

# Package ‘NormalyzerDE’

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**Title** Evaluation of normalization methods and calculation of differential expression analysis statistics

**Version** 1.25.0

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**Description** NormalyzerDE provides screening of normalization methods for LC-MS based expression data. It calculates a range of normalized matrices using both existing approaches and a novel time-segmented approach, calculates performance measures and generates an evaluation report. Furthermore, it provides an easy utility for Limma- or ANOVA- based differential expression analysis.

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---

analyzeNormalizations *Calculate measures for normalization results*

---

**Description**

This function prepares an `NormalizerEvaluationResults` object containing the evaluation measures CV (coefficient of variance), MAD (median absolute deviation), average variance, significance measures (ANOVA between condition groups) and correlation between replicates.

**Usage**

```
analyzeNormalizations(nr, categoricalAnova = FALSE)
```

**Arguments**

`nr` Normalizer results object with calculated results.  
`categoricalAnova` Whether categorical or numerical (ordered) ANOVA should be calculated.

**Value**

Normalizer results with attached evaluation results object.

**Examples**

```
data(example_summarized_experiment)
normObj <- getVerifiedNormalizerObject("job_name", example_summarized_experiment)
normResults <- normMethods(normObj)
normResultsWithEval <- analyzeNormalizations(normResults)
```

---

calculateANOVAPValues *Calculates ANOVA p-values comparing the different condition groups returning a vector of resulting p-values with NA-values where too few values were present in at least one of the groups.*

---

**Description**

Calculates ANOVA p-values comparing the different condition groups returning a vector of resulting p-values with NA-values where too few values were present in at least one of the groups.

**Usage**

```
calculateANOVAPValues(methodList, sampleReplicateGroups, categoricalANOVA)
```

**Arguments**

- methodList      List containing normalized matrices
- sampleReplicateGroups  
                  Condition header
- categoricalANOVA  
                  Whether the ANOVA should be calculated using ordered or categorical groups

**Value**

avgVarianceMat Matrix with average variance for each biological condition

---

calculateAvgMadMem      *Calculate average MAD (Median Absolute Deviation) for each feature in each condition and then calculates the average for each replicate group*

---

**Description**

Calculate average MAD (Median Absolute Deviation) for each feature in each condition and then calculates the average for each replicate group

**Usage**

calculateAvgMadMem(methodList, sampleReplicateGroups)

**Arguments**

- methodList      List containing normalized matrices.
- sampleReplicateGroups  
                  Condition header.

**Value**

condAvgMadMat Matrix with average MAD for each biological condition.

---

```
calculateAvgReplicateVariation
```

*Calculate average variance for each feature in each condition and then calculate the average for each replicate group*

---

### Description

Calculate average variance for each feature in each condition and then calculate the average for each replicate group

### Usage

```
calculateAvgReplicateVariation(methodList, sampleReplicateGroups)
```

### Arguments

methodList      List containing normalized matrices.  
 sampleReplicateGroups  
                   Condition header.

### Value

avgVarianceMat Matrix with average variance for each biological condition

---

```
calculateContrasts
```

*Performs statistical comparisons between the supplied conditions. It uses the design matrix and data matrix in the supplied Normalyzer-Statistics object. A column is supplied specifying which of the columns in the design matrix that is used for deciding the sample groups. The comparisons vector specifies which pairwise comparisons between condition levels that are to be calculated.*

---

### Description

Optionally, a batch column can be specified allowing compensation for covariate variation in the statistical model. This is only compatible with a Limma-based statistical analysis.

### Usage

```
calculateContrasts(  
  nst,  
  comparisons,  
  condCol,  
  batchCol = NULL,  
  splitter = "-",
```

```

    type = "limma",
    leastRepCount = 1
  )

  ## S4 method for signature 'NormalizerStatistics'
  calculateContrasts(
    nst,
    comparisons,
    condCol,
    batchCol = NULL,
    splitter = "-",
    type = "limma",
    leastRepCount = 1
  )

```

### Arguments

nst	Results evaluation object.
comparisons	String with comparisons for contrasts.
condCol	Column name in design matrix containing condition information.
batchCol	Column name in design matrix containing batch information.
splitter	Character dividing contrast conditions.
type	Type of statistical test (Limma or welch).
leastRepCount	Least replicates in each group to be retained for contrast calculations

