Package 'statTarget'

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Type Package

Title Statistical Analysis of Molecular Profiles

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Description A streamlined tool provides a graphical user interface for quality control based signal drift correction (QC-RFSC), integration of data from multi-batch MS-based experiments, and the comprehensive statistical analysis in metabolomics and proteomics.

License LGPL (>= 3)

URL https://stattarget.github.io

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Contents

statTarget-package 2
mdsPlot 3
predict_RF 3
pvimPlot 4
rForest 5
shiftCor 6
shiftCor_dQC (deprecated) 7
statAnalysis 8

Index **11**

`statTarget-package` *Statistical Analysis of Molecular Profiles*

Description

An streamlined tool provides graphical user interface for quality control based signal correction, integration of MS-based data from multiple batches, and the comprehensive statistical analysis for omics studies.

Usage

```
statTarget()
```

Details

Package: statTarget

Type: package

License: LGPL (>= 3)

Value

A description of statTarget. See the details at https://stattarget.github.io

Author(s)

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mdsPlot *MDSplot in statTarget*

Description

Multi-dimensional scaling plot of proximity matrix from randomForest.

Usage

```
mdsPlot(rForest,pimpModel,Labels = TRUE,slink = FALSE,
slinkDat, ...)
```

Arguments

rForest	An object of class randomForest that contains the proximity component from statTarget_rForest function.
pimpModel	An object of permutation-based variable Gini importance measures (PIMP-algorithm) from statTarget_rForest function.
Labels	Labels is TRUE for visible the sample name in the figure else with the index for class.
slink	Logical indicating if slinkDat is active for extenal classID.
slinkDat	A data frame for the extenal classID.
...	A generic MDSplot function in randomForest package

Value

The output of cmdscale on 1 - rf$proximity is returned invisibly.

Author(s)

Hemi Luan, hemi.luan@gmail.com

See Also

MDSplot

predict_RF *preidict function for random forest objects in statTarget*

Description

Prediction of test data using random forest in statTarget.

Usage

```
predict_RF(object, newdata, type='response',...)
```

Arguments

object	An object created by the function statTarget_rForest.
newdata	A data frame or matrix containing new data. (Note: If not given, the out-of-bag prediction in object is returned. see randomForest package.
type	One of response, prob. or votes, indicating the type of output: predicted values, matrix of class probabilities, or matrix of vote counts. class is allowed, but automatically converted to 'response', for backward compatibility.
...	A generic predict function from randomForest package.

Value

A class of predicted values is returned. Object type is classification, for detail see randomForest package.

Author(s)

Hemi Luan, hemi.luan@gmail.com

See Also

randomForest

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pvimPlot *Gini importance and permutation-based variable importance measures plots*

Description

Create plots for Gini importance and permutation-based variable Gini importance measures.

Usage

```
pvimPlot(rForest,pimpModel,nvarRF = 6,border= NA,
space = 0.3,...)
```

Arguments

rForest	an object of class randomForest that contains the proximity component from statTarget rForest function.
pimpModel	an object of permutation-based variable Gini importance measures (PIMP-algorithm) from statTarget rForest function.
nvarRF	The number of variables in importance plot of randomForest.
border	The color to be used for the border of the bars. Use border = NA to omit borders. see also barplot.
space	The amount of space (as a fraction of the average bar width) left before each bar. May be given as a single number or one number per bar. see also barplot
...	A generic barplot function from graphics package.

Value

The output of the name of selected variable importance.

Author(s)

Hemi Luan, hemi.luan@gmail.com

Examples

```
datpath <- system.file('extdata',package = 'statTarget')
statFile <- paste(datpath,'data_example_long.csv', sep='/')
getFile <- read.csv(statFile,header=TRUE)
rFtest <- rForest(getFile,ntree = 10,times = 5)
pvimPlot(rFtest$randomForest,rFtest$pimpTest)
```

---

rForest *Random Forest classfication in statTarget*

Description

rForest provides the Breiman's random forest algorithm for classification and permutation-based variable importance measures (PIMP-algorithm).

