Package ‘msmsEDA’

January 30, 2017

Type Package
Title Exploratory Data Analysis of LC-MS/MS data by spectral counts
Version 1.12.0
Date 2014-01-19
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Depends R (>= 3.0.1), MSnbase
Imports MASS, gplots, RColorBrewer
Description Exploratory data analysis to assess the quality of a set of LC-MS/MS experiments, and visualize the influence of the involved factors.
License GPL-2
Encoding latin1
biocViews Software, MassSpectrometry, Proteomics
NeedsCompilation no

R topics documented:

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msmsEDA-package

Exploratory Data Analysis of label-free LC-MS/MS spectral counts

Description

Exploratory data analysis to assess the quality of a set of label-free LC-MS/MS experiments, quantified by spectral counts, and visualize the influence of the involved factors. Visualization tools to assess quality and to discover outliers and eventual confounding.

Details

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- pp.msms.data: data preprocessing
- gene.table: extract gene symbols from protein description
- count.stats: summaries by sample
- counts.pca: principal components analysis
- counts.hc: hierarchical clustering of samples
- norm.counts: normalization of spectral counts matrix
- counts.heatmap: experiment heatmap
- disp.estimates: dispersion analysis and plots
- filter.flags: flag informative features
- spc.barplots: sample sizes barplots
- spc.boxplots: samples SpC boxplots
- spc.densityplot: samples SpC density plots
- spc.scatterplot: scatterplot comparing two conditions
- batch.neutralize: batch effects correction

Author(s)

Josep Gregori, Alex Sanchez and Josep Villanueva
Maintainer: Josep Gregori <josep.gregori@gmail.com>

References

**batch.neutralize**

**Batch effects correction**

**Description**

Computes the SpC matrix where the fixed effects of a blocking factor are substracted.

**Usage**

```r
batch.neutralize(dat, fbatch, half=TRUE, sqrt.trans=TRUE)
```

**Arguments**

- `dat`: A SpC matrix with proteins in the rows and samples in the columns.
- `fbatch`: A blocking factor of length equal to the number of columns in the expression matrix.
- `half`: When FALSE, the contrast coefficients are of the contr.treatment style. When TRUE, the contrast coefficients are of the contr.sum style, its aim is to distribute equally the effect to each batch level, instead of having untouched reference levels.
- `sqrt.trans`: When TRUE the fit is done on the square root transformed SpC matrix.

**Details**

A model with intercept and the blocking factor is fitted. The batch effects corrected SpC matrix is computed by substracting the estimated effect of the given blocking factor. When there is no clear reference batch level, the default option `half=TRUE` should be preferred. The square root transformation is known to stabilize the variance of Poisson distributed counts (with variance equal to the mean). The linear model fitting gives more accurate errors and p-values on the square root transformed SpC matrix. Nevertheless with exploratory data analysis purposes, both the raw and square root transformed SpC matrix may give good results.

**Value**

The batch effects corrected SpC matrix.

**Author(s)**

Josep Gregori

**See Also**

The `MSnSet` class documentation and `normalize`

**Examples**

```r
data(msms.dataset)
msnset <- pp.msms.data(msms.dataset)
### Plot the PCA on the two first PC, and colour by treatment level
ftreat <- pData(msnset)$treat
counts.pca(msnset, facs=ftreat, do.plot=TRUE, snms=as.character(ftreat))
### Correct the batch effects
```
count.stats <- exprs(msnset)
fbatch <- pData(msnset)$batch
spcm2 <- batch.neutralize(spcm, fbatch, half=TRUE, sqrt.trans=TRUE)
### Plot the PCA on the two first PC, and colour by treatment level
### to visualize the improvement.
exprs(msnset) <- spcm2
counts.pca(msnset, facs=ftreat, do.plot=TRUE, snms=as.character(ftreat))
### Incidence of the correction
summary(as.vector(spcm-spcm2))
plot(density(as.vector(spcm-spcm2)))

---

count.stats  Summary of statistics of spectral counts by sample in the dataset

### Description

Computes the number of proteins identified, the total spectral counts, and a summary of each sample

### Usage

count.stats(msnset)

### Arguments

- **msnset**: A MSnSet with spectral counts in the expression matrix.