### Value

nst Statistics object with statistical measures calculated

### Examples

```

data(example_stat_summarized_experiment)
nst <- NormalizerStatistics(example_stat_summarized_experiment)
results <- calculateContrasts(nst, c("1-2", "2-3"), "group")
resultsBatch <- calculateContrasts(nst, c("1-2", "2-3"), "group", batchCol="batch")

```

---

calculateCorrSum	<i>Calculates internal correlations for each condition having at least two samples and returns a vector with correlation values corresponding to each condition</i>
------------------	---

---

### Description

Calculates internal correlations for each condition having at least two samples and returns a vector with correlation values corresponding to each condition

**Usage**

```
calculateCorrSum(
  methodData,
  allReplicateGroups,
  sampleGroupsWithReplicates,
  corrType
)
```

**Arguments**

methodData      Expression data matrix

allReplicateGroups      Full condition header corresponding to data tables columns

sampleGroupsWithReplicates      Unique conditions where number of replicates exceeds one

corrType      Type of correlation (Pearson or Spearman)

**Value**

corSums

---

calculateFeatureCV	<i>Calculate CV values for each feature. Iterates through each normalization method and calculates a matrix of CV values where each column correspond to a method and each row corresponds to a feature.</i>
--------------------	--

---

**Description**

Calculate CV values for each feature. Iterates through each normalization method and calculates a matrix of CV values where each column correspond to a method and each row corresponds to a feature.

**Usage**

```
calculateFeatureCV(methodList)
```

**Arguments**

methodList      List containing normalized matrices.

sampleReplicateGroups      Condition header.

**Value**

methodFeatureCVMatrix Matrix with feature as rows and normalization method as columns



---

`calculatePercentageAvgDiffInMat`

*General function for calculating percentage difference of average column means in matrix*

---

**Description**

General function for calculating percentage difference of average column means in matrix

**Usage**

```
calculatePercentageAvgDiffInMat(targetMat)
```

**Arguments**

`targetMat`      Matrix for which column means should be compared

**Value**

`percDiffVector` Vector with percentage difference, where first element always will be 100

---

`calculateReplicateCV`    *Calculate CV per replicate group and normalization technique*

---

**Description**

Iterates through each normalization method and calculate average CV values per replicate group.

**Usage**

```
calculateReplicateCV(methodList, sampleReplicateGroups)
```

**Arguments**

`methodList`      List containing normalized matrices.  
`sampleReplicateGroups`  
                    Condition header.

**Value**

`avgCVPerNormAndReplicates` Matrix with group CVs as rows and normalization technique as columns

---

calculateSummarizedCorrelationVector

*Calculates correlation values between replicates for each condition matrix. Finally returns a matrix containing the results for all dataset*

---

### Description

Calculates correlation values between replicates for each condition matrix. Finally returns a matrix containing the results for all dataset

### Usage

```
calculateSummarizedCorrelationVector(
  methodlist,
  allReplicateGroups,
  sampleGroupsWithReplicates,
  corrType
)
```

### Arguments

methodlist	List containing normalized matrices for each normalization method
allReplicateGroups	Vector with condition groups matching the columns found in the normalization methods
sampleGroupsWithReplicates	Unique vector with condition groups present in two or more samples
corrType	Type of correlation (Pearson or Spearman)

### Value

avgCorSum Matrix with column corresponding to normalization approaches and rows corresponding to replicate group

---

createDirectory      *Create directory, or return error if already present*

---

### Description

Create directory, or return error if already present

### Usage

```
createDirectory(targetPath)
```

**Arguments**

targetPath      Path where to attempt to create directory

**Value**

None

---

*detectSingleReplicate*    *Detect single replicate, and assign related logical*

---

**Description**

Detect single replicate, and assign related logical

**Usage**

```
detectSingleReplicate(nds, quiet)

## S4 method for signature 'NormalizerDataset'
detectSingleReplicate(nds, quiet = FALSE)
```

**Arguments**

nds              Normalizer dataset  
quiet            Don't give non-error output

**Value**

bool on whether sample contains only one sample group

---

*detectSingletonSample*    *Detect single sample group*

---

**Description**

Detect single sample group

**Usage**

```
detectSingletonSample(nds, quiet)

## S4 method for signature 'NormalizerDataset'
detectSingletonSample(nds, quiet = FALSE)
```