Usage

```
rForest(file,ntree = 100,times = 100, gDist = TRUE,
seed = 123,...)
```

Arguments

file	An data frame or 'Stat File' from statTarget software.
ntree	Number of trees to grow. This should not be set to too small a number, to ensure that every input row gets predicted at least a few times.
times	The number of permutations for permutation-based variable importance measures.
gDist	If gDist is TRUE the null importance distributions are approximated with Gaussian distributions else with empirical cumulative distributions.
seed	For the same set of random variables and reproducible results.
...	A generic function in randomForest package

Value

Objects Two objects from statTarget_rForest (1. randomForest,rfModel; 2. PIMPresult, pimpModel)

VarImp The original Gini importance

PerVarImp A matrix, where the permuted VarImp measures for the predictor variable.

p-value The probability of observing the original VarImp or a larger value, given the fitted null importance distribution.

p.ks.test The p-values of the Kolmogorov-Smirnov Tests for each row PerVarImp.

Author(s)

Hemi Luan, hemi.luan@gmail.com

References

Altmann A.,Tolosi L.,Sander O. and Lengauer T. (2010) Permutation importance: a corrected feature importance measure, Bioinformatics 26 (10), 1340-1347.

Ender Celik. (2015) vita: Variable Importance Testing Approaches. R package version 1.0.0 https://CRAN.R-project.org/package=vita

Examples

```
datpath <- system.file('extdata',package = 'statTarget')
statFile <- paste(datpath,'data_example_long.csv', sep='/')
getFile <- read.csv(statFile,header=TRUE)
rFtest <- rForest(getFile,ntree = 10,times = 5)
```

`shiftCor` *shiftCor*

Description

shiftCor provides the QC based signal correction for large scale metabolomics and targeted proteomics.

Usage

```
shiftCor(
  samPeno,
  samFile,
  Frule = 0.8,
  MLmethod = "QCRFSC",
  ntree = 500,
  imputeM = "KNN",
  coCV = 30,
  plot = FALSE
)
```

Arguments

`samPeno`	File path. The file with the meta information including the sample name, batches, class and order.
`samFile`	File path. The file with the expression information.
`Frule`	Modified n precent rule function. A variable will be kept if it has a non-zero value for at least n precent of samples in any one group. (Default: 0.8)
`MLmethod`	The machine learning method for QC based signal correction, such as QC based random forest signal correction (QC-RFSC). QC-RLSC was deprecated .
`ntree`	Number of trees to grow in random forest model.

imputeM	The parameter for imputation method i.e., nearest neighbor averaging, 'KNN'; minimum values, 'min'; Half of minimum values, 'minHalf'; median values, 'median'.
coCV	Define the cutoff value (0-100) of CV for controlling the number of features.
plot	Defines if images of feature quality should be generated (TRUE) or not (FALSE). Defaults to FALSE.

Value

the shiftCor files. See the details at https://stattarget.github.io

Examples

```
datpath <- system.file('extdata',package = 'statTarget')
samPeno <- paste(datpath,'MTBLS79_sampleList.csv', sep='/')
samFile <- paste(datpath,'MTBLS79.csv', sep='/')
samPeno
samFile
shiftCor(samPeno,samFile, MLmethod = 'QCRFSC', imputeM = 'KNN',coCV = 30)
```

---

shiftCor_dQC (deprecated)

QC-free based signal correction

Description

shiftCor_dQC provides the QC-free based signal correction for large scale mass spectrometry-based omics data.

Usage

```
shiftCor_dQC(
  samPeno,
  samFile,
  Frule = 0.8,
  imputeM = "KNN",
  MLmethod = "Combat",
  par.prior = TRUE,
  prior.plots = FALSE,
  mod.covariates = FALSE,
  batch.Num = NULL
)
```

Arguments

samPeno	The file with the meta information including the sample name, batches, class and order (denoting other covariates besides batch).
samFile	The file with the expression information.
Frule	Modified n precent rule function. A variable will be kept if it has a non-zero value for at least n precent of samples in any one group. (Default: 0.8)

imputeM	The parameter for imputation method i.e., nearest neighbor averaging, 'KNN'; minimum values, 'min'; Half of minimum values, 'minHalf'; median values, 'median'.
MLmethod	'ComBat' allows users to adjust for batch effects in datasets where the batch covariate is known, using methodology described in Johnson et al. 2007. It uses either parametric or non-parametric empirical Bayes frameworks for adjusting data for batch effects. Users are returned an expression matrix that has been corrected for batch effects.The function was revised accroding to 'sva' package (version = "3.8").
par.prior	TRUE indicates parametric adjustments will be used, FALSE indicates non-parametric adjustments will be used
prior.plots	(Optional) TRUE give prior plots.
mod.covariates	TRUE indicates model matrix for outcome of interest and other covariates besides batch (Column 'order' denotes covariates the in samPeno file).
batch.Num	(Optional) NULL If given, will use the selected batch as a reference for batch adjustment.