### Value

A data frame with one row by sample and with variables:

- **proteins**: Number of identified proteins in sample
- **counts**: Total spectral counts in sample
- **min**: Min spectral counts
- **lwh**: Tukey’s lower hinge spectral counts
- **med**: Median spectral counts
- **hgh**: Tukey’s upper hinge spectral counts
- **max**: Max spectral counts

### Author(s)

Josep Gregori

### See Also

- `MSnSet`, `fivenum`

### Examples

```r
data(msms.dataset)
msnset <- pp.msms.data(msms.dataset)
res <- count.stats(msnset)
res```
Hierarchical clustering on an spectral counts matrix.

Description
Hierarchical clustering of samples in an spectral counts matrix, coloring tree branches according to factor levels.

Usage
```
counts.hc(msnset, do.plot=TRUE, facs=NULL, wait=TRUE)
```

Arguments
- **msnset**: A MSnSet with spectral counts in the expression matrix.
- **do.plot**: A logical indicating whether to plot the dendrograms.
- **facs**: NULL, or a data frame with factors. See details below.
- **wait**: This function may draw different plots, one by given factor in facs. When in interactive mode the default is to wait for confirmation before proceeding to the next plot. When wait is FALSE and R in interactive mode, instructs not to wait for confirmation.

Details
The hierarchical clustering is done by means of hclust with default parameters. If do.plot is TRUE, a dendrogram is plotted for each factor, with branches colored as per factor level. If facs is NULL then the factors are taken from pData(msnset).

Value
Invisibly returns the the value obtained from hclust.

Author(s)
Josep Gregori

See Also
- MSnSet
- hclust

Examples
```
data(msms.dataset)
msnset <- pp.msms.data(msms.dataset)
hc <- counts.hc(msnset)
str(hc)
```
counts.heatmap  

*Heatmap of an spectral counts matrix.*

**Description**

Heatmap showing the clustering of proteins and samples in a matrix of spectral counts.

**Usage**

```r
counts.heatmap(msnset, etit=NULL, fac=NULL, to.pdf=FALSE)
```

**Arguments**

- `msnset`  
  A MSnSet with spectral counts in the expression matrix.

- `etit`  
  The root name of the pdf file names where the heatmaps are sent.

- `fac`  
  A factor which is used for the column color bar.

- `to.pdf`  
  A logical indicating whether the heatmaps are sent to a pdf file.

**Details**

A heatmap of the `msnset` expression matrix is plot. If `to.pdf` is TRUE two heatmaps are plot, the first is fitted on an A4 page, the second is plotted with 3mm by row, allocating enough height to make the rownames readable. If `fac` is not NULL then a column color bar will show the levels of the factor. If `to.pdf` is TRUE the heatmaps are sent to pdf files whose names are the concatenation of `etit` and “-HeatMap.pdf” and “-FullHeatMap.pdf”, otherwise `etit` has no effect.

**Value**

No value is returned.

**Author(s)**

Josep Gregori

**See Also**

`MSnSet`, `heatmap` and `heatmap.2`

**Examples**

