Package 'dGAselID'

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Type Package

Title Genetic Algorithm with Incomplete Dominance for Feature Selection

Version 1.2

Author Nicolae Teodor Melita

Maintainer Nicolae Teodor Melita <nt_melita@yahoo.com>

Description Feature selection from high dimensional data using a diploid genetic algorithm with Incomplete Dominance for genotype to phenotype mapping and Random Assortment of chromosomes approach to recombination.

Depends R (>= 3.3.1), Biobase, MLInterfaces

Imports genefilter, ALL, grDevices, graphics, stats, utils

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LazyData TRUE

RoxygenNote 5.0.1

NeedsCompilation no

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R topics documented:

`AnalyzeResults` *AnalyzeResults*

Description

Ranks individuals according to their fitness and records the results.

Usage

```
AnalyzeResults(individuals, results, randomAssortment = TRUE, chrConf)
```

Arguments

`individuals`	Population of individuals with diploid genotypes.
`results`	Results returned by EvaluationFunction().
`randomAssortment`	Random Assortment of Chromosomes for recombinations. The default value is TRUE.
`chrConf`	Configuration of chromosomes returned by splitChromosomes().

Examples

```
## Not run:
 library(genefilter)
 library(ALL)
 data(ALL)
 bALL = ALL[, substr(ALL$BT,1,1) == "B"]
 smallALL = bALL[, bALL$mol.biol %in% c("BCR/ABL", "NEG")]
 smallALL$mol.biol = factor(smallALL$mol.biol)
 smallALL$BT = factor(smallALL$BT)
 f1 <- pOverA(0.25, log2(100))
 f2 <- function(x) (IQR(x) > 0.5)
 f3 <- ttest(smallALL$mol.biol, p=0.1)
 ff <- filterfun(f1, f2, f3)
 selectedsmallALL <- genefilter(exprs(smallALL), ff)
 smallALL = smallALL[selectedsmallALL, ]
 rm(f1)
 rm(f2)
 rm(f3)
```

```
rm(ff)
rm(bALL)
sum(selectedsmallALL)
set.seed(1357)

population0<-InitialPopulation(smallALL, 14, 10, FALSE)
individuals0<-Individuals(population0)
results0<-EvaluationFunction(smallALL, individuals0, response="mol.biol",
            method=knn.cvI(k=3, l=2), trainTest="LOG")
chrConf0<-splitChromosomes(smallALL)
iterRes0<-AnalyzeResults(individuals0, results0, randomAssortment=TRUE, chrConf0)

## End(Not run)
```

Crossover *Crossover*

Description

Two-point crossover operator.

Usage

```
Crossover(c1, c2, chrConf)
```

Arguments

c1	Set of chromosomes.
c2	Set of chromosomes.
chrConf	Configuration of chromosomes returned by splitChromosomes().

Examples

```
## Not run:
library(ALL)
data(ALL)

demoALL<-ALL[1:12,1:8]
set.seed(1357)
population02<-InitialPopulation(demoALL, 2, 4, FALSE)
chrConf02<-splitChromosomes(demoALL, 2)
chrConf02
population02[1:2,]
Crossover(population02[1,], population02[2,], chrConf02)

## End(Not run)
```

dGAselID *dGAselID*

Description

Initializes and starts the search with the genetic algorithm.

Usage

```
dGAselID(x, response, method = knn.cvI(k = 3, l = 2), trainTest = "LOG",
  startGenes, populationSize, iterations, noChr = 22, elitism = NA,
  ID = "ID1", pMutationChance = 0, nSMutationChance = 0,
  fSMutationChance = 0, lSDeletionChance = 0, wChrDeletionChance = 0,
  transposonChance = 0, randomAssortment = TRUE, embryonicSelection = NA,
  EveryGeneInInitialPopulation = TRUE, nnetSize = NA, nnetDecay = NA,
  rdaAlpha = NA, rdaDelta = NA, ...)
```