**Arguments**

nds	Normalyzer dataset.
quiet	Only print error messages

**Value**

None

---

 elapsedSecondsBetweenSystimes

*Get number of seconds between two Sys.time() objects*


---

**Description**

Get number of seconds between two Sys.time() objects

**Usage**

```
elapsedSecondsBetweenSystimes(start, end)
```

**Arguments**

start	Start-time object
end	End-time object

**Value**

None

---

 example\_data

*Small example dataset used to demonstrate code consistency in testing and as dummy data in the vignette.*


---

**Description**

Small example dataset used to demonstrate code consistency in testing and as dummy data in the vignette.

**Usage**

```
example_data
```

**Format**

A data frame containing annotation and expression data

---

example\_data\_only\_values

*Same data as in "example\_data", but omitting the annotation meaning that it only contains the expression data.*

---

**Description**

Same data as in "example\_data", but omitting the annotation meaning that it only contains the expression data.

**Usage**

example\_data\_only\_values

**Format**

A data frame containing expression data

---

example\_design

*Design matrix corresponding to the small example datasets.*

---

**Description**

Design matrix corresponding to the small example datasets.

**Usage**

example\_design

**Format**

A design matrix corresponding to the dataset "example\_data"

---

example_stat_data	<i>Same data as in "example_data", but normalized and ready for statistical processing.</i>
-------------------	---

---

**Description**

Same data as in "example\_data", but normalized and ready for statistical processing.

**Usage**

```
example_stat_data
```

**Format**

A normalized data frame ready for statistical processing

---

example_stat_summarized_experiment	<i>SummarizedExperiment object prepared with design-matrix, data-matrix and annotation columns for normalized data</i>
------------------------------------	--

---

**Description**

SummarizedExperiment object prepared with design-matrix, data-matrix and annotation columns for normalized data

**Usage**

```
example_stat_summarized_experiment
```

**Format**

An instance of the class SummarizedExperiment with stats data

---

example\_summarized\_experiment

*SummarizedExperiment object prepared with design-matrix, data-matrix and annotation columns loaded for raw data*

---

### **Description**

SummarizedExperiment object prepared with design-matrix, data-matrix and annotation columns loaded for raw data

### **Usage**

```
example_summarized_experiment
```

### **Format**

An instance of the class SummarizedExperiment

---

example\_wide\_data

*Full raw NormalyzerDE matrix used for internal testing*

---

### **Description**

Full raw NormalyzerDE matrix used for internal testing

### **Usage**

```
example_wide_data
```

### **Format**

A data table ready for analysis in NormalyzerDE

---

example_wide_design	<i>Design matrix belonging together with example_wide_data. Used for internal testing.</i>
---------------------	--

---

**Description**

Design matrix belonging together with example\_wide\_data. Used for internal testing.

**Usage**

```
example_wide_design
```

**Format**

A design table ready for analysis in NormalyzerDE

---

filterLowRep	<i>Filter rows with lower than given number of replicates for any condition</i>
--------------	---

---

**Description**

Filter rows with lower than given number of replicates for any condition

**Usage**

```
filterLowRep(df, groups, leastRep = 2)
```

**Arguments**

df	Dataframe with expression data to filter
groups	Condition groups header
leastRep	Minimum number of replicates in each group to retain

**Value**

collDesignDf Reduced design matrix



---

findLowlyVariableFeaturesCVs

*Uses a list of FDR-values to extract features with low variance in the log2-transformed dataset. This is then used to calculate the average CV for these 'lowly variable' features in each normalization approach*

---

### Description

Uses a list of FDR-values to extract features with low variance in the log2-transformed dataset. This is then used to calculate the average CV for these 'lowly variable' features in each normalization approach

### Usage

```
findLowlyVariableFeaturesCVs(referenceFDR, methodList)
```

### Arguments

referenceFDR	List of FDR values used as non-normalized reference
methodList	List containing normalized matrices

### Value

lowVarFeaturesAverageCVs Average CV values for lowly variable features in each normalization approach

