Package: MatrixQCvis (via r-universe)

October 16, 2026

Type Package

Title Shiny-based interactive data-quality exploration for omics data

Version 1.20.2

Date 2026-08-17

VignetteBuilder knitr

Description Data quality assessment is an integral part of preparatory data analysis to ensure sound biological information retrieval. We present here the MatrixQCvis package, which provides shiny-based interactive visualization of data quality metrics at the per-sample and per-feature level. It is broadly applicable to quantitative omics data types that come in matrix-like format (features x samples). It enables the detection of low-quality samples, drifts, outliers and batch effects in data sets. Visualizations include amongst others bar- and violin plots of the (count/intensity) values, mean vs standard deviation plots, MA plots, empirical cumulative distribution function (ECDF) plots, visualizations of the distances between samples, and multiple types of dimension reduction plots. Furthermore, MatrixQCvis allows for differential expression analysis based on the limma (moderated t-tests) and proDA (Wald tests) packages. MatrixQCvis builds upon the popular Bioconductor SummarizedExperiment S4 class and enables thus the facile integration into existing workflows. The package is especially tailored towards metabolomics and proteomics mass spectrometry data, but also allows to assess the data quality of other data types that can be represented in a SummarizedExperiment object.

Depends DT (>= 0.33), SummarizedExperiment (>= 1.20.0), plotly (>= 4.9.3), shiny (>= 1.6.0)

Imports ComplexHeatmap (>= 2.7.9), dplyr (>= 1.0.5), ExperimentHub (>= 2.6.0), ggplot2 (>= 3.3.3), grDevices (>= 4.1.0), Hmisc (>= 4.5-0), htmlwidgets (>= 1.5.3), impute (>= 1.65.0), imputeLCMD (>= 2.0), limma (>= 3.47.12), MASS (>= 7.3-58.1), methods (>= 4.1.0), pcaMethods (>= 1.83.0), proDA (>= 1.5.0), rlang (>=

0.4.10), rmarkdown (>= 2.7), Rtsne (>= 0.15), shinydashboard (>= 0.7.1), shinyhelper (>= 0.3.2), shinyjs (>= 2.0.0), stats (>= 4.1.0), sva (>= 3.52.0), tibble (>= 3.1.1), tidyr (>= 1.1.3), umap (>= 0.2.7.0), UpSetR (>= 1.4.0), vsn (>= 3.59.1)

Suggests BiocGenerics (>= 0.37.4), BiocStyle (>= 2.19.2), hexbin (>= 1.28.2), httr (>= 1.4.7), jpeg (>= 0.1-10), knitr (>= 1.33), statmod (>= 1.5.0), testthat (>= 3.0.2)

biocViews Visualization, ShinyApps, GUI, QualityControl, DimensionReduction, Metabolomics, Proteomics, Transcriptomics

License GPL-3

Encoding UTF-8

RoxygenNote 7.3.1

Config/pak/sysreqs
cmake make libicu-dev libpng-dev libuv1-dev libxml2-dev libssl-dev perl python3 zlib1g-dev

Repository Bioconductor 3.23

Date/Publication 2026-08-17 13:37:18 UTC

RemoteUrl https://github.com/bioc/MatrixQCvis

RemoteRef RELEASE_3_23

RemoteSha c915e167bad19ba0f4f9bfed9687564f7af39e4c

Contents

barplotSamplesMeasuredMissing . . . 3
batchCorrectionAssay . . . 4
createBoxplot . . . 5
createDfFeature . . . 7
cv . . . 8
cvFeaturePlot . . . 8
dimensionReduction . . . 9
dimensionReductionPlot . . . 10
distSample . . . 12
distShiny . . . 13
driftPlot . . . 14
ECDF . . . 15
explVar . . . 16
extractComb . . . 17
featurePlot . . . 18
hist_sample . . . 19
hist_sample_num . . . 20
histFeature . . . 20
histFeatureCategory . . . 21
hoeffDPlot . . . 22
hoeffDValues . . . 23
imputeAssay . . . 24

MAplot 26
MAvalues 27
measuredCategory 28
mosaic 29
normalizeAssay 30
permuteExplVar 31
plotCV 32
plotPCALoadings 33
plotPCAVar 34
plotPCAVarPvalue 35
samplesMeasuredMissing 36
shinyQC 37
sumDistSample 38
tblPCALoadings 39
transformAssay 40
upsetCategory 41
volcanoPlot 42

Index **44**

`barplotSamplesMeasuredMissing` *Barplot of number of measured/missing features of samples*

Description

`barplotSamplesMeasuredMissing` plots the number of measured/missing features of samples as a barplot. The function will take as input the returned `tbl` of `samplesMeasuredMissing`.

Usage

```
barplotSamplesMeasuredMissing(tbl, measured = TRUE)
```

Arguments

`tbl`	`tbl` object
`measured`	`logical`, should the number of measured or missing values be plotted

Value

gg object from `ggplot2`

Examples

```
## create se
a <- matrix(seq_len(100), nrow = 10, ncol = 10,
            dimnames = list(seq_len(10), paste("sample", seq_len(10))))
a[c(1, 5, 8), seq_len(5)] <- NA
set.seed(1)
a <- a + rnorm(100)
cD <- data.frame(name = colnames(a), type = c(rep("1", 5), rep("2", 5)))
rD <- data.frame(spectra = rownames(a))
se <- SummarizedExperiment::SummarizedExperiment(assay = a,
    rowData = rD, colData = cD)

## create the data.frame with information on number of measured/missing
## values
tbl <- samplesMeasuredMissing(se)

## plot number of measured values
barplotSamplesMeasuredMissing(tbl, measured = TRUE)

## plot number of missing values
barplotSamplesMeasuredMissing(tbl, measured = FALSE)
```

---

batchCorrectionAssay *Remove batch effects from (count/intensity) values of a* SummarizedExperiment

---

Description

The function batchCorrectionAssay removes the batch effect of (count/intensity) values of a SummarizedExperiment. It uses either the removeBatchEffect or ComBat functions or no batch effect correction method (pass-through, none).

Usage

```
batchCorrectionAssay(
  se,
  method = c("none", "removeBatchEffect (limma)", "ComBat"),
  batch = NULL,
  batch2 = NULL,
  ...
)
```

Arguments

se	SummarizedExperiment
method	character, one of "none" or "removeBatchEffect"
batch	character, NULL or one of colnames(colData(se))

batch2	character, NULL or one of colnames(colData(se))
...	further arguments passed to removeBatchEffect or ComBat

Details

The column batch in colData(se) contains the information on the batch identity. For method = "removeBatchEffect (limma)", batch2 may indicate a second series of batches. Internal use in shinyQC.

If batch is NULL and method is set to method = "removeBatchEffect (limma)" or method = "ComBat", no batch correction will be performed (equivalent to method = "none").

The method ComBat will only perform batch correction on valid features: (1) more or equal than two observations (no NA) per level and per feature, (2) variance greater than 0 per feature, and (3) more than two valid features as given by (1) and (2). For non-valid features, values are taken from assay(se).

