Package 'SafeQuant'

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Type Package

Title SafeQuant: Proteomics Data Analysis

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Description The SafeQuant Package includes methods for analysis of quantitative Proteomics data. More documentation to come.

Imports affy,
limma,
gplots,
seqinr,
corrplot,
optparse,
data.table,
epiR

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R topics documented:

`addIdQvalues` *Add identification leve q-values to ExpressionSet (calculated based on target-decoy score distribution)*

Description

Add identification leve q-values to ExpressionSet (calculated based on target-decoy score distribution)

Usage

```
addIdQvalues(eset = eset)
```

Arguments

`eset`	ExpressionSet

Details

if ptm column is part if the ExpressionSet q-values are calculated seperately for modified and non-modified features

Value

ExpressionSet object

Note

No note

See Also

`getIdLevelQvals`

Examples

```
print("No examples")
```

`barplotMSSignal` *Barplot of ms-signal per column*

Description

Barplot of ms-signal per column

Usage

```
barplotMSSignal(eset,
  col = as.character(.getConditionColors(eset)[pData(eset)$condition, ]),
  method = "sum", cex.lab = 1.25, cex.axis = 1.25,
  labels = rownames(pData(eset)), ...)
```

Arguments

matrix	matrix of ms-signals
color	color

Details

No details

Note

No note

References

NA

Examples

```
print("No examples")
```

---

createCalibrationCurve

S3 class object describing a calibration curve and storing some figures of merit

---

Description

S3 class object describing a calibration curve and storing some figures of merit

Usage

```
createCalibrationCurve(eset, method = "blank")
```

Arguments

eset	ExpressionSet
method	to calculate Limit of Detection / Limit of Quantification. c("blank","low")

Details

No details

Value

calibrationCurve object

Note

No note

References

Statistical characterization of multiple-reaction monitoring mass spectrometry (MRM-MS) assays for quantitative proteomics, Mani et al. (2012), http://www.ncbi.nlm.nih.gov/pubmed/23176545

Examples

```
print("No examples")
```

`createExpDesign` *Create Experimental Design*

Description

Create Experimental Design

Usage

```
createExpDesign(tag, nbPlex)
```

Arguments

`tag`	user input tag e.g. 1,2,3:4,5,6 indicating two condition with 3 reps each
`nbPlex`	tmt 6 or 10 plex

Details

The first listed condition is always the control condition

Value

expDesign data.frame

Note

No note

References

NA

Examples

```
print("No examples")
```

`createExpressionDataset` *Create ExpressionSet object*

Description

Create ExpressionSet object

Usage

```
createExpressionDataset(expressionMatrix = expressionMatrix,
  expDesign = expDesign, featureAnnotations = featureAnnotations)
```

Arguments

`expressionMatrix`	matrix of expression signals per feature and sample
`expDesign`	experimental design data.frame
`featureAnnotations`	data.frame including e.g: Protein Description, Id score etc.

Details

No details

Value

ExpressionSet object

Note

No note

References

NA

See Also

`ExpressionSet`

Examples

```
print("No examples")
```

cvBoxplot *C.V. boxplot*

Description

C.V. boxplot

Usage

```
cvBoxplot(eset,
  col = as.character(.getConditionColors(eset)[unique(pData(eset)$condition),
  ]), cex.names = 0.9, cex.axis = 1.25, cex.lab = 1.25, ...)
```

Arguments

eset	ExpressionSet

Details

No details

Note

No note

References

NA

Examples

```
print("No examples")
```

expDesignTagToExpDesign *Create experimental design data.frame from user input string*

Description

Create experimental design data.frame from user input string

Usage

```
expDesignTagToExpDesign(tag, expDesignDefault)
```

Arguments

string	tag
data.frame	default expDesign

Details

tag: 1,2:3:4,5,6 condition isControl 1 Condition 1 TRUE 2 Condition 1 TRUE 3 Condition 1 TRUE 4 Condition 2 FALSE 5 Condition 2 FALSE 6 Condition 2 FALSE

Value

data.frame describing experimental design

Note

No note

References

NA

Examples

```
print("No examples")
```

`export.safeQuantAnalysis` *Export content of safeQuantAnalysis object*

Description

Export content of safeQuantAnalysis object

Usage

```
## S3 method for class 'safeQuantAnalysis'
export(sqa, nbRows = nrow(sqa$pValue),
  file = NA)
```

Arguments

`sqa`	safeQuantAnalysis object
`nbRows`	Number of rows to export. Features are ordred by increasing minimal p.value

