

# Package ‘MatrixQCvis’

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**Type** Package

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

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**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)

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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

<code>se</code>	<code>SummarizedExperiment</code>
<code>method</code>	character, one of "none" or "removeBatchEffect"
<code>batch</code>	character, NULL or one of <code>colnames(colData(se))</code>
<code>batch2</code>	character, NULL or one of <code>colnames(colData(se))</code>
<code>...</code>	further arguments passed to <code>removeBatchEffect</code> or <code>ComBat</code>

## 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**

<code>se</code>	SummarizedExperiment containing the (count/intensity) values in the assay slot
<code>orderCategory</code>	character, one of <code>colnames(colData(se))</code>
<code>title</code>	character or numeric of length(1)
<code>log</code>	logical, if TRUE (count/intensity) values are displayed as log values
<code>violin</code>	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	<i>Create data frame of (count/intensity) values for a selected feature along data processing steps</i>
-----------------	---

---

**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  $\text{sd}(y) / \text{mean}(y) * 100$  with  $y$  the column values, thus, the function returns the coefficient of variation in percentage.

## Usage

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

## Arguments

<code>x</code>	matrix
<code>name</code>	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	<i>Plot of feature-wise coefficient of variation values</i>
---------------	---

---

### 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

<code>l</code>	list containing matrices
<code>lines</code>	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	<i>Dimensionality reduction with dimensionReduction methods PCA, PCoA, NMDS, UMAP and tSNE</i>
--------------------	--

---

### 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**

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

**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

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

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

**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**

<code>x</code>	matrix or <code>data.frame</code> with samples in columns and features in rows
<code>method</code>	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**

<code>se</code>	<code>SummarizedExperiment</code>
<code>aggregation</code>	character, type of aggregation of (count/intensity) values
<code>category</code>	character, column of <code>colData(se)</code>
<code>orderCategory</code>	character, column of <code>colData(se)</code>
<code>level</code>	character, from which samples should the LOESS curve be calculated, either "all" or one of the levels of the selected columns of <code>colData(se)</code> ("category")
<code>method</code>	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	<i>Retrieve the explained variance for each principal component (PCA) or axis (PCoA)</i>
---------	--

---

### 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

<code>d</code>	prcomp or list from <code>cmdscale</code>
<code>type</code>	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

<code>se</code>	SummarizedExperiment
<code>combination</code>	character, refers to factors in category
<code>measured</code>	logical
<code>category</code>	character, corresponding to a column name in <code>colData(se)</code>

### 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	<i>Create a plot of (count/intensity) values over the samples</i>
-------------	---

---

**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**

<code>df</code>	<code>data.frame</code>
-----------------	-------------------------

**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(1, "feature 1")
featurePlot(df)
```

---

histFeature	<i>Histogram for measured value per feature</i>
-------------	---

---

**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")
```

---

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	<i>Return the number of a category</i>
-----------------	--

---

### 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")
```

---

hoeffDPlot	<i>Create a plot from a list of Hoeffding's D values</i>
------------	--

---

### 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	<i>Impute missing values in a matrix</i>
-------------	--

---

### Description

The function `impute` imputes missing values based on one of the following principles: Bayesian missing value imputation (BPCA), k-nearest neighbor averaging (kNN), Maximum 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

<code>a</code>	matrix with samples in columns and features in rows
<code>method</code>	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`. 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 Gaussian 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 MValues function
group	character, one of colnames(colData(se)) (se used in MValues) or "all"
plot	character, one of colData(se)\$name (se used in MValues) 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 (referring 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 (except 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)) except 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 $\log_2(\text{assay}(se) + 1)$
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	<i>Obtain the number of measured intensities per sample type</i>
------------------	--

---

### 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

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

### 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	<i>Mosaic plot for two factors in colData(se)</i>
--------	---

---

## 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

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

## 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

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

---

permutExplVar	<i>Permute the expression values and retrieve the explained variance</i>
---------------	--

---

**Description**

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

**Usage**

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

**Arguments**

<code>x</code>	matrix or data.frame, samples in columns and features in rows
<code>n</code>	numeric, number of permutation rounds
<code>center</code>	logical, passed to the function <code>explVar</code>
<code>scale</code>	logical, passed to the function <code>explVar</code>
<code>sample_n</code>	numeric(1), number of features (subset) to be taken for calculation of permuted explained variance, the top <code>sample_n</code> 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` function). The reduced data set is used for feeding into tSNE. By plotting the percentage of variance explained by the Principal 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 lose 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))))
permutExplVar(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	<i>Plot for PCA loadings of features</i>
-----------------	--

---

### 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	<i>Plot of explained variance against the principal components</i>
------------	--

---

**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**

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

**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	<i>Plot p-values for the significance of principal components</i>
------------------	---

---

**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 tibble 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**

tibble 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 (subsetting) SummarizedExperiment object is returned with information on the processing steps (normalization, transformation, batch correction and imputation). The object will only be 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` accesses the list entry `rotation` of the `prcomp` object.

**Value**

tibble

**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	<i>Transform the (count/intensity) values of a data.frame, tbl or matrix</i>
----------------	--

---

### 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

<code>a</code>	matrix with samples in columns and features in rows
<code>method</code>	character, one of "none", "log", "log2", "log10", or "vsn"
<code>.offset</code>	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

<code>se</code>	SummarizedExperiment, containing the intensity values in <code>assay(se)</code> , missing values are encoded by NA
<code>category</code>	character, corresponding to a column in <code>colData(se)</code>
<code>measured</code>	logical, should the measured values ( <code>measured = TRUE</code> ) or missing values ( <code>measured = FALSE</code> ) 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  $-\log_{10}$ (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**

<code>df</code>	data.frame as received from <code>topTable(ttest)</code> or <code>test_diff(proDA)</code>
<code>type</code>	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")
```



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