Value

the shiftCor files. See the details at https://stattarget.github.io

Examples

```
datpath <- system.file('extdata',package = 'statTarget')
samPeno <- paste(datpath,'MTBLS79_dQC_sampleList.csv', sep='/')
samFile <- paste(datpath,'MTBLS79.csv', sep='/')
shiftCor_dQC(samPeno,samFile, Frule = 0.8, MLmethod = "Combat",mod.covariates = FALSE)
shiftCor_dQC(samPeno,samFile, Frule = 0.8, MLmethod = "Combat",mod.covariates = TRUE,batch.Num = 1)
```

---

statAnalysis *statAnalysis for statistical analysis for omics data or others.*

Description

statAnalysis provides the statistical analysis for metabolomics data or others.

Usage

```
statAnalysis(
  file,
  Frule = 0.8,
  normM = "NONE",
  imputeM = "KNN",
  glog = TRUE,
  FDR = TRUE,
  ntree = 500,
  nvarRF = 5,
  scaling = "Pareto",
  plot.volcano = TRUE,
  save.boxplot = FALSE,
```

```
  silt = 20,
  pcax = 1,
  pcay = 2,
  Labels = TRUE,
  upper.lim = 2,
  lower.lim = 0.5,
  sig.lim = 0.05
)
```

Arguments

file	The file with the expression information with long format
Frule	Modified n precent rule function. A variable will be kept if it has a non-zero value for at least n precent of samples in any one group. (Default: 0.8)
normM	The parameter for normalization method (i.e median quotient normalization, 'PQN'; integral normalization , 'SUM', and 'NONE').
imputeM	The parameter for imputation method i.e., nearest neighbor averaging, 'KNN'; minimum values, 'min'; Half of minimum values, 'minHalf'; median values, 'median'.
glog	Generalised logarithm (glog) transformation, with the default value TRUE. The glog is a better behaved log transformation when some data values are zero or just near zero.
FDR	The false discovery rate for conceptualizing the rate of type I errors in null hypothesis testing when conducting multiple comparisons.
ntree	Number of trees to grow for randomForest model. This should not be set to too small a number, to ensure that every input row gets predicted at least a few times.
nvarRF	The number of the variables with top importance in randomforest model
scaling	Scaling method before statistic analysis (PCA or PLS-DA). 'pareto', 'Pareto', 'p' or 'P' can be used for specifying the Pareto scaling. 'auto', 'Auto', 'auto', 'a' or 'A' can be used for specifying the Auto scaling (or unit variance scaling). 'vast', 'Vast', 'v' or 'V' can be used for specifying the vast scaling. 'range', 'Range', 'r' or 'R' can be used for specifying the Range scaling.
plot.volcano	if TRUE, the volcano plot is performed
save.boxplot	if TRUE, the box plot is performed
silt	The number of permutation for PLS-DA model and variable importance of randomForest.
pcax	Principal components in PCA model for the x-axis.
pcay	Principal components in PCA model for the y-axis.
Labels	Name labels for score plot of multiple statistical analysis
upper.lim	The up-regulated metabolites using Fold Changes cut off values in the Volcano plot. Fold change values will be calculated before normalization step.
lower.lim	The down-regulated metabolites using Fold Changes cut off values in the Volcano plot. Fold change values will be calculated before normalization step.
sig.lim	The significance level for metabolites in the Pvalues file in the Volcano plot.

Value

The statAnalsis output files. See the details at https://stattarget.github.io

Author(s)

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Examples

```
datpath <- system.file('extdata',package = 'statTarget')
file <- paste(datpath,'data_example_long.csv', sep='/')
statAnalysis(file,Frule = 0.8, normM = 'NONE', imputeM = 'KNN', glog = TRUE,scaling = 'Pareto')
```

Index

∗ **Controls,Correction**
    shiftCor, 6
    shiftCor_dQC (deprecated), 7
∗ **P-value**
    statAnalysis, 8
∗ **PCA**
    statAnalysis, 8
∗ **PLSDA**
    statAnalysis, 8
∗ **Quality**
    shiftCor, 6
    shiftCor_dQC (deprecated), 7

mdsPlot, 3

predict_RF, 3
pvimPlot, 4

rForest, 5

shiftCor, 6
shiftCor_dQC *(*shiftCor_dQC
        (deprecated)*)*, 7
shiftCor_dQC (deprecated), 7
statAnalysis, 8
statTarget *(*statTarget-package*)*, 2
statTarget-package, 2