---

generateAnnotatedMatrix

*Generate an annotated data frame from statistics object*

---

### Description

Extracts key values (p-value, adjusted p-value, log2-fold change and average expression values) from an NormalyzerStatistics instance and appends these to the annotation- and data-matrices

### Usage

```
generateAnnotatedMatrix(nst, prefixSep = "_", compLabels = NULL)
```

### Arguments

nst	NormalyzerDE statistics object.
prefixSep	Character string for separating the prefix names from the statistics suffix
compLabels	Vector containing strings to use as prefix for statistical comparisons

**Value**

outDf Annotated statistics matrix

**Examples**

```
data(example_stat_summarized_experiment)
statObj <- NormalyzerStatistics(example_stat_summarized_experiment)
statObj <- calculateContrasts(statObj, comparisons=c("1-2", "2-3"), condCol="group", type="limma")
annotDf <- generateAnnotatedMatrix(statObj)
```

---

generatePlots	<i>Generates a number of visualizations for the performance measures calculated for the normalized matrices. These contain both general measures and direct comparisons for different normalization approaches.</i>
---------------	---

---

**Description**

They include:

**Usage**

```
generatePlots(nr, jobdir, plotRows = 3, plotCols = 4, writeAsPngs = FALSE)
```

**Arguments**

nr	Normalyzer results object.
jobdir	Path to output directory for run.
plotRows	Number of plot rows.
plotCols	Number of plot columns.
writeAsPngs	Output the report as PNG-plots instead of a single PDF

**Details**

"Total intensity" Barplot showing the summed intensity in each sample for thelog2-transformed data

"Total missing" Barplot showing the number of missing values found in each sample for the log2-transformed data

Log2-MDS plot: MDS plot where data is reduced to two dimensions allowing inspection of the main global changes in the data

PCV - Intragroup: Mean of intragroup CV of all replicate groups

PMAD - Intragroup: Mean of intragroup median absolute deviation across replicate groups

PEV - Intragroup: Mean of intragroup pooled estimate of variance across the replicate groups

Relative PCV, PMAD and PEV compared to log2: The results from PCV, PMAD and PEV from all normalized data compared to the log2 data

Stable variables plot: 5 analysis of log2 transformed data. Thereafter, global CV of these variables is estimated from different normalized datasets. A plot of global CV of the stable variables from all datasets on the y-axis and PCV-compared to log2 on the x-axis is generated.

CV vs Raw Intensity plots: For the first replicate group in each of the normalized dataset, a plot of PCV of each variable compared to the average intensity of the variable in the replicate group is plotted.

MA plots: Plotted using the plotMA function of the limma package. The first sample in each dataset is plotted against the average of the replicate group that sample belong to.

Scatterplots: The first two samples from each dataset are plotted.

Q-Q plots: QQ-plots are plotted for the first sample in each normalized dataset.

Boxplots: Boxplots for all samples are plotted and colored according to the replicate grouping.

Relative Log Expression (RLE) plots: Relative log expression value plots. Ratio between the expression of the variable and the median expression of this variable across all samples. The samples should be aligned around zero. Any deviation would indicate discrepancies in the data.

Density plots: Density distributions for each sample using the density function. Can capture outliers (if single densities lies far from the others) and see if there is batch effects in the dataset (if for instance there is two clear collections of lines in the data).

MDS plots Multidimensional scaling plot using the cmdscale() function from the stats package. Is often able to show whether replicates group together, and whether there are any clear outliers in the data.

MeanSDplots Displays the standard deviation values against values ordered according to mean. If no dependency on mean is present (as is desired) a flat red line is shown.

Pearson and Spearman correlation Mean of intragroup Pearson and Spearman correlation values for each method.

Dendograms Generated using the hclust function. Data is centered and scaled prior to analysis. Coloring of replicates is done using as.phylo from the ape package.

P-value histograms Histogram plots of p-values after calculating an ANOVA between different condition groups. If no effect is present in the data a flat distribution is expected. If an effect is present a flat distribution is still expected, but with a sharp peak close to zero. If other effects are present it might indicate that the data doesn't support the assumptions of ANOVA, for instance if there are batch effects present in the data.