Value

matrix

Examples

```
## create se
a <- matrix(seq_len(100), nrow = 10, ncol = 10,
    dimnames = list(seq_len(10), paste("sample", seq_len(10))))
a[c(1, 5, 8), seq_len(5)] <- NA
set.seed(1)
a <- a + rnorm(100)
cD <- data.frame(name = colnames(a),
    type = c(rep("1", 5), rep("2", 5)), batch = rep(c(1, 2), 5))
rD <- data.frame(spectra = rownames(a))
se <- SummarizedExperiment::SummarizedExperiment(assay = a,
    rowData = rD, colData = cD)

## method = "removeBatchEffect (limma)"
batchCorrectionAssay(se, method = "removeBatchEffect (limma)",
    batch = "batch", batch2 = NULL)

## method = "ComBat"
batchCorrectionAssay(se, method = "ComBat",
    batch = "batch", batch2 = NULL)
```

---

createBoxplot *Create a boxplot of (count/intensity) values per sample*

Description

The function create_boxplot creates a boxplot per sample for the intensity/count values.

Usage

```
createBoxplot(
  se,
  orderCategory = colnames(colData(se)),
  title = "",
  log = TRUE,
  violin = FALSE
)
```

Arguments

se	SummarizedExperiment containing the (count/intensity) values in the assay slot
orderCategory	character, one of colnames(colData(se))
title	character or numeric of length(1)
log	logical, if TRUE (count/intensity) values are displayed as log values
violin	logical, if FALSE a boxplot is created, if TRUE a violin plot is created

Details

Internal usage in shinyQC.

Value

gg object from ggplot2

Examples

```
## create se
a <- matrix(seq_len(100), nrow = 10, ncol = 10,
    dimnames = list(seq_len(10), paste("sample", seq_len(10))))
a[c(1, 5, 8), seq_len(5)] <- NA
set.seed(1)
a <- a + rnorm(100)
cD <- data.frame(name = colnames(a), type = c(rep("1", 5), rep("2", 5)))
rD <- data.frame(spectra = rownames(a))
se <- SummarizedExperiment::SummarizedExperiment(assay = a,
    rowData = rD, colData = cD)

createBoxplot(se, orderCategory = "name", title = "", log = TRUE,
    violin = FALSE)
```

createDfFeature *Create data frame of (count/intensity) values for a selected feature along data processing steps*

Description

The function createDfFeature takes as input a list of matrices and returns the row Feature of each matrix as a column of a data.frame. The function createDfFeature provides the input for the function featurePlot.

Usage

```
createDfFeature(l, feature)
```

Arguments

l	list containing matrices at different processing steps
feature	character, element of rownames of the matrices in l

Details

Internal usage in shinyQC

Value

data.frame

Examples

```
set.seed(1)
x1 <- matrix(rnorm(100), ncol = 10, nrow = 10,
    dimnames = list(paste("feature", seq_len(10)),
        paste("sample", seq_len(10))))
x2 <- x1 + 5
x3 <- x2 + 10

l <- list(x1 = x1, x2 = x2, x3 = x3)
createDfFeature(l, "feature 1")
```

cv *Calculate coefficient of variation*

Description

The function cv calculates the coefficient of variation from columns of a matrix. The coefficients of variation are calculated according to the formula `sd(y) / mean(y) * 100` with y the column values, thus, the function returns the coefficient of variation in percentage.

Usage

```
cv(x, name = "raw")
```

Arguments

x	matrix
name	character, the name of the returned list

Details

The function returned a named `list` (the name is specified by the `name` argument) containing the coefficient of variation of the columns of `x`.

Value

`list`

Examples

```
x <- matrix(seq_len(10), ncol = 2)
cv(x)
```

cvFeaturePlot *Plot of feature-wise coefficient of variation values*

Description

The function `cvFeaturePlot` returns a `plotly` plot of coefficient of variation values. It will create a violin plot and superseded points of coefficient of variation values per list entry of `l`.

Usage

```
cvFeaturePlot(l, lines = FALSE)
```

Arguments

l	list containing matrices
lines	logical

Details

lines = TRUE will connect the points belonging to the same feature with a line. If there are less than two features, the violin plot will not be plotted. The violin plots will be ordered according to the order in l

Value

plotly

Examples

```
x1 <- matrix(seq_len(100), ncol = 10, nrow = 10,
    dimnames = list(paste("feature", seq_len(10)),
        paste("sample", seq_len(10))))
x2 <- x1 + 5
x3 <- x2 + 10
l <- list(x1 = x1, x2 = x2, x3 = x3)
cvFeaturePlot(l, lines = FALSE)
```

---

dimensionReduction *Dimensionality reduction with dimensionReduction methods PCA, PCoA, NMDS, UMAP and tSNE*

Description

The function dimensionReduction creates a data.frame with the coordinates of the projected data (first entry of returned output). The function allows for the following projections: Principal Component Analysis (PCA), Principal Coordinates Analysis/Multidimensional Scaling (PCoA), Non-metric Multidimensional scaling (NMDS), t-distributed stochastic neighbor embedding (tSNE), and Uniform Manifold Approximation and Projection (UMAP).

The second list entry will contains the object returned from prcomp (PCA), cmdscale (PCoA), isoMDS (NMDS), Rtsne (tSNE), or umap (UMAP).

Usage

```
dimensionReduction(
  x,
  type = c("PCA", "PCoA", "NMDS", "tSNE", "UMAP"),
  params = list()
)
```

Arguments

x	matrix, containing no missing values, samples are in columns and features are in rows
type	character, specifying the type/method to use for dimensionality reduction. One of PCA, PCoA, NMDS, tSNE, or UMAP.
params	list, arguments/parameters given to the functions stats::prcomp, stats::dist, Rtsne::Rtsne, umap::umap

Details

The function dimensionReduction is a wrapper around the following functions stats::prcomp (PCA), stats::cmdscale (PCoA), MASS::isoMDS (NMDS), Rtsne::Rtsne (tSNE), and umap::umap (UMAP). For the function umap::umap the method is set to naive.

Value

list, first entry contains a tbl, second entry contains the object returned from prcomp (PCA), cmdscale (PCoA), isoMDS (NMDS), Rtsne (tSNE), or umap (UMAP)

Author(s)

Thomas Naake

Examples

```
x <- matrix(rnorm(seq_len(10000)), ncol = 100)
rownames(x) <- paste("feature", seq_len(nrow(x)))
colnames(x) <- paste("sample", seq_len(ncol(x)))
params <- list(method = "euclidean", ## dist
    initial_dims = 10, max_iter = 100, dims = 3, perplexity = 3, ## tSNE
    min_dist = 0.1, n_neighbors = 15, spread = 1) ## UMAP
dimensionReduction(x, type = "PCA", params = params)
dimensionReduction(x, type = "PCoA", params = params)
dimensionReduction(x, type = "NMDS", params = params)
dimensionReduction(x, type = "tSNE", params = params)
dimensionReduction(x, type = "UMAP", params = params)
```

---

dimensionReductionPlot

Plot the coordinates from dimensionReduction *values*

Description

The function dimensionReductionPlot creates a dimension reduction plot. The function takes as input the tbl object obtained from the dimensionReduction function. The tbl contains transformed values by one of the dimension reduction methods.