Arguments

x	Dataset in ExpressionSet format.
response	Response variable
method	Supervised classifier for fitness evaluation. Most of the supervised classifiers in MLInterfaces are acceptable. The default is knn.cvI(k=3, l=2).
trainTest	Cross-validation method. The default is "LOG".
startGenes	Genes in the genotypes at initialization.
populationSize	Number of genotypes in initial population.
iterations	Number of iterations.
noChr	Number of chromosomes. The default value is 22.
elitism	Elite population in percentages.
ID	Dominance. The default value is "ID1". Use "ID2" for Incomplete Dominance.
pMutationChance	Chance for a Point Mutation to occur. The default value is 0.
nSMutationChance	Chance for a Non-sense Mutation to occur. The default value is 0.
fSMutationChance	Chance for a Frameshift Mutation to occur. The default value is 0.
lSDeletionChance	Chance for a Large Segment Deletion to occur. The default value is 0.
wChrDeletionChance	Chance for a Whole Chromosome Deletion to occur. The default value is 0.
transposonChance	Chance for a Transposon Mutation to occur. The default value is 0.

randomAssortment
: Random Assortment of Chromosomes for recombinations. The default value is TRUE.

embryonicSelection
: Remove chromosomes with fitness < specified value. The default value is NA.

EveryGeneInInitialPopulation
: Request for every gene to be present in the initial population. The default value is TRUE.

nnetSize
: for nnetI. The default value is NA.

nnetDecay
: for nnetI. The default value is NA.

rdaAlpha
: for rdaI. The default value is NA.

rdaDelta
: for rdaI. The default value is NA.

...
: Additional arguments.

Value

The output is a list containing 5 named vectors, records of the evolution:

DGenes
: The occurrences in selected genotypes for every gene,

dGenes
: The occurrences in discarded genotypes for every gene,

MaximumAccuracy
: Maximum accuracy in every generation,

MeanAccuracy
: Average accuracy in every generation,

MinAccuracy
: Minimum accuracy in every generation,

BestIndividuals
: Best individual in every generation.

Examples

```
## Not run:
 library(genefilter)
 library(ALL)
 data(ALL)
 bALL = ALL[, substr(ALL$BT,1,1) == "B"]
 smallALL = bALL[, bALL$mol.biol %in% c("BCR/ABL", "NEG")]
 smallALL$mol.biol = factor(smallALL$mol.biol)
 smallALL$BT = factor(smallALL$BT)
 f1 <- pOverA(0.25, log2(100))
 f2 <- function(x) (IQR(x) > 0.5)
 f3 <- ttest(smallALL$mol.biol, p=0.1)
 ff <- filterfun(f1, f2, f3)
 selectedsmallALL <- genefilter(exprs(smallALL), ff)
 smallALL = smallALL[selectedsmallALL, ]
 rm(f1)
 rm(f2)
 rm(f3)
 rm(ff)
 rm(bALL)
```

```
sum(selectedsmallALL)

set.seed(149)
res<-dGAselID(smallALL, "mol.biol", trainTest=1:79, startGenes=12, populationSize=200,
              iterations=150, noChr=5, pMutationChance=0.0075, elitism=4)

## End(Not run)
```

Elitism *Elitism*

Description

Operator for elitism.

Usage

```
Elitism(results, elitism, ID)
```

Arguments

results	Results returned by EvaluationFunction().
elitism	Elite population in percentages.
ID	Dominance. The default value is "ID1". Use "ID2" for Incomplete Dominance.

Examples

```
## Not run:
 library(genefilter)
 library(ALL)
 data(ALL)
 bALL = ALL[, substr(ALL$BT,1,1) == "B"]
 smallALL = bALL[, bALL$mol.biol %in% c("BCR/ABL", "NEG")]
 smallALL$mol.biol = factor(smallALL$mol.biol)
 smallALL$BT = factor(smallALL$BT)
 f1 <- pOverA(0.25, log2(100))
 f2 <- function(x) (IQR(x) > 0.5)
 f3 <- ttest(smallALL$mol.biol, p=0.1)
 ff <- filterfun(f1, f2, f3)
 selectedsmallALL <- genefilter(exprs(smallALL), ff)
 smallALL = smallALL[selectedsmallALL, ]
 rm(f1)
 rm(f2)
 rm(f3)
 rm(ff)
 rm(bALL)
 sum(selectedsmallALL)
 set.seed(1357)
```

```
 population0<-InitialPopulation(smallALL, 14, 8, FALSE)
 individuals0<-Individuals(population0)
 results0<-EvaluationFunction(smallALL, individuals0, response="mol.biol",
            method=knn.cvI(k=3, l=2), trainTest="LOG")
 Elitism(results0, 25, ID="ID1")
 Elitism(results0, 25, ID="ID2")

## End(Not run)
```