Details

NA

Note

No note

References

NA

See Also

safeQuantAnalysis

Examples

```
print("No examples")
```

`getAllCV` *Calculate Coefficiant of Variance per feature (Relative standard Deviation) per Condition*

Description

Calculate Coefficiant of Variance per feature (Relative standard Deviation) per Condition

Usage

```
getAllCV(eset)
```

Arguments

`eset`	ExpressionSet

Details

CV = sd / mean

Value

data.frame of CVs per condition

Note

No note

References

NA

See Also

getCV

Examples

```
print("No examples")
```

`getAllEBayes` *Perform statistical test (mderated t-test), comparing all case to control*

Description

Perform statistical test (mderated t-test), comparing all case to control

Usage

```
getAllEBayes(eset = eset, adjust = F, log = T, method = "pairwise")
```

Arguments

`eset`	ExpressionSet
`adjust`	TRUE/FALSE adjust for multiple testing using Benjamini & Hochberg (1995) method log T/F log-transform expression values
`method`	c("pairwise","all")

Details

No details

Value

ExpressionSet object

Note

No note

References

Empirical Bayes method, Smyth (2004), http://www.ncbi.nlm.nih.gov/pubmed/16646809

See Also

`eBayes`

Examples

```
print("No examples")
```

getBaselineIntensity *Get signal at zscore x (x standard deviations below mean)*

Description

Get signal at zscore x (x standard deviations below mean)

Usage

```
getBaselineIntensity(intensities, promille = 5)
```

Arguments

intensities	refrence run signals
percentile	baseline value set as specified promille

Value

baseline value

Note

No note

References

NA

Examples

```
print("No examples")
```

getCV *Calculate Coefficiant of Variance per feature (Relative standard Deviation)*

Description

Calculate Coefficiant of Variance per feature (Relative standard Deviation)

Usage

```
getCV(data)
```

Arguments

data	data.frame of replicate signals

Details

CV = sd / mean

Value

vector of CVs

Note

No note

References

NA

Examples

```
print("No examples")
```

`getExpDesignProgenesisCsv` *Parse Experimental Design from Progenesis Csv Export*

Description

Parse Experimental Design from Progenesis Csv Export

Usage

```
getExpDesignProgenesisCsv(file,
  expressionColIndices = .getProgenesisCsvExpressionColIndices(file))
```

Arguments

`file`	path to progenesis csv file

Details

No details

Value

data.frame describing experimental design

Note

No note

References

NA

Examples

```
print("No examples")
```

`getGlobalNormFactors` *Get normalization factors. calculated as summed/median signal per run (column) over summed/median of first run.*

Description

Get normalization factors. calculated as summed/median signal per run (column) over summed/median of first run.

Usage

```
getGlobalNormFactors(eset, method = "sum")
```

Arguments

`eset`	ExpressionSet

Details

No details

Value

vector of normalization factors

Note

No note

References

NA

Examples

```
print("No examples")
```

`getIBAQEset` *Calculate intensity-based absolute-protein-quantification (iBAQ) metric per protein*

Description

Calculate intensity-based absolute-protein-quantification (iBAQ) metric per protein

Usage

```
getIBAQEset(eset, proteinDB = NA, peptideLength = c(5, 36),
  nbMiscleavages = 0, proteaseRegExp = .getProteaseRegExp("trypsin"))
```

Arguments

eset	protein level ExpressionSet
peptideLength	peptide length interval (to get number of peptides used for normalization)
nbMiscleavages	number of mis-cleavages allowed when digesting protein sequneces in silico (to get number of peptides used for normalization)
proteaseRegExp	protease Reg Exp cleavage rule
list	protein sequneces

Details

No details

Value

ExpressionSet

Note

No note

References

Global quantification of mammalian gene expression control, Schwanhausser (2011), http://www.ncbi.nlm.nih.gov/pubmed/21593866, Critical assessment of proteome-wide label-free absolute abundance estimation strategies. Ahrne (2013), http://www.ncbi.nlm.nih.gov/pubmed/23794183

Examples

```
print("No examples")
```

---

getIdLevelQvals — *Calculates identification level q-values based on target-decoy score distributions*

Description

Calculates identification level q-values based on target-decoy score distributions

Usage

```
getIdLevelQvals(scores, isDecoy)
```

Arguments

scores	peptide/protein identficationscore
isDecoy	vector of TRUE/FALSE

Details

q-value = (Nb. Decoy Entries at idScore Threshold S*) / (Nb. Target Entries at idScore Threshold S). (* idScore >= S)