Usage

```
dimensionReductionPlot(
  tbl,
  se,
  color = c("none", colnames(se@colData)),
  size = c("none", colnames(se@colData)),
  explainedVar = NULL,
  x_coord,
  y_coord,
  height = 600,
  interactive = TRUE
)
```

Arguments

tbl	tbl as obtained by the function dimensionReduction
se	SummarizedExperiment
color	character, one of "none" or colnames(se@colData)
size	character, one of "none" or colnames(se@colData)
explainedVar	NULL or named numeric, if numeric explainedVar contains the explained variance per principal component (names of explainedVar corresponds to the principal components)
x_coord	character, column name of tbl that stores x coordinates
y_coord	character, column name of tbl that stores y coordinates
height	numeric, specifying the height of the plot (in pixels)
interactive	logical(1), if TRUE dimensionReductionPlot will return a plotly object, if FALSE dimensionReductionPlot will return a gg object

Details

The function dimensionReductionPlot is a wrapper for a ggplot/ggplotly expression.

Value

plotly or gg

Author(s)

Thomas Naake

Examples

```
library(SummarizedExperiment)

## create se
a <- matrix(seq_len(100), nrow = 10, ncol = 10, byrow = TRUE,
            dimnames = list(seq_len(10), paste("sample", seq_len(10))))
```

```
set.seed(1)
a <- a + rnorm(100)
cD <- data.frame(name = colnames(a), type = c(rep("1", 5), rep("2", 5)),
  median_vals = apply(a, 2, median))
rD <- data.frame(spectra = rownames(a))
se <- SummarizedExperiment(assay = a, rowData = rD, colData = cD)

pca <- dimensionReduction(x = assay(se), type = "PCA", params = list())[[1]]

dimensionReductionPlot(tbl = pca, se = se, color = "type", size = "median_vals",
    x_coord = "PC1", y_coord = "PC2")
```

`distSample` *Create a heatmap using distance information between samples*

Description

The function `distSample` creates a heatmap from a distance matrix created by the function `distShiny`. The heatmap is annotated by the column specified by the `label` column in `colData(se)`.

Usage

```
distSample(d, se, label = "name", title = "raw", ...)
```

Arguments

`d`	`matrix` containing distances, obtained from `distShiny`
`se`	`SummarizedExperiment`
`label`	`character`, refers to a column in `colData(se)`
`title`	`character`
`...`	further arguments passed to `ComplexHeatmap::Heatmap`

Details

Internal use in `shinyQC`

Value

`Heatmap` object from `ComplexHeatmap`

Examples

```
## create se
a <- matrix(seq_len(100), nrow = 10, ncol = 10,
            dimnames = list(seq_len(10), paste("sample", seq_len(10))))
a[c(1, 5, 8), seq_len(5)] <- NA
set.seed(1)
a <- a + rnorm(100)
a_i <- imputeAssay(a, method = "MinDet")
cD <- data.frame(name = colnames(a_i),
    type = c(rep("1", 5), rep("2", 5)))
rD <- data.frame(spectra = rownames(a_i))
se <- SummarizedExperiment::SummarizedExperiment(assay = a_i, rowData = rD,
    colData = cD)

dist <- distShiny(a_i)
distSample(dist, se, label = "type", title = "imputed",
    show_row_names = TRUE)
```

`distShiny` *Create distance matrix from numerical matrix*

Description

The function `distShiny` takes as an input a numerical `matrix` or `data.frame` and returns the distances between the rows and columns based on the defined `method` (e.g. euclidean distance).

Usage

```
distShiny(x, method = "euclidean")
```

Arguments

`x`	`matrix` or `data.frame` with samples in columns and features in rows
`method`	`character`, method for distance calculation

Details

Internal use in `shinyQC`.

Value

`matrix`

Examples

```
x <- matrix(seq_len(100), nrow = 10, ncol = 10,
        dimnames = list(seq_len(10), paste("sample", seq_len(10))))
distShiny(x = x)
```

`driftPlot` *Plot the trend line for aggregated values*

Description

The function `driftPlot` aggregates the (count/intensity) values from the `assay()` slot of a `SummarizedExperiment` by the `median` or `sum` of the (count/intensity) values. `driftPlot` then visualizes these aggregated values and adds a trend line (using either LOESS or a linear model) from (a subset of) the aggregated values. The subset is specified by the arguments `category` and `level`.

Usage

```
driftPlot(
  se,
  aggregation = c("median", "sum"),
  category = colnames(colData(se)),
  orderCategory = colnames(colData(se)),
  level = c("all", unique(colData(se)[, category])),
  method = c("loess", "lm")
)
```

Arguments

`se`	`SummarizedExperiment`
`aggregation`	`character`, type of aggregation of (count/intensity) values
`category`	`character`, column of `colData(se)`
`orderCategory`	`character`, column of `colData(se)`
`level`	`character`, from which samples should the LOESS curve be calculated, either `"all"` or one of the levels of the selected columns of `colData(se)` (`"category"`)
`method`	`character`, either `"loess"` or `"lm"`

Details

The x-values are sorted according to the `orderCategory` argument: The levels of the corresponding column in `colData(se)` are pasted with the sample names (in the column `name`) and factorized. Internal usage in `shinyQC`.

Value

gg object from `ggplot2`

Examples

```
#' ## create se
set.seed(1)
a <- matrix(rnorm(1000), nrow = 10, ncol = 100,
    dimnames = list(seq_len(10), paste("sample", seq_len(100))))
a[c(1, 5, 8), seq_len(5)] <- NA
cD <- data.frame(name = colnames(a), type = c(rep("1", 50), rep("2", 50)))
rD <- data.frame(spectra = rownames(a))
se <- SummarizedExperiment::SummarizedExperiment(assay = a,
    rowData = rD, colData = cD)

driftPlot(se, aggregation = "sum", category = "type",
    orderCategory = "type", level = "1", method = "loess")
```

ECDF *Create ECDF plot of a sample against a reference*

Description

The function ECDF creates a plot of the empirical cumulative distribution function of a specified sample and an outgroup (reference). The reference is specified by the group argument. The row-wise (feature) mean values of the reference are calculated after excluding the specified sample.

Usage

```
ECDF(se, sample = colnames(se), group = c("all", colnames(colData(se))))
```

Arguments

se	SummarizedExperiment object
sample	character, name of the sample to compare against the group
group	character, either "all" or one of colnames(colData(se))

Details

Internal use in shinyQC.

The function ECDF uses the ks.test function from stats to perform a two-sample Kolmogorov-Smirnov test. The Kolmogorov-Smirnov test is run with the alternative "two.sided" (null hypothesis is that the true distribution function of the sample is equal to the hypothesized distribution function of the group).

The exact argument in ks.test is set to NULL, meaning that an exact p-value is computed if the product of the sample sizes is less than 10000 of sample and group. Otherwise, asymptotic distributions are used whose approximations might be inaccurate in low sample sizes.

Value

gg object from ggplot2

Examples

```
## create se
set.seed(1)
a <- matrix(rnorm(1000), nrow = 100, ncol = 10,
    dimnames = list(seq_len(100), paste("sample", seq_len(10))))
a[c(1, 5, 8), seq_len(5)] <- NA
cD <- data.frame(name = colnames(a), type = c(rep("1", 5), rep("2", 5)))
rD <- data.frame(spectra = rownames(a))
se <- SummarizedExperiment(assay = a, rowData = rD, colData = cD)

ECDF(se, sample = "sample 1", group = "all")
```

`explVar` *Retrieve the explained variance for each principal component (PCA) or axis (PCoA)*

Description

The function `explVar` calculates the proportion of explained variance for each principal component (PC, `type = "PCA"`) and axis (`type = "PCoA"`).