```r
data(msms.dataset)
msnset <- pp.msms.data(msms.dataset)
counts.heatmap(msnset, fac = pData(msnset)$treat)
```
counts.pca

Principal components analysis of an spectral counts matrix.

Description

A summary and different plots are given as a result of principal components analysis of an spectral counts matrix.

Usage

counts.pca(msnset, facs = NULL, do.plot = TRUE, snms = NULL, wait = TRUE)

Arguments

msnset   A MSnSet with spectral counts in the expression matrix.
do.plot A logical indicating whether to plot the PCA PC1/PC2 map.
facs     NULL or a data frame with factors. See details below.
snms     Character vector with sample short names to be plotted. If NULL then `Xnn` is plotted where `nn` is the column number in the dataset.
wait     This function may draw different plots, one by given factor in facs. When in interactive mode the default is to wait for confirmation before proceeding to the next plot. When wait is FALSE and R in interactive mode, instructs not to wait for confirmation.

Details

The spectral counts matrix is decomposed by means of prcomp. If do.plot is TRUE, a plot is generated for each factor showing the PC1/PC2 samples map, with samples colored as per factor level. If facs is NULL then the factors are taken from pData(msnset).

Value

Invisibly returns a list with values:

pca   The return value obtained from prcomp.
pc.vars   The percentage of variability corresponding to each principal component.

Author(s)

Josep Gregori

See Also

MSnSet, prcomp

Examples

data(msms.dataset)
msnset <- pp.msms.data(msms.dataset)
lst <- counts.pca(msnset)
str(lst)
print(lst$pc.vars[,1:4])
disp.estimates

Residual dispersion estimates

Description

Estimates the residual dispersion of each row of a spectral counts matrix as the ratio residual variance to mean of mean values by level, for each factor in facs. Different plots are drawn to help in the interpretation of the results.

Usage

disp.estimates(msnset, facs=NULL, do.plot=TRUE, etit=NULL, to.pdf=FALSE, wait=TRUE)

Arguments

msnset: A MSnSet with spectral counts in the expression matrix.
facs: A factor or a data frame with factors.
do.plot: A logical indicating whether to produce dispersion distribution plots.
etit: Root name of the pdf file where to send the plots.
to.pdf: A logical indicating whether a pdf file should be produced.
wait: This function draws different plots, two by given factor in facs. When in interactive mode and to.pdf FALSE, the default is to wait for confirmation before proceeding to the next plot. When wait is FALSE and R in interactive mode and to.pdf FALSE, instructs not to wait for confirmation.

details

Estimates the residual dispersion of each protein in the spectral counts matrix, for each factor in facs, and returns the quantiles at c(0.25, 0.5, 0.75, 0.9, 0.95, 0.99, 1) of the distribution of dispersion values for each factor. If facs is NULL the factors are taken from pData(msnset). If do.plot is TRUE this function produces a density plot of dispersion values, and the scatterplot of residual variance vs mean values, in log10 scale. If do.pdf is TRUE etit provides the root name for the pdf file name, ending with "-DispPlots.pdf". If etit is NULL a default value of "MSMS" is provided. A different set of plots is produced for each factor in facs.

Value

Invisibly returns a matrix with the quantiles at c(0.25, 0.5, 0.75, 0.9, 0.95, 0.99, 1) of the residual dispersion estimates. Each row has the residual dispersion values attributable to each factor in facs.

Author(s)

Josep Gregori

Examples

data(msms.dataset)
msnset <- pp.msms.data(msms.dataset)
disp.q <- disp.estimates(msnset)
disp.q
filter.flags

*Flag proteins with a minimum signal and/or sufficient dispersion.*

**Description**

In general the spectral counts (SpC) matrix of a LC-MS/MS experiment is a sparse matrix, where most of the features have very low signal. Besides, the features with low variance to mean ratio (dispersion) will be scarcely informative in a biomarker discovery experiment. Given a minimum number of spectral counts and/or a fraction of the features to be excluded by low dispersion, this function returns a vector of logicals flagging all features with values above the given thresholds.

**Usage**

```r
filter.flags(data,minSpC=2,frac.out=0.4)
```

**Arguments**

- `data`: A SpC matrix with proteins in the rows and samples in the columns.
- `minSpC`: All features with SpC below this threshold will be flagged as FALSE.
- `frac.out`: The fraction of features to be excluded, with the lowest observed dispersion. These will be flagged as FALSE.

**Details**

The less informative features in a SpC matrix are flagged as FALSE. Those with high enough signal and dispersion are flagged as TRUE. This vector of logicals may be used to filter the SpC matrix which is used in plots where only the relevant information matters, and where the high number of 0 may distort the plot and difficult its interpretation.

**Value**

A vector of logical values.

**Author(s)**

Josep Gregori

**Examples**