Value

vector of q.values

Note

No note

References

NA

Examples

```
print("No examples")
```

`getImpuritiesMatrix` *Get Thermo TMT impurity matrix*

Description

Get Thermo TMT impurity matrix

Usage

```
getImpuritiesMatrix(plexNb = 6, test = F)
```

Arguments

`plexNb`	integer, 6 or 10 plex

Details

No details

Value

impurity matrix matrix

Note

No note

References

NA

Examples

```
print("No examples")
```

`getIntSumPerProtein` *Sum up raw intensities per protein and channel. keep track of number of summed spectra and unique peptides*

Description

Sum up raw intensities per protein and channel. keep track of number of summed spectra and unique peptides

Usage

```
getIntSumPerProtein(intData, proteinACs, peptides, minNbPeptPerProt = 1)
```

Arguments

`intData`	data.frame of intensities per channel
`proteinACs`	vector of protein accession numbers
`peptides`	vector of peptide sequneces
`minNbPeptPerProt`	minimal number of peptides per protein

Details

NA

Value

list containing 3 objects 1) data.frame of channel intensities per protein ac, 2) vector listing number of summed spectra per protein, 3) vector listing number of summed peptides per protein

Note

No note

References

NA

Examples

```
print("No examples")
```

getLoocvFoldError *Leave-One-Out Cross Validate Qunatification Model*

Description

Leave-One-Out Cross Validate Qunatification Model

Usage

```
getLoocvFoldError(df)
```

Arguments

data.frame	of two columns 1) "signal" - ms metric 2) "cpc" absolute quantity

Details

No details

Value

data.frame of fold errors per (left-out) protein

Note

No note

References

NA

See Also

NA

Examples

```
print("No examples")
```

getMeanCenteredRange *Get modification coordinates on protein*

Description

Get modification coordinates on protein

Usage

```
getMeanCenteredRange(d, nbSd = 4)
```

Arguments

d	numeric vector
nbSd	range spanning number of sd frmo mean

Details

NA

Value

vector range boundries

Note

No note

References

NA

Examples

```
print("No examples")
```

getModifProteinCoordinates *Get modification coordinates on protein*

Description

Get modification coordinates on protein

Usage

```
getModifProteinCoordinates(modifAnnot, peptideSeq, proteinSeq)
```

Arguments

modifAnnot	modifcation as annotated by progenesis. E.g. '[15] Phospho (ST)|[30] Phospho (ST)'
peptideSeq	peptide sequence
proteinSeq	protein sequence

Details

NA

Value

vector of protein coordinates (mmodification residue number)

Note

No note

References

NA

Examples

```
print("No examples")
```

---

getMotifX *Create motif-x peptide annotation*

Description

Create motif-x peptide annotation

Usage

```
getMotifX(modifPos, peptide, proteinSeq, motifLength = 4)
```

Arguments

modifPos	vector positions
peptide	peptide sequence
proteinSeq	protein sequence
motifLength	motif flanking sequence

Details

motif-x example PGDYS*TTPG

Value

vector of motifs

Note

No note

References

NA

Examples

```
print("No examples")
```

`getNbDetectablePeptides` *Get number peptides passing defined length criteria*

Description

Get number peptides passing defined length criteria

Usage

```
getNbDetectablePeptides(peptides, peptideLength = c(5, 36))
```

Arguments

`peptides`	list of peptides
`vector`	of two integers defining peptide length range

Details

No details

Value

integer corresponding to number of detectable peptides

Note

No note

Examples

```
print("No examples")
```

getNbMisCleavages *Get number of mis-cleavages perp peptide*

Description

Get number of mis-cleavages perp peptide

Usage

```
getNbMisCleavages(peptide, protease = "trypsin")
```

Arguments

peptide	character vector
protease	regular expression

Details

NA

Value

vector ofintegers

Note

No note

References

NA

Examples

```
print("No examples")
```

getNbPeptidesPerProtein *Get number of peptides per protein*

Description

Get number of peptides per protein

Usage

```
getNbPeptidesPerProtein(eset)
```

Arguments

eset	ExpressionSet

Details

NA

Value

table

Note

No note

References

NA

Examples

```
print("No examples")
```

---

getPeptides *Digest protein*

Description

Digest protein

Usage

```
getPeptides(proteinSeq, proteaseRegExp = .getProteaseRegExp("trypsin"),
  nbMiscleavages = 0)
```