Usage

```
explVar(d, type = c("PCA", "PCoA"))
```

Arguments

`d`	`prcomp` or `list` from `cmdscale`
`type`	`character`, one of `"PCA"` or `"PCoA"`

Details

`explVar` uses the function `prcomp` from the `stats` package to retrieve the explained standard deviation per PC (`type = "PCA"`) and the function `cmdscale` from the `stats` package to retrieve the explained variation based on eigenvalues per Axis (`type = "PCoA"`).

Value

`numeric` vector with the proportion of explained variance for each PC or Axis

Author(s)

Thomas Naake

Examples

```
x <- matrix(seq_len(100), nrow = 10, ncol = 10,
    dimnames = list(seq_len(10), paste("sample", seq_len(10))))
set.seed(1)
x <- x + rnorm(100)

## run for PCA
pca <- dimensionReduction(x = x,
    params = list(center = TRUE, scale = TRUE), type = "PCA")[[2]]
explVar(d = pca, type = "PCA")

## run for PCoA
pcoa <- dimensionReduction(x = x,
    params = list(method = "euclidean"), type = "PCoA")[[2]]
explVar(d = pcoa, type = "PCoA")
```

`extractComb` *Obtain the features that are present in a specified set*

Description

The function `extractComb` extracts the features that match a `combination` depending if the features was measured or missing. The function will return the sets that match the `combination`, thus, the function might be useful when answering questions about which features are measured/missing under certain combinations (e.g. sample types or experimental conditions).

Usage

```
extractComb(se, combination, measured = TRUE, category = "type")
```

Arguments

`se`	`SummarizedExperiment`
`combination`	`character`, refers to factors in `category`
`measured`	`logical`
`category`	`character`, corresponding to a column name in `colData(se)`

Details

The function `extractComb` uses the `make_comb_mat` function from `ComplexHeatmap` package.

Presence is defined by a feature being measured in at least one sample of a set.

Absence is defined by a feature with only missing values (i.e. no measured values) of a set.

Value

`character`

Examples

```
## create se
a <- matrix(seq_len(100), nrow = 10, ncol = 10,
            dimnames = list(seq_len(10), paste("sample", seq_len(10))))
a[c(1, 5, 8), seq_len(5)] <- NA
set.seed(1)
a <- a + rnorm(100)
cD <- data.frame(name = colnames(a), type = c(rep("1", 5), rep("2", 5)))
rD <- data.frame(spectra = rownames(a))
se <- SummarizedExperiment::SummarizedExperiment(assay = a, rowData = rD, colData = cD)

extractComb(se, combination = "2", measured = TRUE, category = "type")
```

`featurePlot` *Create a plot of (count/intensity) values over the samples*

Description

The function `featurePlot` creates a plot of (count/intensity) values for different data processing steps (referring to columns in the `data.frame`) over the different samples (referring to rows in the `data.frame`).

Usage

```
featurePlot(df)
```

Arguments

`df`	`data.frame`

Details

Internal usage in `shinyQC`.

Value

gg object from `ggplot2`

Examples

```
set.seed(1)
x1 <- matrix(rnorm(100), ncol = 10, nrow = 10,
    dimnames = list(paste("feature", seq_len(10)),
        paste("sample", seq_len(10))))
x2 <- x1 + 5
x3 <- x2 + 10
l <- list(x1 = x1, x2 = x2, x3 = x3)
df <- createDfFeature(l, "feature 1")
```

```
featurePlot(df)
```

`hist_sample` *Plot a histogram of the number of a category*

Description

`hist_sample` plots the number of a category (e.g. sample types) as a histogram. It use the returned `tbl` from `hist_sample_num`.

Usage

```
hist_sample(tbl, category = "type")
```

Arguments

`tbl`	`tbl` as returned by `hist_sample_num`
`category`	`character`, x-axis label of the plot

Value

gg object from `ggplot2`

Examples

```
## create se
a <- matrix(seq_len(100), nrow = 10, ncol = 10,
            dimnames = list(seq_len(10), paste("sample", seq_len(10))))
a[c(1, 5, 8), seq_len(5)] <- NA
set.seed(1)
a <- a + rnorm(100)
cD <- data.frame(name = colnames(a), type = c(rep("1", 4), rep("2", 6)))
rD <- data.frame(spectra = rownames(a))
se <- SummarizedExperiment::SummarizedExperiment(assay = a,
    rowData = rD, colData = cD)

tbl <- hist_sample_num(se, category = "type")
hist_sample(tbl)
```

hist_sample_num *Return the number of a category*

Description

hist_sample_num returns the number of a category (e.g. sample types) as a tbl. The function will retrieve first the column category in colData(se). The function will return a tbl containing the numerical values of the quantities.

Usage

```
hist_sample_num(se, category = "type")
```

Arguments

se	SummarizedExperiment object
category	character, corresponding to a column in colData(se)

Value

tbl

Examples

```
## create se
a <- matrix(seq_len(100), nrow = 10, ncol = 10,
    dimnames = list(seq_len(10), paste("sample", seq_len(10))))
a[c(1, 5, 8), seq_len(5)] <- NA
set.seed(1)
a <- a + rnorm(100)
cD <- data.frame(name = colnames(a), type = c(rep("1", 4), rep("2", 6)))
rD <- data.frame(spectra = rownames(a))
se <- SummarizedExperiment::SummarizedExperiment(assay = a,
    rowData = rD, colData = cD)

hist_sample_num(se, category = "type")
```

histFeature *Histogram for measured value per feature*

Description

The function histFeature creates a histogram with the number of measured/missing values per feature.

Usage

```
histFeature(x, measured = TRUE, ...)
```

Arguments

x	matrix containing intensities. Missing values are encoded as NA.
measured	logical, should the measured values (measured = TRUE) or missing values (measured = FALSE) be taken
...	additional parameters passed to geom_histogram, e.g. binwidth.

Value

plotly object from ggplotly

Examples

```
x <- matrix(c(c(1, 1, 1), c(1, NA, 1), c(1, NA, 1),
    c(1, 1, 1), c(NA, 1, 1), c(NA, 1, 1)), byrow = FALSE, nrow = 3)
colnames(x) <- c("A_1", "A_2", "A_3", "B_1", "B_2", "B_3")
histFeature(x, binwidth = 1)
```

---

histFeatureCategory *Histogram of features per sample type*

Description

The function histFeatureCategory creates histogram plots for each sample type in se.

Usage

```
histFeatureCategory(se, measured = TRUE, category = "type", ...)
```

Arguments

se	SummarizedExperiment, the assay slot contains the intensity values per sample. Missing values are encoded as NA.
measured	logical, should the measured values (measured = TRUE) or missing values (measured = FALSE) be taken
category	character, corresponding to a column in colData(se)
...	additional parameters passed to geom_histogram, e.g. binwidth.

Value

plotly object from ggplotly

Examples

```
## create se
a <- matrix(seq_len(100), nrow = 10, ncol = 10,
            dimnames = list(seq_len(10), paste("sample", seq_len(10))))
a[c(1, 5, 8), seq_len(5)] <- NA
set.seed(1)
a <- a + rnorm(100)
cD <- data.frame(name = colnames(a), type = c(rep("1", 5), rep("2", 5)))
rD <- data.frame(spectra = rownames(a))
se <- SummarizedExperiment::SummarizedExperiment(assay = a,
    rowData = rD, colData = cD)

histFeatureCategory(se, measured = TRUE, category = "type")
```

`hoeffDPlot` *Create a plot from a list of Hoeffding's D values*

Description

The function `hoeffDPlot` creates via `ggplot` a violin plot per factor, a jitter plot of the data points and (optionally) connects the points via lines. `hoeffDPlot` uses the `plotly` package to make the figure interactive.