```r
data(msms.dataset)
fraction <- 0.3
msnset <- pp.msms.data(msms.dataset)
flags <- filter.flags(exprs(msnset),minSpC=2,frac.out=fraction)
cat("\nNumber of informative features:",sum(flags),"\n")
```
**gene.table**

*Gene symbols associated to protein accessions*

**Description**

Given a character vector with protein accessions, and a character vector with protein descriptions including gene symbols, returns a character vector with gene symbols whose names are the protein accessions. A character pattern should also be given to match the gene symbols.

**Usage**

```r
gene.table(Accession, Protein, patt = "GN=[A-Z0-9_]\*", off = 3)
```

**Arguments**

- **Accession**: A character vector with protein accessions.
- **Protein**: A character vector of protein descriptions including gene name symbols.
- **patt**: A character pattern to match the gene symbol within the protein description.
- **off**: Offset from the first character in the pattern corresponding to the gene symbol.

**Details**

NA is inserted where no match is found.

**Value**

A character vector with gene symbols, whose names are the corresponding protein accessions.

**Author(s)**

Josep Gregori

**Examples**

```r
data(pnms)
head(pnms)
gene.smb <- gene.table(pnms$Accession, pnms$Proteins)
head(gene.smb)
```
Description

A MSnSet with a spectral counts matrix as expression and two factors in the phenoData. The spectral counts matrix has samples in the columns, and proteins in the rows. The factors give the treatment and batch conditions of each sample in the dataset.

Usage

data(msms.dataset)

Format

A MSnSet

References


Laurent Gatto and Kathryn S. Lilley, MSnbase - an R/Bioconductor package for isobaric tagged mass spectrometry data visualization, processing and quantitation, Bioinformatics 28(2), 288-289 (2012).

See Also

See MSnSet for detail on the class, and the exprs and pData accessors.

Examples

data(msms.dataset)
msms.dataset
dim(msms.dataset)
head(exprs(msms.dataset))
head(pData(msms.dataset))
table(pData(msms.dataset)$treat)
table(pData(msms.dataset)$batch)
table(pData(msms.dataset)$treat, pData(msms.dataset)$batch)
**Spectral counts matrix normalization**

**Description**
An spectral counts matrix is normalized by means of a set of samples divisors.

**Usage**

```r
norm.counts(msnset, div)
```

**Arguments**

- `msnset`: A MSnSet with spectral counts in the expression matrix.
- `div`: A vector of divisors by sample.

**Details**
Each column in the data matrix is divided by the corresponding divisor to obtain the normalized matrix.

**Value**
A MSnSet object with the normalized spectral counts.

**Author(s)**
Josep Gregori

**See Also**
The `MSnSet` class documentation and `normalize`

**Examples**