Arguments

proteinSeq	protein sequence

Details

No details

Value

vector of peptides

Note

No note

Examples

```
print("No examples")
```

getRatios *Calculate ratios, comparing all case to control*

Description

Calculate ratios, comparing all case to control

Usage

```
getRatios(eset, method = "median", log2 = T)
```

Arguments

eset	ExpressionSet
method	median or mean

Details

No details

Value

ExpressionSet object

Note

No note

References

NA

Examples

```
print("No examples")
```

getRTNormFactors *Get retentiontime base normalization factors*

Description

Get retentiontime base normalization factors

Usage

```
getRTNormFactors(eset, minFeaturesPerBin = 100)
```

Arguments

eset	ExpressionSet
minFeaturesPerBin	minumum number of features per bin. If nb. features are < minFeaturesPerBin -> include neighbouring bins.

Details

No details

Value

data.frame normalization factors per retention time bin (minute)

Note

No note

References

In Silico Instrumental Response Correction Improves Precision of Label-free Proteomics and Accuracy of Proteomics-based Predictive Models, Lyutvinskiy et al. (2013), http://www.ncbi.nlm.nih.gov/pubmed/23589346

Examples

```
print("No examples")
```

---

getScoreCutOff *Get score cutoff for a given fdr cut-off*

Description

Get score cutoff for a given fdr cut-off

Usage

```
getScoreCutOff(scores, isDecoy, fdrCutOff = 0.01)
```

Arguments

scores	peptide/protein identficationscore
isDecoy	vector of TRUE/FALSE
fdrCutOff	[0,1]

Details

NA

Value

scoreCutoff

Note

No note

References

NA

Examples

```
print("No examples")
```

`getSignalPerCondition` *Summarize replicate signal per condition (min)*

Description

Summarize replicate signal per condition (min)

Usage

```
getSignalPerCondition(eset, method = "median")
```

Arguments

`method`	median (default), mean, max, min, sd
`data`	data.frame of replicate signals

Details

No details

Value

data.frame of per condition signals

Note

No note

References

NA

Examples

```
print("No examples")
```

getTopX *Roll up feature intensites per unique colum combination*

Description

Roll up feature intensites per unique colum combination

Usage

```
getTopX(entryData, topX = 3)
```

Arguments

entryData	data.frame listing feature intensities of one entry Typically rows corresponds to Peptide entries of one protein
topX	best X flyers
eset	ExpressionSet
featureDataColumnName	vector of column names e.g. peptide or proteinName
method	"sum", "mean" or "top3"
isProgressBar	TRUE/FALSE display progress bar

Details

featureDataColumnName = c("peptide","charge","ptm"), method= c("sum"), sums up intensities per peptie modification charge state

Value

ExpressionSet object

vector of topX intensities per column (sample)

Note

No note

No note

References

No references

Absolute quantification of proteins by LCMSE: A virtue of parallel MS acquisition, Silva (2006), http://www.ncbi.nlm.nih.gov/pubmed/16219938, Critical assessment of proteome-wide label-free absolute abundance estimation strategies. Ahrne (2013), http://www.ncbi.nlm.nih.gov/pubmed/23794183

See Also

topX

Examples

```
print("No examples")
Calculate Mean of X most intense features
```

`getUserOptions` *Read User Specified Command Line Options*

Description

Read User Specified Command Line Options

Usage

```
getUserOptions(version = version)
```

Arguments

`version`	Safequant version number

Details

No details

Value

user options list

Note

No note

References

NA

Examples

```
print("No examples")
```

`globalNormalize` *Normalize, Norm factors calculated as median signal per run (column) over median of first run.*

Description

Normalize, Norm factors calculated as median signal per run (column) over median of first run.

Usage

```
globalNormalize(eset, globalNormFactors)
```

Arguments

`eset`	ExpressionSet

Details

No details

Value

eset ExpressionSet

Note

No note

References

NA

See Also

getGlobalNormFactors

Examples

```
print("No examples")
```

hClustHeatMap — *Hierarchical clustering heat map, cluster by runs intensity, features by ratio and display log2 ratios to control median*

Description

Hierarchical clustering heat map, cluster by runs intensity, features by ratio and display log2 ratios to control median

Usage

```
hClustHeatMap(eset, conditionColors = .getConditionColors(eset),
  breaks = seq(-2, 2, length = 20), ...)
```