## Value

None

## Examples

```
data(example_summarized_experiment)
normObj <- getVerifiedNormalizerObject("job_name", example_summarized_experiment)
normResults <- normMethods(normObj)
normResultsWithEval <- analyzeNormalizations(normResults)
outputDir <- tempdir()
generatePlots(normResultsWithEval, outputDir)
```

---

`generateStatsReport`     *Generate full output report plot document. Plots p-value histograms for each contrast in the `NormalizerStatistics` instance and writes these to a PDF report.*

---

## Description

Generate full output report plot document. Plots p-value histograms for each contrast in the `NormalizerStatistics` instance and writes these to a PDF report.

## Usage

```
generateStatsReport(  
  nst,  
  jobName,  
  jobDir,  
  sigThres = 0.1,  
  sigThresType = "fdr",  
  log2FoldThres = 0,  
  plotRows = 3,  
  plotCols = 4,  
  writeAsPngs = FALSE  
)
```

## Arguments

<code>nst</code>	NormalizerDE statistics object.
<code>jobName</code>	Name of processing run.
<code>jobDir</code>	Path to output directory.
<code>sigThres</code>	Significance threshold for indicating as significant
<code>sigThresType</code>	Type of significance threshold (FDR or p)
<code>log2FoldThres</code>	log2 fold-change required for being counted as significant
<code>plotRows</code>	Number of plot rows.
<code>plotCols</code>	Number of plot columns.
<code>writeAsPngs</code>	Output the report as separate PNG files instead of a single PDF file

## Value

None

**Examples**

```
data(example_stat_summarized_experiment)
statObj <- NormalyzerStatistics(example_stat_summarized_experiment)
statObj <- calculateContrasts(statObj, comparisons=c("1-2", "2-3"),
  condCol="group", type="limma")
outputDir <- tempdir()
generateStatsReport(statObj, "jobName", outputDir)
```

---

getCombinedMatrix      *Merge multiple dataframes using provided function*

---

**Description**

Merge multiple dataframes using provided function

**Usage**

```
getCombinedMatrix(mList, combFunc)
```

**Arguments**

mList              List containing dataframes of same shape  
combFunc            Function performing elementwise merge of matrices

**Value**

combinedMatrix A single dataframe with combined data

---

getIndexList              *Return list containing vector positions of values in string*

---

**Description**

Return list containing vector positions of values in string

**Usage**

```
getIndexList(targetVector)
```

**Arguments**

targetVector

**Value**

indexList List where key is condition level and values are indices for the condition

---

`getLowCountSampleFiltered`*Verify that samples contain at least a lowest number of values*

---

**Description**

Verify that samples contain at least a lowest number of values

**Usage**

```
getLowCountSampleFiltered(  
  dataMatrix,  
  groups,  
  threshold = 15,  
  stopIfTooFew = TRUE  
)
```

**Arguments**

<code>dataMatrix</code>	Dataframe with processed input data.
<code>groups</code>	Vector containing condition levels.
<code>threshold</code>	Lowest number of allowed values in a column.
<code>stopIfTooFew</code>	Abort run if lower than threshold number of values in column

**Value**

None

---

`getReplicateSortedData`*Get dataframe with raw data column sorted on replicates*

---

**Description**

Get dataframe with raw data column sorted on replicates

**Usage**

```
getReplicateSortedData(rawDataOnly, groups)
```

**Arguments**

<code>rawDataOnly</code>	Dataframe with unparsed input data matrix.
<code>groups</code>	Vector containing condition levels.

**Value**

rawData sorted on replicate

---

getRowNAFilterContrast

*Get contrast vector (TRUE/FALSE-values) indicating whether both at least half values are present, and each sample has at least one non-NA value*

---

**Description**

Get contrast vector (TRUE/FALSE-values) indicating whether both at least half values are present, and each sample has at least one non-NA value

**Usage**

```
getRowNAFilterContrast(dataMatrix, replicateHeader, minCount = 1)
```

**Arguments**

dataMatrix	Matrix with expression values for entities in replicate samples.
replicateHeader	Header showing how samples in matrix are replicated.
minCount	Minimum number of required values present in samples.

**Value**

Contrast vector

---

getRTNormalizedMatrix *Perform RT-segmented normalization by performing the supplied normalization over retention-time sliced data*

---

**Description**

The function orders the retention times and steps through them using the supplied step size (in minutes). If smaller than a fixed lower boundary the window is expanded to ensure a minimum amount of data in each normalization step. An offset can be specified which can be used to perform multiple RT-segmentations with partial overlapping windows.