```r
data(msms.dataset)
msnset <- pp.msms.data(msms.dataset)
(tspc <- apply(exprs(msnset), 2, sum))
div <- tspc/median(tspc)
e.norm <- norm.counts(msnset, div)
apply(exprs(e.norm), 2, sum)
e.norm
```
### pnms

<table>
<thead>
<tr>
<th>pnms</th>
<th>Accessions and gene symbols</th>
</tr>
</thead>
</table>

**Description**

A data frame with accessions in one column, and protein description including gene symbols in the second column.

**Usage**

data(pnms)

**Format**

A data frame with 1160 observations on the following 2 variables.

- **Accession**: a character vector with the protein accessions
- **Proteins**: a character vector with a description of each protein, including the gene symbol

**Examples**

data(pnms)
str(pnms)
head(pnms)

### pp.msms.data

**Spectral counts matrix pre-processing**

**Description**

Given a MSnSet, possibly subsetted from a bigger dataset, removes the all zero rows, and those with row names (accessions) ending with `-R` in the corresponding expression matrix. NAs are replaced by zeroes, as usually a NA in a spectral counts matrix corresponds to a protein not identified in a sample.

**Usage**

pp.msms.data(msnset)

**Arguments**

- **msnset**: A MSnSet with spectral counts in the expression matrix.

**Details**

An `-R` protein corresponds to an artefactual identification.
Rows with all zeros are uninformative and may give rise to errors in the analysis.
A NA is understood as a unidentified protein in a sample.
Value

Returns an updated MSnSet object. Its processingData slot shows that the object has been processed by pp.msms.data.

Author(s)

Josep Gregori

See Also

MSnSet

Examples

data(msms.dataset)
dim(msms.dataset)
msnset <- pp.msms.data(msms.dataset)
dim(msnset)

spc.barplots

Set of SpC barplots by sample

Description

Draws bars of height proportional to the sample size of each column in a SpC matrix. The sizes are scaled to the median of the total SpC by sample.

Usage

spc.barplots(msms.counts,fact=NULL,...)

Arguments

msms.counts  A SpC matrix with proteins in the rows and samples in the columns.
fact  NULL or a factor of length equal to the number of columns in the expression matrix. If provided the bars are colored by factor level.
...  Extra parameters passed to the plot function.

Details

.

Author(s)

Josep Gregori

Examples

data(msms.dataset)
spc.barplots(exprs(msms.dataset),fact=pData(msms.dataset)[,1],
    main="UPS1 200fm vs 600fm")
spc.boxplots

Set of SpC boxplots by sample

Description

Draws a boxplot for each column (sample) in a SpC matrix. The SpC are previously transformed by log2, with an offset of 0.1. If a factor is provided the boxplots are colored by factor level to better visualize the differences.

Usage

spc.boxplots(msms.counts,fact=NULL,minSpC=2,...)

Arguments

msms.counts A SpC matrix with proteins in the rows and samples in the columns.
minSpC All matrix cells with values below this threshold are excluded.
fact NULL or a factor of length equal to the number of columns in the expression matrix. If provided the boxplots are colored by factor level.
... Extra parameters passed to the plot function.

Details

More informative plots are obtained when excluding the cells with values below 2, the default for minSpC.

Author(s)

Josep Gregori

Examples

data(msms.dataset)
spc.boxplots(exprs(msms.dataset),fact=pData(msms.dataset)[,1],
  main="UPS1 200fm vs 600fm")

spc.densityplots

SpC density plots of a SpC matrix

Description

Draws superposed density plots, one for each column (sample) in a SpC matrix. The SpC are previously transformed by log2, with an offset of 0.1. If a factor is provided the density curves are colored by factor level to better visualize the differences.

Usage

spc.densityplots(msms.counts,fact=NULL,minSpC=2,...)
spc.scatterplot

Arguments

- **msms.counts**: A SpC matrix with proteins in the rows and samples in the columns.
- **minSpC**: All matrix cells with values below this threshold are excluded.
- **fact**: NULL or a factor of length equal to the number of columns in the expression matrix. If provided, the density curves are colored by factor level.
- **...**: Extra parameters passed to the plot function.

Details

More informative plots are obtained when excluding the cells with values below 2, the default for minSpC.

Author(s)

Josep Gregori

Examples

data(msms.dataset)
sc.densityplots(exprs(msms.dataset), fact=pData(msms.dataset)[,1],
               main="UP81 200fm vs 600fm")

spc.scatterplot  Scatterplot of SpC means comparing two conditions

Description

Given a SpC matrix and a two levels factor, draws a scatterplot with SpC means of one condition in the x axis and SpC means of the second condition in the y axis.

Usage

spc.scatterplot(msms.counts, treat, trans="log2", minSpC=2, minLFC=1, ...)

Arguments

- **msms.counts**: A SpC matrix with proteins in the rows and samples in the columns.
- **treat**: A two level factor of length equal to the number of columns in the expression matrix. The two levels represent the conditions to be compared.
- **trans**: The transformation made on the means before plotting. One among "log2", "sqrt", or "none". The default is "log2".
- **minSpC**: Used as signal threshold.
- **minLFC**: Used as size effect threshold.
- **...**: Extra parameters passed to the plot function.

Details

The transformed means are plotted, one condition versus the other. The borders representing absolute log fold change 1 are drawn as dashed lines. All features with log fold change equal to or greater than minLFC and with mean SpC in the most abundant condition equal to or greater than minSpC are colored in red.
Author(s)
Josep Gregori

Examples

data(msms.dataset)
spc.scatterplot(exprs(msms.dataset), treat=pData(msms.dataset)[,1], trans="log2",
   minSpC=2, minLFC=1, main="UPS1 200fm vs 600fm")
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