Package ‘genalg’

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plot.rbga

Description

Plots features of the genetic algorithm optimization run. The default plot shows the minimal and mean evaluation value, indicating how far the GA has progressed.

The "hist" plot shows for binary chromosome the gene selection frequency, i.e. the times one gene in the chromosome was selected in the current population. In case of floats chromosomes, it will make histograms for each variable to indicate the selected values in the population.

The "vars" plot the evaluation function versus the variable value. This is useful to look at correlations between the variable and the evaluation values.
Usage

```r
## S3 method for class 'rbga'
plot(x, type="default", breaks=10, ...)
```

Arguments

- `x`: a rbga object.
- `type`: one of "hist", "vars" or "default".
- `breaks`: the number of breaks in a histogram.
- `...`: options directly passed to the plot function.

Examples

```r
evaluate <- function(string=c()) {
  returnVal = 1 / sum(string);
  returnVal
}

rbga.results = rbga.bin(size=10, mutationChance=0.01, zeroToOneRatio=0.5,
  evalFunc=evaluate)

plot(rbga.results)
plot(rbga.results, type="hist")
```

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**rbga**

*R Based Genetic Algorithm (floating point chromosome)*

Description

A R based genetic algorithm that optimizes, using a user set evaluation function, a set of floats. It takes as input minimum and maximum values for the floats to optimizes. The optimum is the chromosome for which the evaluation value is minimal.

It requires an `evalFunc` method to be supplied that takes as argument the chromosome, a vector of floats. Additionally, the GA optimization can be monitored by setting a `monitorFunc` that takes a `rbga` object as argument.

Results can be visualized with `plot.rbga` and summarized with `summary.rbga`.

Usage

```r
rbga(stringMin=c(), stringMax=c(),
  suggestions=NULL,
  popSize=200, iters=100,
  mutationChance=NA,
  elitism=NA,
  monitorFunc=NULL, evalFunc=NULL,
  showSettings=FALSE, verbose=FALSE)
```
Arguments

stringMin  vector with minimum values for each gene.
stringMax  vector with maximum values for each gene.
suggestions  optional list of suggested chromosomes
popSize  the population size.
iters  the number of iterations.
mutationChance  the chance that a gene in the chromosome mutates. By default 1/(size+1). It affects the convergence rate and the probing of search space: a low chance results in quicker convergence, while a high chance increases the span of the search space.
elitism  the number of chromosomes that are kept into the next generation. By default is about 20% of the population size.
monitorFunc  Method run after each generation to allow monitoring of the optimization
evalFunc  User supplied method to calculate the evaluation function for the given chromosome
showSettings  if true the settings will be printed to screen. By default False.
verbose  if true the algorithm will be more verbose. By default False.

References


See Also

rbga.bin plot.rbga

Examples

```r
# optimize two values to match pi and sqrt(50)
evaluate <- function(string=c()) {
  returnVal = NA;
  if (length(string) == 2) {
    returnVal = abs(string[1]-pi) + abs(string[2]-sqrt(50));
  } else {
    stop("Expecting a chromosome of length 2!");
  }
  returnVal
}

monitor <- function(obj) {
  # plot the population
  xlim = c(obj$stringMin[1], obj$stringMax[1]);
  # plot the population
  # xlab = "Population size",
  # ylab = "Fitness",
  # main = "Fitness vs Population Size",
  # sub = "rbaa"
}
```
ylim = c(obj$stringMin[2], obj$stringMax[2]);
plot(obj$population, xlim=xlim, ylim=ylim,
     xlab="pi", ylab="sqrt(50)");
}

rbga.results = rbga(c(1, 1), c(5, 10), monitorFunc=monitor,
                     evalFunc=evaluate, verbose=TRUE, mutationChance=0.01)

plot(rbga.results)
plot(rbga.results, type="hist")
plot(rbga.results, type="vars")

---

**rbga.bin**  
*R Based Genetic Algorithm (binary chromosome)*

**Description**

A R based genetic algorithm that optimizes, using a user set evaluation function, a binary chromosome which can be used for variable selection. The optimum is the chromosome for which the evaluation value is minimal.

It requires a `evalFunc` method to be supplied that takes as argument the binary chromosome, a vector of zeros and ones. Additionally, the GA optimization can be monitored by setting a `monitorFunc` that takes a `rbga` object as argument.

Results can be visualized with `plot.rbga` and summarized with `summary.rbga`.