**Usage**

```
getRTNormalizedMatrix(
  rawMatrix,
  retentionTimes,
  normMethod,
  stepSizeMinutes = 1,
  windowMinCount = 100,
  offset = 0,
  noLogTransform = FALSE
)
```

**Arguments**

`rawMatrix` Target matrix to be normalized

`retentionTimes` Vector of retention times corresponding to `rawMatrix`

`normMethod` The normalization method to apply to the time windows

`stepSizeMinutes` Size of windows to be normalized

`windowMinCount` Minimum number of values for window to not be expanded.

`offset` Whether time window should shifted half step size

`noLogTransform` Don't log-transform the data

**Value**

Normalized matrix

**Examples**

```
data(example_data_small)
data(example_design_small)
data(example_data_only_values)
dataMat <- example_data_only_values
retentionTimes <- as.numeric(example_data[, "Average.RT"])
performCyclicLoessNormalization <- function(rawMatrix) {
  log2Matrix <- log2(rawMatrix)
  normMatrix <- limma::normalizeCyclicLoess(log2Matrix, method="fast")
  colnames(normMatrix) <- colnames(rawMatrix)
  normMatrix
}
rtNormMat <- getRTNormalizedMatrix(dataMat, retentionTimes,
performCyclicLoessNormalization, stepSizeMinutes=1, windowMinCount=100)
```



---

`getSmoothedRTNormalizedMatrix`

*Generate multiple RT time-window normalized matrices where one is shifted. Merge them using a specified method (mean or median) and return the result.*

---

### Description

Uses the function `getRTNormalizedMatrix` to generate multiple normalized matrices which are shifted respective to each other and finally merged into a single matrix. This could potentially reduce effect of fluctuations within individual windows.

### Usage

```
getSmoothedRTNormalizedMatrix(  
  rawMatrix,  
  retentionTimes,  
  normMethod,  
  stepSizeMinutes,  
  windowShifts = 2,  
  windowMinCount = 100,  
  mergeMethod = "mean",  
  noLogTransform = FALSE  
)
```

### Arguments

<code>rawMatrix</code>	Target matrix to be normalized
<code>retentionTimes</code>	Vector of retention times corresponding to <code>rawMatrix</code>
<code>normMethod</code>	The normalization method to apply to the time windows
<code>stepSizeMinutes</code>	Size of windows to be normalized
<code>windowShifts</code>	Number of frame shifts.
<code>windowMinCount</code>	Minimum number of features within window.
<code>mergeMethod</code>	Layer merging approach. Mean or median.
<code>noLogTransform</code>	Don't log transform the input

### Value

Normalized matrix

**Examples**

```

data(example_data_small)
data(example_data_only_values)
data(example_design_small)
retentionTimes <- as.numeric(example_data[, "Average.RT"])
dataMat <- example_data_only_values
performCyclicLoessNormalization <- function(rawMatrix) {
  log2Matrix <- log2(rawMatrix)
  normMatrix <- limma::normalizeCyclicLoess(log2Matrix, method="fast")
  colnames(normMatrix) <- colnames(rawMatrix)
  normMatrix
}
rtNormMat <- getSmoothedRTNormalizedMatrix(dataMat, retentionTimes,
  performCyclicLoessNormalization, stepSizeMinutes=1, windowMinCount=100,
  windowShifts=2, mergeMethod="median")

```

---

```
getVerifiedNormalizerObject
```

*Verify that input data is in correct format, and if so, return a generated NormalizerDE data object from that input data*

---

**Description**

This function performs a number of checks on the input data and provides informative error messages if the data isn't fulfilling the required format. Checks include verifying that the design matrix matches to the data matrix, that the data matrix contains valid numbers and that samples have enough values for analysis

**Usage**

```

getVerifiedNormalizerObject(
  jobName,
  summarizedExp,
  threshold = 15,
  omitSamples = FALSE,
  requireReplicates = TRUE,
  quiet = FALSE,
  noLogTransform = FALSE,
  tinyRunThres = 50
)

```

**Arguments**

jobName	Name of ongoing run.
summarizedExp	Summarized experiment input object
threshold	Minimum number of features.
omitSamples	Automatically omit invalid samples from analysis.

requireReplicates      Require there to be at least to samples per condition  
 quiet                  Don't print output messages during processing  
 noLogTransform      Don't log-transform the provided data  
 tinyRunThres        If less features in run, a limited run is performed

**Value**

Normalizer data object representing verified input data.