Usage

```
hoeffDPlot(df, lines = TRUE)
```

Arguments

`df`	`data.frame` containing one or multiple columns containing the Hoeffding's D statistics
`lines`	`logical`, should points belonging to the same sample be connected

Details

The function `hoeffDPlot` will create the violin plot and jitter plot according to the specified order given by the colnames of `df`. `hoeffDPlot` will thus internally refactor the `colnames` of the supplied `data.frame` according to the order of the `colnames`.

Value

gg object from `ggplot2`

Examples

```
## create se
set.seed(1)
a <- matrix(rnorm(10000), nrow = 1000, ncol = 10,
            dimnames = list(seq_len(1000), paste("sample", seq_len(10))))
a[c(1, 5, 8), seq_len(5)] <- NA
cD <- data.frame(name = colnames(a), type = c(rep("1", 5), rep("2", 5)))
rD <- data.frame(spectra = rownames(a))
se <- SummarizedExperiment::SummarizedExperiment(assay = a,
    rowData = rD, colData = cD)

tbl <- MAvalues(se, log = FALSE, group = "all")
hd_r <- hoeffDValues(tbl, "raw")

## normalized values
se_n <- se
assay(se_n) <- normalizeAssay(a, "sum")
tbl_n <- MAvalues(se_n, log = FALSE, group = "all")
hd_n <- hoeffDValues(tbl_n, "normalized")

df <- data.frame(raw = hd_r, normalized = hd_n)
hoeffDPlot(df, lines = TRUE)
hoeffDPlot(df, lines = FALSE)
```

`hoeffDValues` *Create values of Hoeffding's D statistics from M and A values*

Description

The function creates and returns Hoeffding's D statistics values from MA values.

In case `sample_n` is set to a numerical value (e.g. 10000), a random subset containing `sample_n` is taken to calculate Hoeffding's D values to speed up the calculation. In case there are less features than `sample_n`, all features are taken.

Usage

```
hoeffDValues(tbl, name = "raw", sample_n = NULL)
```

Arguments

`tbl`	`tibble`, as obtained from the function `MAvalues`
`name`	`character(1)`, name of the returned list
`sample_n`	`numeric(1)`, number of features (subset) to be taken for calculation of Hoeffding's D values

Details

The function uses the function `hoeffd` from the `Hmisc` package to calculate the values.

Value

named list with Hoeffding's D values per sample

Examples

```
## create se
a <- matrix(seq_len(100), nrow = 10, ncol = 10,
            dimnames = list(seq_len(10), paste("sample", seq_len(10))))
a[c(1, 5, 8), seq_len(5)] <- NA
set.seed(1)
a <- a + rnorm(100)
cD <- data.frame(name = colnames(a), type = c(rep("1", 5), rep("2", 5)))
rD <- data.frame(spectra = rownames(a))
se <- SummarizedExperiment::SummarizedExperiment(assay = a,
    rowData = rD, colData = cD)

tbl <- MAvalues(se)
hoeffDValues(tbl, "raw")

## normalized values
se_n <- se
assay(se_n) <- normalizeAssay(a, "sum")
tbl_n <- MAvalues(se_n, group = "all")
hoeffDValues(tbl_n, "normalized")

## transformed values
se_t <- se
assay(se_t) <- transformAssay(a, "log")
tbl_t <- MAvalues(se_t, group = "all")
hoeffDValues(tbl_t, "transformed")
```

---

imputeAssay *Impute missing values in a* `matrix`

Description

The function `impute` imputes missing values based on one of the following principles: Bayesian missing value imputation (`BPCA`), k-nearest neighbor averaging (`kNN`), Malimum likelihood-based imputation method using the EM algorithm (`MLE`), replacement by the smallest non-missing value in the data (`Min`), replacement by the minimal value observed as the q-th quantile (`MinDet`, default `q = 0.01`), and replacement by random draws from a Gaussian distribution centred to a minimal value (`MinProb`).

Usage

```
imputeAssay(
  a,
  method = c("BPCA", "kNN", "MLE", "Min", "MinDet", "MinProb", "none")
)
```

Arguments

a	matrix with samples in columns and features in rows
method	character, one of "BPCA", "kNN", "MLE", "Min", "MinDet", "MinProb", or "none"

Details

BPCA wrapper for pcaMethods::pca with methods = "bpca". BPCA is a missing at random (MAR) imputation method.

kNN wrapper for impute::impute.knn with k = 10, rowmax = 0.5, colmax = 0.5, maxp = 1500. kNN is a MAR imputation method.

MLE wrapper for imputeLCMD::impute.MAR with method = "MLE", model.selector = 1/imputeLCMD::impute.wrapper.MI MLE is a MAR imputation method.

Min imputes the missing values by the observed minimal value of x. Min is a missing not at random (MNAR) imputation method.

MinDet is a wrapper for imputeLCMD::impute.MinDet with q = 0.01. MinDet performs the imputation using a deterministic minimal value approach. The missing entries are replaced with a minimal value, estimated from the q-th quantile from each sample. MinDet is a MNAR imputation method.

MinProb is a wrapper for imputeLCMD::impute.MinProb with q = 0.01 and tune.sigma = 1. MinProb performs the imputation based on random draws from a Gaussion distribution with the mean set to the minimal value of a sample. MinProb is a MNAR imputation method.

MinProb does not impute values (not available within shiny application).

Value

matrix

Examples

```
a <- matrix(seq_len(100), nrow = 10, ncol = 10,
    dimnames = list(seq_len(10), paste("sample", seq_len(10))))
a[c(1, 5, 8), seq_len(5)] <- NA

imputeAssay(a, method = "kNN")
imputeAssay(a, method = "Min")
imputeAssay(a, method = "MinDet")
imputeAssay(a, method = "MinProb")
```

MAplot *Create a MA plot*

Description

The function creates a 2D histogram of M and A values.

Usage

```
MAplot(
  tbl,
  group = c("all", colnames(tbl)),
  plot = c("all", unique(tbl[["name"]]))
)
```

Arguments

tbl	tibble containing the M and A values, as obtained from the MAvalues function
group	character, one of colnames(colData(se)) (se used in MAvalues) or "all"
plot	character, one of colData(se)$name (se used in MAvalues) or "all"

Details

MAplot returns a 2D hex histogram instead of a classical scatterplot due to computational reasons and better visualization of overlaying points. The argument plot specifies the sample (refering to colData(se)$name) to be plotted. If plot = "all", MA values for all samples will be plotted (samples will be plotted in facets). If the number of features (tbl$Features) is below 1000, points will be plotted (via geom_points), otherwise hexagons will be plotted (via geom_hex).

Value

gg object from ggplot2

Examples

```
## create se
set.seed(1)
a <- matrix(rnorm(10000), nrow = 1000, ncol = 10,
            dimnames = list(seq_len(1000), paste("sample", seq_len(10))))
a[c(1, 5, 8), seq_len(5)] <- NA
cD <- data.frame(name = colnames(a), type = c(rep("1", 5), rep("2", 5)))
rD <- data.frame(spectra = rownames(a))
se <- SummarizedExperiment::SummarizedExperiment(assay = a,
    rowData = rD, colData = cD)

tbl <- MAvalues(se, log = FALSE, group = "all")
MAplot(tbl, group = "all", plot = "all")
```

MAvalues *Create values (M and A) for MA plot*

Description

The function MAvalues will create MA values as input for the function MAplot and hoeffDValues. M and A are specified relative to specified samples which is determined by the group argument. In case of group == "all", all samples (expect the specified one) are taken for the reference calculation. In case of group != "all" will use the samples belonging to the same group given in colnames(colData(se)) expect the specified one.