Arguments

eset	ExpressionSet
conditionColors	data.frame of colors per condition

Details

No details

Note

No note

References

NA

Examples

```
print("No examples")
```

isCon — *Check if protein is a contaminant entry*

Description

Check if protein is a contaminant entry

Usage

```
isCon(ac)
```

Arguments

ac	vector of protein accession numbers

Details

contanminants proteins are typically annotated as: CON_P0000

Value

vector TRUE/FALSE

Note

No note

References

NA

Examples

```
print("No examples")
```

---

isDecoy *Check if protein is a decoy entry*

Description

Check if protein is a decoy entry

Usage

```
isDecoy(ac)
```

Arguments

ac	vector of protein accession numbers

Details

decoy proteins are typically annotated as: REV_P0000

Value

vector TRUE/FALSE

Note

No note

References

NA

Examples

```
print("No examples")
```

`isStrippedACs` *Check if ACs are in "non-stripped" uniprot format e.g. "sp|Q8CHJ2|AQP12_MOUSE"*

Description

Check if ACs are in "non-stripped" uniprot format e.g. "sp|Q8CHJ2|AQP12_MOUSE"

Usage

```
isStrippedACs(acs)
```

Arguments

`acs`	accession numbers

Details

TRUE if less than 10

Value

boolean TRUE/FALSE

Note

No note

References

NA

Examples

```
print("No examples")
```

`missinValueBarplot` *Plot Percentage of Features with with missing values*

Description

Plot Percentage of Features with with missing values

Usage

```
missinValueBarplot(eset,
  col = as.character(.getConditionColors(eset)[pData(eset)$condition, ]),
  cex.axis = 1.25, cex.lab = 1.25, ...)
```

Arguments

eset	ExpressionSet

Details

No details

Note

No note

References

NA

Examples

```
print("No examples")
```

---

pairsAnnot *Plot lower triangle Pearsons R^2. Diagonal text, upper triangle all against all scatter plots with lm abline*

Description

Plot lower triangle Pearsons R^2. Diagonal text, upper triangle all against all scatter plots with lm abline

Usage

```
pairsAnnot(data, textCol = rep(1, ncol(data)), diagText = c(),
  col = rgb(0, 100, 0, 50, maxColorValue = 255), ...)
```

Arguments

data	data.frame

Details

No details

Note

No note

References

NA

Examples

```
print("No examples")
```

`parseMaxQuantProteinGroupTxt` *Parse MaxQuant Protein Group Txt*

Description

Parse MaxQuant Protein Group Txt

Usage

```
parseMaxQuantProteinGroupTxt(file = file, expDesign = expDesign,
  method = "auc")
```

Arguments

`file`	path to MaxQuant Protein txt file
`expDesign`	experimental design data.frame
`method`	auc (area under curve) or spc (spectral count)

Details

No details

Value

ExpressionSet object

Note

No note

References

NA

See Also

`ExpressionSet`

Examples

```
print("No examples")
```

parseProgenesisFeatureCsv *Parse Progenesis Feature Csv Export*

Description

Parse Progenesis Feature Csv Export

Usage

```
parseProgenesisFeatureCsv(file = file,
  expDesign = getExpDesignProgenesisCsv(file), method = "auc")
```

Arguments

file	path to Progenesis Feature csv file
expDesign	experimental design data.frame
method	auc (area under curve) or spc (spectral count)

Details

No details

Value

ExpressionSet object

Note

No note

References

NA

See Also

ExpressionSet

Examples

```
print("No examples")
```

parseProgenesisPeptideMeasurementCsv
Parse Progenesis Peptide Measurement Csv Export

Description

Parse Progenesis Peptide Measurement Csv Export

Usage

```
parseProgenesisPeptideMeasurementCsv(file, expDesign = expDesign,
  method = "auc",
  expressionColIndices = .getProgenesisCsvExpressionColIndices(file, method =
  method))
```

Arguments

file	path to Progenesis Peptide Measurement csv file
expDesign	experimental design data.frame
method	auc (area under curve) or spc (spectral count)

Details

No details

Value

ExpressionSet object

Note

No note

References

NA

See Also

ExpressionSet

Examples

```
print("No examples")
```

parseProgenesisProteinCsv *Parse Progenesis Protein Csv*

Description

Parse Progenesis Protein Csv

Usage

```
parseProgenesisProteinCsv(file = file, expDesign = expDesign,
  method = "auc")
```

Arguments

file	path to Progenesis Protein csv file
expDesign	experimental design data.frame
method	auc (area under curve) or spc (spectral count)

