotting system

GA <- gaisl(...)
out <- plot(GA)
library(reshape2)
df <- melt(out, id.var = "iter")
library(ggplot2)
ggplot(df, aes(x = iter, y = value, group = variable, colour = variable)) +
  xlab("Generation") + ylab("Fitness values") +
  geom_line(size = 0.8) +
  scale_colour_brewer(palette = "Paired") +
  theme_bw() +
  theme(legend.title = element_blank())

# End(Not run)
```
Arguments

- object: an object of class `ga-class`.
- x: an object of class `summary.ga`.
- digits: number of significant digits.
- ...: further arguments passed to or from other methods.

Value

The `summary` function returns an object of class `summary.ga` which can be printed by the corresponding `print` method. The function also returns invisibly a list with the information from the genetic algorithm search.

Author(s)

Luca Scrucca

See Also

gai

Examples

```r
f <- function(x) abs(x)+cos(x)
GA <- ga(type = "real-valued",
        fitness = function(x) -f(x),
        min = -20, max = 20, run = 50)
out <- summary(GA)
print(out)
str(out)
```

Description

Summary method for class `gaisl-class`.

Usage

```r
# S4 method for signature 'gaisl'
summary(object, ...)

# S3 method for class 'summary.gaisl'
print(x, digits = getOption("digits"), ...)
```
summary.gaisl-method

Arguments

object an object of class \textit{gaisl-class}.
x an object of class \textit{summary.gaisl}.
digits number of significant digits.
... further arguments passed to or from other methods.

Value

The \textit{summary} function returns an object of class \textit{summary.gaisl} which can be printed by the corresponding \textit{print} method. The function also returns invisibly a list with the information from the islands genetic algorithm search.

Author(s)

Luca Scrucca

See Also

gaisl

Examples

\begin{verbatim}
f <- function(x) abs(x)+cos(x) 
GA <- gaisl(type = "real-valued", 
             fitness = function(x) -f(x), 
             min = -20, max = 20, run = 10, 
             numIslands = 4, parallel = 2) # CRAN check limits ncores = 2 
out <- summary(GA) 
print(out) 
str(out)
\end{verbatim}
Index

*Topic **classes**
  ga-class, 11
  gaisl-class, 18
  numericOrNA-class, 26

*Topic **hplof**
  palettes, 26
  persp3d, 28
  plot.ga-method, 30
  plot.gaisl-method, 31

*Topic **methods**
  parNames-methods, 27
  plot.ga-method, 30
  plot.gaisl-method, 31

*Topic **optimize**
  ga, 5
  ga-class, 11
  gaisl, 13
  gaisl-class, 18
  summary.ga-method, 32
  summary.gaisl-method, 33

*Topic **package**
  GA-package, 2
  binary2decimal, 3, 4
  binary2gray, 3, 4
  bl2gr.colors (palettes), 26
  colors, 27
  decimal2binary (binary2decimal), 3
  detectCores, 7, 16

GA (GA-package), 2
  ga, 5, 11, 13, 16, 17, 19–26, 28, 31, 33
  ga-class, 11, 27
  GA-package, 2
  ga_Crossover, 6, 9, 15, 20
  ga_lrSelection (ga_Selection), 25
  ga_Mutation, 6, 9, 15, 22, 23
  ga_nlrSelection (ga_Selection), 25
  ga_pmutation, 23
  ga_Population, 6, 9, 15, 24
  ga_rwSelection (ga_Selection), 25
  ga_Selection, 6, 9, 15, 25
  ga_spCrossover (ga_Crossover), 20
  ga_tourSelection (ga_Selection), 25
  gabin_lrSelection (ga_Selection), 25
  gabin_nlrSelection (ga_Selection), 25
  gabin_Population (ga_Population), 24
  gabin_raMutation (ga_Mutation), 22
  gabin_RWSelection (ga_Selection), 25
  gabin_spCrossover (ga_Crossover), 20
  gabin_tourSelection (ga_Selection), 25
  gabin_uCrossover (ga_Crossover), 20
  gaControl, 8, 9, 12
  gaisl, 13, 18, 19, 32, 34
  gaisl-class, 18
  gaislMonitor, 16
  gaislMonitor (gaMonitor), 19
  gaislMonitor2, 16
  gaislMonitor2 (gaMonitor), 19
  gaMonitor, 7, 19
  gaMonitor2, 7
  gaMonitor2 (gaMonitor), 19
  gaperm_cxCrossover (ga_Crossover), 20
  gaperm_dmMutation (ga_Mutation), 22
  gaperm_ismMutation (ga_Mutation), 22
  gaperm_lrSelection (ga_Selection), 25
  gaperm_nlrSelection (ga_Selection), 25
  gaperm_oxCrossover (ga_Crossover), 20
  gaperm_pbxCrossover (ga_Crossover), 20
  gaperm_pmxCrossover (ga_Crossover), 20
  gaperm_Population (ga_Population), 24
  gaperm_rwSelection (ga_Selection), 25
  gaperm_scrMutation (ga_Mutation), 22
  gaperm_simMutation (ga_Mutation), 22
  gaperm_swMutation (ga_Mutation), 22
  gaperm_tourSelection (ga_Selection), 25
  gareal_blxCrossover (ga_Crossover), 20
gareal_lacrossover (ga_Crossover), 20
  gareal_laplaceCrossover (ga_Crossover), 20
  gareal_lrSelection (ga_Selection), 25
  gareal_lsSelection (ga_Selection), 25
  gareal_nlrSelection (ga_Selection), 25
  gareal_nraMutation (ga_Mutation), 22
  gareal_Population (ga_Population), 24
  gareal_powMutation (ga_Mutation), 22
  gareal_raMutation (ga_Mutation), 22
  gareal_rsMutation (ga_Mutation), 22
  gareal_rwSelection (ga_Selection), 25
  gareal_sigaSelection (ga_Selection), 25
  gareal_spCrossover (ga_Crossover), 20
  gareal_tuSelection (ga_Selection), 25
  gareal_waCrossover (ga_Crossover), 20
  gaSummary, 20
  gray2binary (binary2gray), 4
jet.colors (palettes), 26
matplot, 31
numericOrNA-class, 26
optim, 7, 16
palettes, 26
parNames (parNames-methods), 27
parNames, ga-method (parNames-methods), 27
parNames-methods, 27
persp, 29
persp3d, 28
plot, ga-method (plot.ga-method), 30
plot, gaisl-method (plot.gaisl-method), 31
plot.default, 31
plot.ga (plot.ga-method), 30
plot.ga-method, 30
plot.gaisl (plot.gaisl-method), 31
plot.gaisl-method, 31
print, ga-method (ga), 5
print, gaisl-method (gaisl), 13
print.summary.ga (summary.ga-method), 32
print.summary.gaisl (summary.gaisl-method), 33
rgb, 27
setClassUnion, 26
show, ga-method (ga), 5
show, gaisl-method (gaisl), 13
spectral.colors (palettes), 26
summary, ga-method (summary.ga-method), 32
summary, gaisl-method
  (summary.gaisl-method), 33
summary.ga (summary.ga-method), 32
summary.ga-method, 32
summary.gaisl (summary.gaisl-method), 33
summary.gaisl-method, 33