Usage

```
MAvalues(se, log2 = TRUE, group = c("all", colnames(colData(se))))
```

Arguments

se	SummarizedExperiment
log2	logical, specifies if values are log2-transformed prior to calculating M and A values. If the values are already transformed, log2 should be set to FALSE. If log2 = TRUE and if there are values in assay(se) that are 0, the log2 values are calculated by log2(assay(se) + 1)
group	character, either "all" or one of colnames(colData(se))

Value

tbl with columns Feature, name (sample name), A, M and additional columns of colData(se)

Examples

```
## create se
set.seed(1)
a <- matrix(rnorm(10000), nrow = 1000, ncol = 10,
            dimnames = list(seq_len(1000), paste("sample", seq_len(10))))
a[c(1, 5, 8), seq_len(5)] <- NA
cD <- data.frame(name = colnames(a), type = c(rep("1", 5), rep("2", 5)))
rD <- data.frame(spectra = rownames(a))
se <- SummarizedExperiment(assay = a, rowData = rD, colData = cD)

MAvalues(se, log = FALSE, group = "all")
```

measuredCategory *Obtain the number of measured intensities per sample type*

Description

The function measuredCategory creates a tbl with the number of measured values per feature. 0 means that there were only missing values (NA) for the feature and sample type. measuredCategory will return a tbl where columns are the unique sample types and rows are the features as in assay(se).

Usage

```
measuredCategory(se, measured = TRUE, category = "type")
```

Arguments

se	SummarizedExperiment
measured	logical, should the measured values (measured = TRUE) or missing values (measured = FALSE) be taken
category	character, corresponds to a column name in colData(se)

Details

measuredCategory is a helper function.

Value

matrix with number of measured/missing features per category type

Examples

```
## create se
set.seed(1)
a <- matrix(rnorm(100), nrow = 10, ncol = 10,
            dimnames = list(seq_len(10), paste("sample", seq_len(10))))
a[c(1, 5, 8), seq_len(5)] <- NA
cD <- data.frame(name = colnames(a), type = c(rep("1", 5), rep("2", 5)))
rD <- data.frame(spectra = rownames(a))
se <- SummarizedExperiment::SummarizedExperiment(assay = a,
    rowData = rD, colData = cD)

measuredCategory(se, measured = TRUE, category = "type")
```

mosaic *Mosaic plot for two factors in colData(se)*

Description

The function mosaic creates a mosaic plot of two factors from an SummarizedExperiment object. The columns f1 and f2 are taken from colData(se).

Usage

```
mosaic(se, f1, f2)
```

Arguments

se	SummarizedExperiment object
f1	character, f1 is one of the column names in colData(se)
f2	character, f2 is one of the column names in colData(se)

Details

Code partly taken from https://stackoverflow.com/questions/21588096/pass-string-to-facet-grid-ggplot2

Value

gg object from ggplot2

Examples

```
## create se
set.seed(1)
a <- matrix(rnorm(100), nrow = 10, ncol = 10,
            dimnames = list(seq_len(10), paste("sample", seq_len(10))))
a[c(1, 5, 8), seq_len(5)] <- NA
cD <- data.frame(name = colnames(a),
    type = c(rep("1", 5), rep("2", 5)),
    cell_type = c("A", "B"))
rD <- data.frame(spectra = rownames(a))
se <- SummarizedExperiment::SummarizedExperiment(assay = a,
    rowData = rD, colData = cD)

mosaic(se, "cell_type", "type")
```

normalizeAssay *Normalize a data sets (reduce technical sample effects)*

Description

The function normalizeAssay performs normalization by sum of the (count/intensity) values per sample (method = "sum"), quantile division per sample (method = "quantile division"), or by quantile normalization (adjusting the value distributions that they become identical in statistical properties, method = "quantile"). The value for quantile division (e.g., the 75 specified by the probs argument. Quantile normalization is performed by using the normalizeQuantiles function from limma.

For the methods "sum" and "quantile division", normalization will be done depending on the multiplyByNormalizationValue parameter. If set to TRUE, normalization values (e.g. sum or quantile) will be calculated per sample. In a next step, adjusted normalization values will be calculated for each sample in relation to the median normalization values across all samples. Finally, the values in a are multiplied by these adjusted normalization values. If multiplyByNormalizationValue is set to FALSE, normalization values (e.g. sum or quantile) will be calculated per sample. The values in a are sample-wise divided by the normalization values.

Usage

```
normalizeAssay(
  a,
  method = c("none", "sum", "quantile division", "quantile"),
  probs = 0.75,
  multiplyByNormalizationValue = FALSE
)
```

Arguments

a	matrix with samples in columns and features in rows
method	character, one of "none", "sum", "quantile division", "quantile"
probs	numeric, ranging between [0, 1). probs is used as the divisor for quantile division in method = "quantile division"
multiplyByNormalizationValue	logical, if TRUE, normalization values will be calculated and the values in a will be multiplied by the values The parameter is only relavant for method = "sum" and method = "quantile division"

Details

Internal usage in shinyQC. If method is set to "none", the object x is returned as is (pass-through).

If probs is NULL, probs is internally set to 0.75 if method = "quantile division".

Depending on the values in a, if multiplyByNormalizationValue is set to TRUE the returned normalized values will be in the same order of magnitude than the original values, while if FALSE, the returned values will be in a smaller order of magnitude.

Value

matrix

Examples

```
a <- matrix(seq_len(100), nrow = 10, ncol = 10,
        dimnames = list(seq_len(10), paste("sample", seq_len(10))))
normalizeAssay(a, "sum")
```

---

permuteExplVar *Permute the expression values and retrieve the explained variance*

Description

The function permuteExplVar determines the explained variance of the permuted expression matrix (x). It is used to determine the optimal number of PCs for tSNE.

Usage

```
permuteExplVar(x, n = 10, center = TRUE, scale = TRUE, sample_n = NULL)
```

Arguments

x	matrix or data.frame, samples in columns and features in rows
n	numeric, number of permutation rounds
center	logical, passed to the function explVar
scale	logical, passed to the function explVar
sample_n	numeric(1), number of features (subset) to be taken for calculation of permuted explained variance, the top sample_n varying values based on their standard deviation will be taken

Details

For the input of tSNE, typically, we want to reduce the initial number of dimensions linearly with PCA (used as the initial_dims arguments in the Rtsne funtion). The reduced data set is used for feeding into tSNE. By plotting the percentage of variance explained by the Princical Components (PCs) we can estimate how many PCs we keep as input into tSNE. However, if we select too many PCs, noise will be included as input to tSNE; if we select too few PCs we might loose the important data structures. To get a better understanding how many PCs to include, randomization will be employed and the observed variance will be compared to the permuted variance.