Details

No details

Value

ExpressionSet object

Note

No note

References

NA

See Also

ExpressionSet

Examples

```
print("No examples")
```

`parseScaffoldRawFile` *Parse scaffold output .xls file (RAW export)*

Description

Parse scaffold output .xls file (RAW export)

Usage

```
parseScaffoldRawFile(fileName, expDesign = expDesign,
  keepFirstAcOnly = FALSE, isPurityCorrect = T)
```

Arguments

`expDesign`	experimental design data.frame
`keepFirstAcOnly`	TRUE/FALSE If multiple ACs in Accession.Numbers filed. Then keep the first one only
`file`	path to Scaffold file

Details

No details

Value

ExpressionSet object

Note

No note

References

NA

See Also

`ExpressionSet`

Examples

```
print("No examples")
```

perFeatureNormalization *Per Feature Normalization*

Description

Per Feature Normalization

Usage

```
perFeatureNormalization(eset, normFactors)
```

Arguments

eset	ExpressionSet
matrix	normalization factors (logged) (row names are proteins)

Details

Example Usage: Normalize phospho peptide signals for Protein Changes

Value

ExpressionSet object

Note

No note

References

No references

See Also

topX

Examples

```
print("No examples")
```

plotAbsEstCalibrationCurve *Plot absolut Estimation calibration Curve*

Description

Plot absolut Estimation calibration Curve

Usage

```
plotAbsEstCalibrationCurve(fit, dispElements = c("formula", "lowess",
  "stats"), xlab = "Conc. (CPC) ", ylab = "Pred. Conc. (CPC) ",
  predictorName = paste("log10(", names(coef(fit))[2], ")", sep = ""),
  text = F, cex.lab = 1, cex.axis = 1, cex.text = 1, cex.dot = 1, ...,
  main = "")
```

Arguments

fit	simple log-linear model
dispElements	c("formula","lowess","stats")
cex.lab=	expansion factor for axis labels
cex.axis=	expansion factor for axis
cex.text=	expansion factor for legend
cex.dot=	expansion factor for plotted dots

Note

No note

References

NA

Examples

```
print("No examples")
```

plotExpDesign *Display experimental design, high-lighting the control condition*

Description

Display experimental design, high-lighting the control condition

Usage

```
plotExpDesign(eset, condColors = .getConditionColors(eset), version = "X")
```

Arguments

eset	ExpressionSet

Details

No details

Note

No note

References

NA

Examples

```
print("No examples")
```

---

plotIdScoreVsFDR *Plot FDR vs. identification score*

Description

Plot FDR vs. identification score

Usage

```
plotIdScoreVsFDR(idScore, qvals, qvalueThrs = 0.01,
  ylab = "False Discovery Rate", xlab = "Identification Score", lwd = 1.5,
  ...)
```

Arguments

idScore	vector of identification scores
qvals	vector of q-valres
qvalueThrs	threshold indicated by horizontal line

Details

No details

Note

No note

References

NA

Examples

```
print("No examples")
```

plotMSSignalDistributions
Plot ms.signal distributions

Description

Plot ms.signal distributions

Usage

```
plotMSSignalDistributions(d, col = 1:100, cex.axis = 1, cex.lab = 1,
  ylab = "Frequnecy", xlab = "MS-Signal", ...)
```

Arguments

matrix	matrix of ms-signals
color	color

Details

No details

Note

No note

References

NA

Examples

```
print("No examples")
```

plotNbIdentificationsVsRT
Plot the number of identified Features per Reteintion Time minute.

Description

Plot the number of identified Features per Reteintion Time minute.

Usage

```
plotNbIdentificationsVsRT(eset, cex.axis = 1.25, cex.lab = 1.25,
  col = "blue", lwd = 2, ...)
```

Arguments

eset	ExpressionSet

Note

No note

References

NA

Examples

```
print("No examples")
```

`plotNbValidDeFeaturesPerFDR` *Plot Total Number of diffrentially Abundant Features (applying ratio cutoff) vs. qValue/pValue for all conditions*

Description

Plot Total Number of diffrentially Abundant Features (applying ratio cutoff) vs. qValue/pValue for all conditions

Usage

```
plotNbValidDeFeaturesPerFDR(sqa, upRegulated = T, log2RatioCufOff = log2(1),
  pvalRange = c(0, 0.3), pvalCutOff = 1, isLegend = T, isAdjusted = T,
  ylab = "Nb. Features", ...)
```