EmbryonicSelection *EmbryonicSelection*

Description

Function for deleting individuals with a fitness below a specified threshold.

Usage

```
EmbryonicSelection(population, results, embryonicSelection)
```

Arguments

population	Population of individuals with diploid genotypes.
results	Results returned by EvaluationFunction().
embryonicSelection	Threshold value. The default value is NA.

Examples

```
## Not run:
 library(genefilter)
 library(ALL)
 data(ALL)
 bALL = ALL[, substr(ALL$BT,1,1) == "B"]
 smallALL = bALL[, bALL$mol.biol %in% c("BCR/ABL", "NEG")]
 smallALL$mol.biol = factor(smallALL$mol.biol)
 smallALL$BT = factor(smallALL$BT)
 f1 <- pOverA(0.25, log2(100))
 f2 <- function(x) (IQR(x) > 0.5)
 f3 <- ttest(smallALL$mol.biol, p=0.1)
 ff <- filterfun(f1, f2, f3)
 selectedsmallALL <- genefilter(exprs(smallALL), ff)
 smallALL = smallALL[selectedsmallALL, ]
 rm(f1)
 rm(f2)
 rm(f3)
 rm(ff)
 rm(bALL)
 sum(selectedsmallALL)
```

```
 set.seed(1357)

 population0<-InitialPopulation(smallALL, 14, 8, FALSE)
 individuals0<-Individuals(population0)
 results0<-EvaluationFunction(smallALL, individuals0, response="mol.biol",
             method=knn.cvI(k=3, l=2), trainTest="LOG")
 EmbryonicSelection(individuals0, results0, 0.5)

## End(Not run)
```

EvaluationFunction *EvaluationFunction*

Description

Evaluates the individuals' fitnesses.

Usage

```
EvaluationFunction(x, individuals, response, method, trainTest, nnetSize = NA,
  nnetDecay = NA, rdaAlpha = NA, rdaDelta = NA, ...)
```

Arguments

x	Dataset in ExpressionSet format.
individuals	Population of individuals with diploid genotypes.
response	Response variable.
method	Supervised classifier for fitness evaluation. Most of the supervised classifiers in MLInterfaces are acceptable. The default is knn.cvI(k=3, l=2).
trainTest	Cross-validation method. The default is "LOG".
nnetSize	for nnetI. The default value is NA.
nnetDecay	for nnetI. The default value is NA.
rdaAlpha	for rdaI. The default value is NA.
rdaDelta	for rdaI. The default value is NA.
...	Additional arguments.

Examples

```
## Not run:
 library(genefilter)
 library(ALL)
 data(ALL)
 bALL = ALL[, substr(ALL$BT,1,1) == "B"]
 smallALL = bALL[, bALL$mol.biol %in% c("BCR/ABL", "NEG")]
 smallALL$mol.biol = factor(smallALL$mol.biol)
 smallALL$BT = factor(smallALL$BT)
```

```
f1 <- pOverA(0.25, log2(100))
f2 <- function(x) (IQR(x) > 0.5)
f3 <- ttest(smallALL$mol.biol, p=0.1)
ff <- filterfun(f1, f2, f3)
selectedsmallALL <- genefilter(exprs(smallALL), ff)
smallALL = smallALL[selectedsmallALL, ]
rm(f1)
rm(f2)
rm(f3)
rm(ff)
rm(bALL)
sum(selectedsmallALL)
set.seed(1357)

population0<-InitialPopulation(smallALL, 14, 8, FALSE)
individuals0<-Individuals(population0)
results<-EvaluationFunction(smallALL, individuals0, response="mol.biol",
            method=knn.cvI(k=3, l=2), trainTest="LOG")

## End(Not run)
```

`frameShiftMutation` *frameShiftMutation*

Description

Operator for the frameshift mutation.