Value

matrix with explained variance

Author(s)

Thomas Naake

Examples

```
x <- matrix(seq_len(100), nrow = 10, ncol = 10,
    dimnames = list(seq_len(10), paste("sample", seq_len(10))))
permuteExplVar(x = x, n = 10, center = TRUE, scale = TRUE, sample_n = NULL)
```

---

plotCV *Plot CV values*

Description

The function plotCV displays the coefficient of variation values of set of values supplied in a data.frame object. The function will create a plot using the ggplot2 package and will print the values in the different columns in different colors.

Usage

```
plotCV(df)
```

Arguments

df	data.frame containing one or multiple columns containing the coefficients of variation

Details

Internal usage in shinyQC.

Value

gg object from ggplot2

Examples

```
x1 <- matrix(seq_len(10), ncol = 2)
x2 <- matrix(seq(11, 20), ncol = 2)
x3 <- matrix(seq(21, 30), ncol = 2)
x4 <- matrix(seq(31, 40), ncol = 2)

## calculate cv values
cv1 <- cv(x1, "x1")
cv2 <- cv(x2, "x2")
cv3 <- cv(x3, "x3")
cv4 <- cv(x4, "x4")
```

```
df <- data.frame(cv1, cv2, cv3, cv4)
plotCV(df)
```

---

plotPCALoadings *Plot for PCA loadings of features*

Description

The function plotPCALoadings creates a loadings plot of the features.

Usage

```
plotPCALoadings(tbl, x_coord, y_coord)
```

Arguments

tbl	tbl as obtained by the function dimensionReduction
x_coord	character, column name of tbl that stores x coordinates
y_coord	character, column name of tbl that stores y coordinates

Details

The function takes as input the output of the function tblPlotPCALoadings. It uses the ggplotly function from plotly to create an interactive plotly plot.

Value

plotly

Author(s)

Thomas Naake

Examples

```
x <- matrix(rnorm(seq_len(10000)), ncol = 100)
rownames(x) <- paste("feature", seq_len(nrow(x)))
colnames(x) <- paste("sample", seq_len(ncol(x)))
params <- list(method = "euclidean", ## dist
    initial_dims = 10, max_iter = 100, dims = 3, perplexity = 3, ## tSNE
    min_dist = 0.1, n_neighbors = 15, spread = 1) ## UMAP
tbl <- tblPCALoadings(x, params)
plotPCALoadings(tbl, x_coord = "PC1", y_coord = "PC2")
```

plotPCAVar *Plot of explained variance against the principal components*

Description

The function plotPCAVar plots the explained variance (in y-axis against the principal components for the measured and permuted values.

Usage

```
plotPCAVar(var_x, var_perm = NULL)
```

Arguments

var_x	numeric (named numeric vector)
var_perm	matrix with the explained variance obtained by permutation (function permuteExplVar)

Details

The argument var_perm is optional and visualization of permuted values can be omitted by setting var_perm = NULL.

Value

gg object from ggplot

Author(s)

Thomas Naake

Examples

```
x <- matrix(seq_len(100), ncol = 10)
pca <- dimensionReduction(x = x, params = list(center = TRUE, scale = TRUE),
    type = "PCA")[[2]]
var_x <- explVar(d = pca, type = "PCA")
var_perm <- permuteExplVar(x = x, n = 100, center = TRUE, scale = TRUE)
plotPCAVar(var_x = var_x, var_perm = var_perm)
```

plotPCAVarPvalue *Plot p-values for the significance of principal components*

Description

The function plotPCAVarPvalue plots the p-values of significances of principal components. Using the visual output, the optimal number of principal components can be selected.

Usage

```
plotPCAVarPvalue(var_x, var_perm)
```

Arguments

var_x	numeric, measured variances
var_perm	matrix, variances obtained by permutation

Details

Internal usage in shinyQC.

Value

gg object from ggplot

Author(s)

Thomas Naake

Examples

```
x <- matrix(seq_len(100), ncol = 10)
pca <- dimensionReduction(x = x, params = list(center = TRUE, scale = TRUE),
    type = "PCA")[[2]]
var_x <- explVar(d = pca, type = "PCA")
var_perm <- permuteExplVar(x = x, n = 100, center = TRUE, scale = TRUE)
plotPCAVarPvalue(var_x = var_x, var_perm = var_perm)
```

samplesMeasuredMissing *Create tibble containing number of measured/missing features of samples*

Description

samplesMeasuredMissing returns a tbl with the number of measured/missing features of samples. The function will take as input a SummarizedExperiment object and will access its assay() slot

Usage

```
samplesMeasuredMissing(se)
```

Arguments

se	SummarizedExperiment object

Value

tbl with number of measured/missing features per sample

Examples

```
## create se
a <- matrix(seq_len(100), nrow = 10, ncol = 10,
            dimnames = list(seq_len(10), paste("sample", seq_len(10))))
a[c(1, 5, 8), seq_len(5)] <- NA
set.seed(1)
a <- a + rnorm(100)
sample <- data.frame(name = colnames(a), type = c(rep("1", 5), rep("2", 5)))
featData <- data.frame(spectra = rownames(a))
se <- SummarizedExperiment::SummarizedExperiment(assay = a,
    rowData = featData, colData = sample)

## create the data.frame with information on number of measured/missing
## values
samplesMeasuredMissing(se)
```

shinyQC *Shiny application for initial QC exploration of -omics data sets*

Description

The shiny application allows to explore -omics data sets especially with a focus on quality control. shinyQC gives information on the type of samples included (if this was previously specified within the SummarizedExperiment object). It gives information on the number of missing and measured values across features and across sets (e.g. quality control samples, control, and treatment groups, only displayed for SummarizedExperiment objects that contain missing values).

shinyQC includes functionality to display (count/intensity) values across samples (to detect drifts in intensity values during the measurement), to display mean-sd plots, MA plots, ECDF plots, and distance plots between samples. shinyQC includes functionality to perform dimensionality reduction (currently limited to PCA, PCoA, NMDS, tSNE, and UMAP). Additionally, it includes functionality to perform differential expression analysis (currently limited to moderated t-tests and the Wald test).

Usage

```
shinyQC(se, app_server = FALSE)
```

Arguments

se	SummarizedExperiment object (can be omitted)
app_server	logical (set to TRUE if run under a server environment)

Details

rownames(se) should be set to the corresponding name of features, while colnames(se) should be set to the sample IDs. rownames(se) and colnames(se) are not allowed to be NULL. colnames(se), colnames(assay(se)) and rownames(colData(se)) all have to be identical.

shinyQC allows to subset the supplied SummarizedExperiment object.

On exit of the shiny application, the (subsetted) SummarizedExperiment object is returned with information on the processing steps (normalization, transformation, batch correction and imputation). The object will only returned if app_server = FALSE and if the function call is assigned to an object, e.g. tmp <- shinyQC(se).

If the se argument is omitted the app will load an interface that allows for data upload.

Value

shiny application, SummarizedExperiment upon exiting the shiny application

Author(s)

Thomas Naake

Examples

```
library(dplyr)
library(SummarizedExperiment)

## create se
set.seed(1)
a <- matrix(rnorm(100, mean = 10, sd = 2), nrow = 10, ncol = 10,
            dimnames = list(seq_len(10), paste("sample", seq_len(10))))
a[c(1, 5, 8), seq_len(5)] <- NA
cD <- data.frame(name = colnames(a), type = c(rep("1", 5), rep("2", 5)))
rD <- data.frame(spectra = rownames(a))
se <- SummarizedExperiment(assay = a, rowData = rD, colData = cD)

shinyQC(se)
```

`sumDistSample` *Plot the sum of distances to other samples*

Description

The function `sumDistSample` creates a plot showing the sum of distance of a sample to other samples.