Arguments

`sqa`	SafeQuantAnalysis Object
`upRegulated`	TRUE/FALSE select for upregulated features
`log2RatioCufOff`	log2 ratio cut-off
`pvalRange`	pValue/qValue range
`pvalCutOff`	pValue/qValue cut-off
`isLegend`	TRUE/FALSE display legend
`isAdjusted`	TRUE/FALSE qValues/pValue on x-axis

Details

No details

Note

No note

References

NA

Examples

```
print("No examples")
```

`plotPrecMassErrorDistrib` *Plot Precursor Mass Error Distribution*

Description

Plot Precursor Mass Error Distribution

Usage

```
plotPrecMassErrorDistrib(eset, pMassTolWindow = c(-10, 10), ...)
```

Arguments

`eset`	ExpressionSet
`pMassTolWindow`	Precursor Mass Error Tolerance Window

Details

No details

Note

No note

References

NA

Examples

```
print("No examples")
```

`plotPrecMassErrorVsScore` *Plot precursorMass error v.s score highlighting decoy and displaying user specified user specified precursor mass filter*

Description

Plot precursorMass error v.s score highlighting decoy and displaying user specified user specified precursor mass filter

Usage

```
plotPrecMassErrorVsScore(eset, pMassTolWindow = c(-10, 10), ...)
```

Arguments

eset	ExpressionSet
pMassTolWindow	Precursor Mass Error Tolerance Window

Details

No details

Note

No note

References

NA

Examples

```
print("No examples")
```

---

plotROC *Plot Number of Identifications vs. FDR*

Description

Plot Number of Identifications vs. FDR

Usage

```
plotROC(qvals, qvalueThrs = 0.01, xlab = "False Discovery Rate",
  ylab = "# Valid Identifications", xlim = c(0, 0.1), breaks = 100,
  col = "blue", lwd = 1.5, ...)
```

Arguments

qvals	vector of q-values
qvalueThrs	threshold indicated by vertical line
breaks	see breaks for hist function

Details

No details

Note

No note

References

NA

Examples

```
print("No examples")
```

`plotRTNorm` *Plot all retention time profile overalying ratios*

Description

Plot all retention time profile overalying ratios

Usage

```
plotRTNorm(rtNormFactors, eset, samples = 1:ncol(rtNormFactors), main = "",
  ...)
```

Arguments

`rtNormFactors`	data.frame of normalization factor per r.t bin and sample, obtained by getRTNormFactors
`eset`	ExprsssionSet
`samples`	specify samples (sample numbers) to be plotted

Details

No details

Note

No note

References

In Silico Instrumental Response Correction Improves Precision of Label-free Proteomics and Accuracy of Proteomics-based Predictive Models, Lyutvinskiy et al. (2013), http://www.ncbi.nlm.nih.gov/pubmed/23589346

See Also

`getRTNormFactors`

Examples

```
print("No examples")
```

`plotRTNormSummary` *Plot all retention time normalization profiles*

Description

Plot all retention time normalization profiles

Usage

```
plotRTNormSummary(eset,
  col = as.character(.getConditionColors(eset)[pData(eset)$condition, 1]),
  ...)
```

Arguments

`rtNormFactors`	data.frame of normalization factor per r.t bin and sample, obtained by getRTNormFactors
`condNames`	vector of condition names

Details

No details

Note

No note

References

In Silico Instrumental Response Correction Improves Precision of Label-free Proteomics and Accuracy of Proteomics-based Predictive Models, Lyutvinskiy et al. (2013), http://www.ncbi.nlm.nih.gov/pubmed/23589346

See Also

`getRTNormFactors`

Examples

```
print("No examples")
```

`plotScoreDistrib` *Plot identifications target decoy distribution*

Description

Plot identifications target decoy distribution

Usage

```
plotScoreDistrib(targetScores, decoyScores, xlab = "Identification Score",
  ylab = "Counts", ...)
```

Arguments

`targetScores`

`decoyScores`

Details

No details

Note

No note

References

NA

Examples

```
print("No examples")
```

`plotVolcano` *Plots volcano, data points colored by max cv of the 2 compared conditions*

Description

Plots volcano, data points colored by max cv of the 2 compared conditions

Usage

```
plotVolcano(obj, ratioThrs = 1, pValueThreshold = 0.01, adjusted = T, ...)
```

Arguments

obj	safeQuantAnalysis object or data.frame
adjusted	TRUE/FALSE plot qValues or pValues on y-axis
ratioCutOffAbsLog2	ratio abline
absLog10pValueCutOff	pValue abline

Details

data.frame input object should contain 3 columns (ratio,qValue,cv)