**Examples**

```
data(example_summarized_experiment)
normObj <- getVerifiedNormalizerObject("job_name", example_summarized_experiment)
```

---

getWidenedRTRange	<i>Pick datapoints before and after window until a minimum number is reached Expects the start and end retention times to match actual retention times present in the data</i>
-------------------	--

---

**Description**

Pick datapoints before and after window until a minimum number is reached Expects the start and end retention times to match actual retention times present in the data

**Usage**

```
getWidenedRTRange(
  rtStart,
  rtEnd,
  minimumDatapoints,
  retentionTimes,
  allowTooWideData = FALSE
)
```

**Arguments**

rtStart              Original retention time start point  
 rtEnd                Original retention time end point  
 minimumDatapoints      Required number of datapoints to fulfill  
 retentionTimes      Vector with all retention times

**Value**

Vector with start and end of new RT range

---

**globalIntensityNormalization**

*The normalization divides the intensity of each variable in a sample with the sum of intensities of all variables in the sample and multiplies with the median of sum of intensities of all variables in all samples. The normalized data is then log2-transformed.*

---

**Description**

The normalization divides the intensity of each variable in a sample with the sum of intensities of all variables in the sample and multiplies with the median of sum of intensities of all variables in all samples. The normalized data is then log2-transformed.

**Usage**

```
globalIntensityNormalization(rawMatrix, noLogTransform = FALSE)
```

**Arguments**

`rawMatrix` Target matrix to be normalized  
`noLogTransform` Assumes no need for log transformation

**Value**

Normalized and log-transformed matrix

**Examples**

```
data(example_data_only_values_small)  
normMatrix <- globalIntensityNormalization(example_data_only_values)
```

---

**loadData**

*Load raw data into dataframe*

---

**Description**

General function which allows specifying different types of input data including "proteios", "maxquant-pep" (peptide output from MaxQuant) and "maxquantprot" (protein output from MaxQuant) formats.

**Usage**

```
loadData(dataPath, inputFormat = "default")
```

**Arguments**

dataPath        File path to design matrix.  
inputFormat    If input is given in standard NormalyzerDE format, Proteios format or in MaxQuant protein or peptide format

**Value**

rawData Raw data loaded into data frame

**Examples**

```
## Not run:  
df <- loadData("data.tsv")  
  
## End(Not run)
```

---

loadDesign	<i>Load raw design into dataframe</i>
------------	---------------------------------------

---

**Description**

Takes a design path, loads the matrix and ensures that the sample column is in character format and that the group column is in factor format.

**Usage**

```
loadDesign(designPath, sampleCol = "sample", groupCol = "group")
```

**Arguments**

designPath        File path to design matrix.  
sampleCol        Column name for column containing sample names.  
groupCol         Column name for column containing condition levels.

**Value**

designMatrix Design data loaded into data frame

**Examples**

```
## Not run:  
df <- loadDesign("design.tsv")  
  
## End(Not run)
```

---

loadRawDataFromFile	<i>Try reading raw Normalyzer matrix from provided filepath</i>
---------------------	---

---

**Description**

Try reading raw Normalyzer matrix from provided filepath

**Usage**

```
loadRawDataFromFile(inputPath)
```

**Arguments**

inputPath      Path to Normalyzer data.

**Value**

Table containing raw data from input file.

---

meanNormalization	<i>Intensity of each variable in a given sample is divided by the mean of sum of intensities of all variables in the sample and then multiplied by the mean of sum of intensities of all variables in all samples. The normalized data is then transformed to log2.</i>
-------------------	---

---

**Description**

Intensity of each variable in a given sample is divided by the mean of sum of intensities of all variables in the sample and then multiplied by the mean of sum of intensities of all variables in all samples. The normalized data is then transformed to log2.