Usage

```
frameShiftMutation(individuals, chrConf, mutationChance)
```

Arguments

`individuals`	dataset returned by Individuals().
`chrConf`	Configuration of chromosomes returned by splitChromosomes().
`mutationChance`	Chance for a frameshift mutation to occur.

Examples

```
## Not run:
library(ALL)
data(ALL)

demoALL<-ALL[1:12,1:8]

set.seed(1234)
population<-InitialPopulation(demoALL, 4, 9)
individuals<-Individuals(population)
```

```
chrConf<-splitChromosomes(demoALL, 2)
chrConf
individuals

set.seed(123)
frameShiftMutation(individuals, chrConf, 20)

## End(Not run)
```

`Individuals` *Individuals*

Description

Generates individuals with diploid genotypes.

Usage

```
Individuals(population)
```

Arguments

`population`	Population of haploid genotypes.

Examples

```
## Not run:
library(ALL)
data(ALL)

demoALL<-ALL[1:12,1:8]

population02<-InitialPopulation(demoALL, 20, 4, FALSE)
individuals02<-Individuals(population02)

## End(Not run)
```

`InitialPopulation` *InitialPopulation*

Description

Generates an initial randomly generated population of haploid genotypes.

Usage

```
InitialPopulation(x, populationSize, startGenes,
  EveryGeneInInitialPopulation = TRUE)
```

Arguments

x	Dataset in ExpressionSet format.
populationSize	Number of genotypes in initial population.
startGenes	Genes in the genotypes at initialization.
EveryGeneInInitialPopulation	Request for every gene to be present in the initial population. The default value is TRUE.

Examples

```
## Not run:
library(ALL)
data(ALL)

demoALL<-ALL[1:12,1:8]

population01<-InitialPopulation(demoALL, 4, 4)
population02<-InitialPopulation(demoALL, 20, 4, FALSE)

## End(Not run)
```

---

largeSegmentDeletion *largeSegmentDeletion*

Description

Operator for the large segment deletion.

Usage

```
largeSegmentDeletion(individuals, chrConf, mutationChance)
```

Arguments

individuals	dataset returned by Individuals().
chrConf	Configuration of chromosomes returned by splitChromosomes().
mutationChance	Chance for a large segment deletion mutation to occur.

Examples

```
## Not run:
library(ALL)
data(ALL)

demoALL<-ALL[1:12,1:8]

set.seed(1234)
```

```
population<-InitialPopulation(demoALL, 4, 9)
individuals<-Individuals(population)

chrConf<-splitChromosomes(demoALL, 2)
chrConf
individuals

set.seed(123)
largeSegmentDeletion(individuals, chrConf, 20)

## End(Not run)
```

---

nonSenseMutation *nonSenseMutation*

Description

Operator for the nonsense mutation.

Usage

```
nonSenseMutation(individuals, chrConf, mutationChance)
```

Arguments

individuals	dataset returned by Individuals().
chrConf	Configuration of chromosomes returned by splitChromosomes().
mutationChance	Chance for a nonsense mutation to occur.

Examples

```
## Not run:
library(ALL)
data(ALL)

demoALL<-ALL[1:12,1:8]

set.seed(1234)
population<-InitialPopulation(demoALL, 4, 9)
individuals<-Individuals(population)

chrConf<-splitChromosomes(demoALL, 2)
chrConf
individuals

set.seed(123)
nonSenseMutation(individuals, chrConf, 20)

## End(Not run)
```

PlotGenAlg *PlotGenAlg*

Description

Function for graphically representing the evolution.

Usage

```
PlotGenAlg(DGenes, dGenes, maxEval, meanEval)
```

Arguments

DGenes	Occurences of genes as dominant.
dGenes	Occurences of genes as recessive. For future developments.
maxEval	Maximum fitness.
meanEval	Average fitness.