Usage

```
sumDistSample(d, title = "raw")
```

Arguments

`d`	`matrix` containing distances, obtained from `distShiny`
`title`	`character` specifying the title to be added to the plot

Value

gg object from `ggplot2`

Examples

```
a <- matrix(seq_len(100), nrow = 10, ncol = 10,
            dimnames = list(seq_len(10), paste("sample", seq_len(10))))
dist <- distShiny(a)

sumDistSample(dist, title = "raw")
```

tblPCALoadings *Return tibble with PCA loadings for features*

Description

The function tblPCALoadings returns a tibble with loadings values for the features (row entries) in x.

Usage

```
tblPCALoadings(x, params)
```

Arguments

x	matrix, containing no missing values
params	list, arguments/parameters given to the function stats::prcomp

Details

The function tblPCALoadings acccesses the list entry rotation of the prcomp object.

Value

tbl

Author(s)

Thomas Naake

Examples

```
set.seed(1)
x <- matrix(rnorm(seq_len(10000)), ncol = 100)
rownames(x) <- paste("feature", seq_len(nrow(x)))
colnames(x) <- paste("sample", seq_len(ncol(x)))
params <- list(method = "euclidean", ## dist
    initial_dims = 10, max_iter = 100, dims = 3, perplexity = 3, ## tSNE
    min_dist = 0.1, n_neighbors = 15, spread = 1) ## UMAP
tblPCALoadings(x, params)
```

transformAssay *Transform the (count/intensity) values of a* data.frame*,* tbl *or* matrix

Description

The function transformAssay transforms the (count/intensity) values of a matrix. It uses either log, log2, log10, variance stabilizing normalisation (vsn) or no transformation method (pass-through, none). The object x has the samples in the columns and the features in the rows.

Usage

```
transformAssay(
  a,
  method = c("none", "log", "log2", "log10", "vsn"),
  .offset = 1
)
```

Arguments

a	matrix with samples in columns and features in rows
method	character, one of "none", "log", "log2", "log10", or "vsn"
.offset	numeric(1), offset to add when method set to "log", "log2", or "log10" and a contains values of 0, default to 1

Details

Internal use in shinyQC.

Value

matrix

Examples

```
a <- matrix(seq_len(1000), nrow = 100, ncol = 10,
        dimnames = list(seq_len(100), paste("sample", seq_len(10))))
transformAssay(a, "none")
transformAssay(a, "log")
transformAssay(a, "log2")
transformAssay(a, "vsn")
```

upsetCategory *UpSet plot to display measures values across sample types*

Description

The function upsetCategory displays the frequency of measured values per feature with respect to class/sample type to assess difference in occurrences. Internally, the measured values per sample are obtained via the measuredCategory function: this function will access the number of measured/missing values per category and feature. From this, a binary tbl will be created specifying if the feature is present/missing, which will be given to the upset function from the UpSetR package.

Usage

```
upsetCategory(se, category = colnames(colData(se)), measured = TRUE)
```

Arguments

se	SummarizedExperiment, containing the intensity values in assay(se), missing values are encoded by NA
category	character, corresponding to a column in colData(se)
measured	logical, should the measured values (measured = TRUE) or missing values (measured = FALSE) be taken

Details

Presence is defined by a feature being measured in at least one sample of a set.

Absence is defined by a feature with only missing values (i.e. no measured values) of a set.

Value

upset plot

Examples

```
## create se
a <- matrix(seq_len(100), nrow = 10, ncol = 10,
            dimnames = list(seq_len(10), paste("sample", seq_len(10))))
a[c(1, 5, 8), seq_len(5)] <- NA
set.seed(1)
a <- a + rnorm(100)
cD <- data.frame(name = colnames(a), type = c(rep("1", 5), rep("2", 5)))
rD <- data.frame(spectra = rownames(a))
se <- SummarizedExperiment::SummarizedExperiment(assay = a,
    rowData = rD, colData = cD)

upsetCategory(se, category = "type")
```

volcanoPlot *Volcano plot of fold changes/differences against p-values*

Description

The function ComplexHeatmap creates a volcano plot. On the y-axis the -log10(p-values) are displayed, while on the x-axis the fold changes/differences are displayed. The output of the function differs depending on the type parameter. For type == "ttest", the fold changes are plotted; for type == "proDA", the differences are plotted.

Usage

```
volcanoPlot(df, type = c("ttest", "proDA"))
```

Arguments

df	data.frame as received from topTable (ttest) or test_diff (proDA)
type	character

Details

Internal use in shinyQC.

Value

plotly

Examples

```
## create se
a <- matrix(seq_len(100), nrow = 10, ncol = 10,
            dimnames = list(seq_len(10), paste("sample", seq_len(10))))
a[c(1, 5, 8), seq_len(5)] <- NA
set.seed(1)
a <- a + rnorm(100)
a_i <- imputeAssay(a, method = "MinDet")
cD <- data.frame(sample = colnames(a),
    type = c(rep("1", 5), rep("2", 5)))
rD <- data.frame(spectra = rownames(a))
se <- SummarizedExperiment::SummarizedExperiment(assay = a,
                                rowData = rD, colData = cD)
se_i <- SummarizedExperiment::SummarizedExperiment(assay = a_i,
                                rowData = rD, colData = cD)

## create model and contrast matrix
modelMatrix_expr <- stats::formula("~ 0 + type")
contrast_expr <- "type1-type2"
modelMatrix <- model.matrix(modelMatrix_expr, data = colData(se))
contrastMatrix <- limma::makeContrasts(contrasts = contrast_expr,
```

```
                                levels = modelMatrix)

## ttest
fit <- limma::lmFit(a_i, design = modelMatrix)
fit <- limma::contrasts.fit(fit, contrastMatrix)
fit <- limma::eBayes(fit, trend = TRUE)
df_ttest <- limma::topTable(fit, n = Inf, adjust = "fdr", p = 0.05)
df_ttest <- cbind(name = rownames(df_ttest), df_ttest)

## plot
volcanoPlot(df_ttest, type = "ttest")

## proDA

fit <- proDA::proDA(a, design = modelMatrix)
df_proDA <- proDA::test_diff(fit = fit, contrast = contrast_expr,
        sort_by = "adj_pval")

## plot
volcanoPlot(df_proDA, type = "proDA")
```

Index

barplotSamplesMeasuredMissing, 3
batchCorrectionAssay, 4

createBoxplot, 5
createDfFeature, 7
cv, 8
cvFeaturePlot, 8

dimensionReduction, 9
dimensionReductionPlot, 10
distSample, 12
distShiny, 13
driftPlot, 14

ECDF, 15
explVar, 16
extractComb, 17

featurePlot, 18

hist_sample, 19
hist_sample_num, 20
histFeature, 20
histFeatureCategory, 21
hoeffDPlot, 22
hoeffDValues, 23

imputeAssay, 24

MAplot, 26
MAvalues, 27
measuredCategory, 28
mosaic, 29

normalizeAssay, 30

permuteExplVar, 31
plotCV, 32
plotPCALoadings, 33
plotPCAVar, 34
plotPCAVarPvalue, 35

samplesMeasuredMissing, 36
shinyQC, 37
sumDistSample, 38

tblPCALoadings, 39
transformAssay, 40

upsetCategory, 41

volcanoPlot, 42