**Usage**

```r
rbga.bin(size=10,  
suggestions=NULL,  
popSize=200, iters=100,  
mutationChance=NA,  
elitism=NA, zeroToOneRatio=10,  
monitorFunc=NULL, evalFunc=NULL,  
showSettings=FALSE, verbose=FALSE)
```

**Arguments**

- `size`  
  the number of genes in the chromosome.

- `popSize`  
  the population size.

- `iters`  
  the number of iterations.

- `mutationChance`  
  the chance that a gene in the chromosome mutates. By default 1/(size+1). It affects the convergence rate and the probing of search space: a low chance results in quicker convergence, while a high chance increases the span of the search space.

- `elitism`  
  the number of chromosomes that are kept into the next generation. By default is about 20% of the population size.
zeroToOneRatio the change for a zero for mutations and initialization. This option is used to control the number of set genes in the chromosome. For example, when doing variable selection this parameter should be set high to

monitorFunc Method run after each generation to allow monitoring of the optimization

evalFunc User supplied method to calculate the evaluation function for the given chromosome

showSettings if true the settings will be printed to screen. By default False.

verbose if true the algorithm will be more verbose. By default False.

suggestions optional list of suggested chromosomes

References


See Also

rbgaplot.rbga

Examples

# a very simplistic optimization
evaluate <- function(string=c()) {
  returnVal = 1 / sum(string);
  returnVal
}

rbga.results = rbga.bin(size=10, mutationChance=0.01, zeroToOneRatio=0.5,
  evalFunc=evaluate)

plot(rbga.results)

# in this example the four variables in the IRIS data
# set are complemented with 36 random variables.
# Variable selection should find the four original
# variables back (example by Ron Wehrens).
## Not run:
data(iris)
library(MASS)
X <- cbind(scale(iris[,1:4]), matrix(rnorm(36*150), 150, 36))
Y <- iris[,5]
iris.evaluate <- function(indices) {
  result = 1
  if (sum(indices) > 2) {
    huhn <- lda(X[,indices==1], Y, CV=TRUE)$posterior
  }
result = sum(Y != dimnames(huhn)[[2]][apply(huhn, 1,
    function(x)
    which(x == max(x)))] / length(Y)
}
result
}

monitor <- function(obj) {
    minEval = min(obj$evaluations);
    plot(obj, type="hist");
}
woppa <- rbga.bin(size=40, mutationChance=0.05, zeroToOneRatio=10,
    evalFunc=iris.evaluate, verbose=TRUE, monitorFunc=monitor)

## End(Not run)

# another realistic example: wavelenght selection for PLS on NIR data
## Not run:
library(pls.pcr)
data(NIR)

numberOfWavelenghts = ncol(NIR$Xtrain)
evaluateNIR <- function(chromosome=c()) {
    returnVal = 100
    minLV = 2
    if (sum(chromosome) < minLV) {
        returnVal
    } else {
        xtrain = NIR$Xtrain[,chromosome == 1];
        pls.model = pls(xtrain, NIR$Ytrain, validation="CV", grpsize=1,
            ncomp=2:min(10,sum(chromosome)))
    returnVal = pls.model$val$RMS[pls.model$val$nLV-(minLV-1)]
    returnVal
}
}

monitor <- function(obj) {
    minEval = min(obj$evaluations);
    filter = obj$evaluations == minEval;
    bestObjectCount = sum(rep(1, obj$popSize)[filter]);
    # ok, deal with the situation that more than one object is best
    if (bestObjectCount > 1) {
        bestSolution = obj$population[filter,,1,];
    } else {
        bestSolution = obj$population[filter,,];
    }
    outputBest = paste(obj$iter, " #selected=", sum(bestSolution),
        " Best (Error=" , minEval, ",") : ", sep="";
    for (var in 1:length(bestSolution)) {
        outputBest = paste(outputBest,
            bestSolution[var], " ",
            sep="";
    }
summary.rbga

R Based Genetic Algorithm Summary Function

Description

Summarizes the genetic algorithm results.

Usage

## S3 method for class 'rbga'
summary(object, echo=FALSE, ...)

Arguments

object       a rbga object.
echo         if true, the summary will be printed to STDOUT as well as returned.
...           other options (ignored)

Examples

evaluate <- function(string=c()) {
  returnVal = 1 / sum(string);
  returnVal
}

rbga.results = rbga.bin(size=10, mutationChance=0.01, zeroToOneRatio=0.5, evalFunc=evaluate)

summary(rbga.results)
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