Note

No note

References

NA

Examples

```
print("No examples")
```

---

plotXYDensity *Scatter plot with density coloring*

Description

Scatter plot with density coloring

Usage

```
plotXYDensity(x, y, isFitLm = T, legendPos = "bottomright",
  disp = c("abline", "R", "Rc"), ...)
```

Arguments

x	number vector
y	number vector

Note

No note

References

NA

Examples

```
print("No examples")
```

`print.safeQuantAnalysis` *Print content of safeQuantAnalysis object*

Description

Print content of safeQuantAnalysis object

Usage

```
## S3 method for class 'safeQuantAnalysis'
print(sqa)
```

Arguments

`sqa`	safeQuantAnalysis object

Details

NA

Note

No note

References

NA

See Also

`safeQuantAnalysis`

Examples

```
print("No examples")
```

`purityCorrectTMT` *Correct channel intensities based on Reporter ion Isotopic Distributions*

Description

Correct channel intensities based on Reporter ion Isotopic Distributions

Usage

```
purityCorrectTMT(tmtData, impurityMatrix = impurityMatrix,
  invalidReplace = "allNA")
```

Arguments

tmtData	data.frame containing tmt channel intensities
method	to deal with NA and negative values c("","allZero","allNA","allOrg")

Details

Same method as MSnbase, and described in Breitwieser et al. 2012 (Book Chapter)

Value

data.frame of corrected tmt intensities

Note

No note

References

NA

Examples

```
print("No examples")
```

---

removeOutliers *Set value to NA if it deviatves with more than 1.5 * IQR from lower/upper quantile*

Description

Set value to NA if it deviatves with more than 1.5 * IQR from lower/upper quantile

Usage

```
removeOutliers(x, na.rm = TRUE, ...)
```

Arguments

vector	numeric
a	logical indicating whether missing values should be removed.

Details

No details

Value

vector numeric

Note

No note

References

NA

See Also

NA

Examples

```
print("No examples")
```

`rollUp` *Roll up feature intensites per unique colum combination*

Description

Roll up feature intensites per unique colum combination

Usage

```
rollUp(eset, method = "sum", featureDataColumnName = c("proteinName"))
```

Arguments

`eset`	ExpressionSet
`method`	"sum", "mean" or "top3"
`featureDataColumnName`	vector of column names e.g. peptide or proteinName

Details

featureDataColumnName = c("peptide","charge","ptm"), method= c("sum"), sums up intensities per peptie modification charge state

Value

ExpressionSet object

Note

No note

References

No references

See Also

`topX`

Examples

```
print("No examples")
```

`rtNormalize` *Normalization data per retention time bin*

Description

Normalization data per retention time bin

Usage

```
rtNormalize(eset, rtNormFactors)
```

Arguments

`eset`	ExpressionSet
`rtNormFactors`	obtained using getRTNormFactors

Details

Normalize for variations in elelctrospray ionization current.

Value

data.frame normalization factors per retention time bin (minute)

Note

No note

References

In Silico Instrumental Response Correction Improves Precision of Label-free Proteomics and Accuracy of Proteomics-based Predictive Models, Lyutvinskiy et al. (2013), http://www.ncbi.nlm.nih.gov/pubmed/23589346

See Also

`getRTNormFactors`

Examples

```
print("No examples")
```

`setNbPeptidesPerProtein` *Set nbPeptides coulmn of featureData*

Description

Set nbPeptides coulmn of featureData

Usage

```
setNbPeptidesPerProtein(eset)
```

Arguments

`eset`	ExpressionSet

Details

NA

Value

eset

Note

No note

References

NA

Examples

```
print("No examples")
```

`sqNormalize` *Normalize*

Description

Normalize

Usage

```
sqNormalize(eset, method = "global")
```

Arguments

`eset`	ExpressionSet
`method`	c("global","rt")

Details

No details

Value

eset ExpressionSet

Note

No note

References

NA

See Also

getGlobalNormFactors, getRTNormFactors

Examples

```
print("No examples")
```

---

stripACs *strip uniprot format e.g. "sp|Q8CHJ2|AQP12_MOUSE" -> Q8CHJ2*

Description

strip uniprot format e.g. "sp|Q8CHJ2|AQP12_MOUSE" -> Q8CHJ2

Usage

```
stripACs(acs)
```

Arguments

acs	accession numbers

Details

TRUE if less than 10

Value

vector character

Note

No note

References

NA

Examples

```
print("No examples")
```

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