Examples

```
## Not run:
#Graphical representation of the evolution after each generation.
#Intended to be used by dGAselID() only.
#Please refer to the example for dGAselID().

## End(Not run)
```

pointMutation *pointMutation*

Description

Operator for the point mutation.

Usage

```
pointMutation(individuals, mutationChance)
```

Arguments

individuals	dataset returned by Individuals().
mutationChance	chance for a point mutation to occur.

Examples

```
## Not run:
library(ALL)
data(ALL)

demoALL<-ALL[1:12,1:8]

set.seed(1234)
population<-InitialPopulation(demoALL, 4, 9)
individuals<-Individuals(population)

individuals
set.seed(123)
pointMutation(individuals, 4)

## End(Not run)
```

RandomAssortment *RandomAssortment*

Description

Random assortment of chromosomes operator.

Usage

```
RandomAssortment(newChrs, chrConf)
```

Arguments

newChrs	Set of chromosomes.
chrConf	Configuration of chromosomes returned by splitChromosomes().

Examples

```
## Not run:
library(ALL)
data(ALL)

demoALL<-ALL[1:12,1:8]

population02<-InitialPopulation(demoALL, 2, 4, FALSE)
chrConf02<-splitChromosomes(demoALL, 4)

set.seed(1357)
cr1<-Crossover(population02[1,], population02[2,], chrConf02)
RandomAssortment(cr1, chrConf02)
cr1
chrConf02
```

```
## End(Not run)
```

RandomizePop *RandomizePop*

Description

Generates a random population for the next generation.

Usage

```
RandomizePop(population)
```

Arguments

population	Population of chromosome sets in current generation.

Examples

```
## Not run:
library(ALL)
data(ALL)

demoALL<-ALL[1:12,1:8]

population01<-InitialPopulation(demoALL, 4, 4)
population01
RandomizePop(population01)

## End(Not run)
```

---

splitChromosomes *splitChromosomes*

Description

Divides the genotypes into sets with a desired number of chromosomes.

Usage

```
splitChromosomes(x, noChr = 22)
```

Arguments

x	Dataset in ExpressionSet format.
noChr	Desired number of chromosomes. The default value is 22.

Examples

```
## Not run:
library(ALL)
data(ALL)

demoALL<-ALL[1:12,1:8]

splitChromosomes(demoALL, 3)
splitChromosomes(demoALL)


## End(Not run)
```

`transposon` *transposon*

Description

Operator for transposons.

Usage

```
transposon(individuals, chrConf, mutationChance)
```

Arguments

`individuals`	dataset returned by Individuals().
`chrConf`	Configuration of chromosomes returned by splitChromosomes().
`mutationChance`	Chance for a transposon mutation to occur.

Examples

```
## Not run:
library(ALL)
data(ALL)

demoALL<-ALL[1:12,1:8]

set.seed(1234)
population<-InitialPopulation(demoALL, 4, 9)
individuals<-Individuals(population)

chrConf<-splitChromosomes(demoALL, 2)
chrConf
individuals

set.seed(123)
transposon(individuals, chrConf, 20)

## End(Not run)
```

wholeChromosomeDeletion *wholeChromosomeDeletion*

Description

Operator for the deletion of a whole chromosome.

Usage

```
wholeChromosomeDeletion(individuals, chrConf, mutationChance)
```

Arguments

individuals	dataset returned by Individuals().
chrConf	Configuration of chromosomes returned by splitChromosomes().
mutationChance	Chance for a deletion of a whole chromosome mutation to occur.

Examples

```
## Not run:
library(ALL)
data(ALL)

demoALL<-ALL[1:12,1:8]

set.seed(1234)
population<-InitialPopulation(demoALL, 4, 9)
individuals<-Individuals(population)

chrConf<-splitChromosomes(demoALL, 2)
chrConf
individuals

set.seed(123)
wholeChromosomeDeletion(individuals, chrConf, 20)

## End(Not run)
```

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