**Usage**

```
meanNormalization(rawMatrix, noLogTransform = FALSE)
```

**Arguments**

rawMatrix      Target matrix to be normalized  
noLogTransform Assumes no need for log transformation

**Value**

Normalized and log-transformed matrix

**Examples**

```
data(example_data_only_values_small)
normMatrix <- meanNormalization(example_data_only_values)
```

---

medianNormalization	<i>Intensity of each variable in a given sample is divided by the median of intensities of all variables in the sample and then multiplied by the mean of median of sum of intensities of all variables in all samples. The normalized data is then log2-transformed.</i>
---------------------	---

---

### Description

Intensity of each variable in a given sample is divided by the median of intensities of all variables in the sample and then multiplied by the mean of median of sum of intensities of all variables in all samples. The normalized data is then log2-transformed.

### Usage

```
medianNormalization(rawMatrix, noLogTransform = FALSE)
```

### Arguments

rawMatrix      Target matrix to be normalized  
noLogTransform   Assumes no need for log transformation

### Value

Normalized and log-transformed matrix

### Examples

```
data(example_data_only_values_small)  
normMatrix <- medianNormalization(example_data_only_values)
```

---

normalyzer	<i>NormalyzerDE pipeline entry point</i>
------------	--

---

### Description

This function is the main execution point for the normalization part of the NormalyzerDE analysis pipeline. When executed it performs the following steps:

**Usage**

```

normalyzer(
  jobName,
  designPath = NULL,
  dataPath = NULL,
  experimentObj = NULL,
  outputDir = ".",
  forceAllMethods = FALSE,
  omitLowAbundSamples = FALSE,
  sampleAbundThres = 5,
  tinyRunThres = 50,
  requireReplicates = TRUE,
  normalizeRetentionTime = TRUE,
  plotRows = 3,
  plotCols = 4,
  zeroToNA = FALSE,
  sampleColName = "sample",
  groupColName = "group",
  inputFormat = "default",
  skipAnalysis = FALSE,
  quiet = FALSE,
  noLogTransform = FALSE,
  writeReportAsPngs = FALSE,
  rtStepSizeMinutes = 1,
  rtWindowMinCount = 100,
  rtWindowShifts = 1,
  rtWindowMergeMethod = "mean"
)

```

**Arguments**

<code>jobName</code>	Give the current run a name.
<code>designPath</code>	Path to file containing design matrix.
<code>dataPath</code>	Specify an output directory for generated files. Defaults to current working directory.
<code>experimentObj</code>	SummarizedExperiment object, can be provided as input as alternative to 'designPath' and 'dataPath'
<code>outputDir</code>	Directory where results folder is created.
<code>forceAllMethods</code>	Debugging function. Run all normalizations even if they aren't in the recommended range of number of values
<code>omitLowAbundSamples</code>	Automatically remove samples with fewer non-NA values compared to threshold given by <code>sampleAbundThres</code> . Will otherwise stop with error message if such sample is encountered.
<code>sampleAbundThres</code>	Threshold for omitting low-abundant samples. Is by default set to 15.



<code>tinyRunThres</code>	If total number of features is less than this, a limited run is performed.
<code>requireReplicates</code>	Require multiple samples per condition to pass input validation.
<code>normalizeRetentionTime</code>	Perform normalizations over retention time.
<code>plotRows</code>	Number of plot-rows in output documentation.
<code>plotCols</code>	Number of plot-columns in output documentation.
<code>zeroToNA</code>	Convert zero values to NA.
<code>sampleColName</code>	Column name in design matrix containing sample IDs.
<code>groupColName</code>	Column name in design matrix containing condition IDs.
<code>inputFormat</code>	Type of input format.
<code>skipAnalysis</code>	Only perform normalization steps.
<code>quiet</code>	Omit status messages printed during run.
<code>noLogTransform</code>	Don't log-transform the input.
<code>writeReportAsPngs</code>	Output the evaluation report as PNG files instead of a single PDF
<code>rtStepSizeMinutes</code>	Retention time normalization window size.
<code>rtWindowMinCount</code>	Minimum number of datapoints in each retention-time segment.
<code>rtWindowShifts</code>	Number of layered retention time normalized windows.
<code>rtWindowMergeMethod</code>	Merge approach for layered retention time windows.

## Details

1: Loads the data matrix containing expression values and optional annotations, as well as the design matrix containing the experimental setup 2: Performs input data verification to validate that the data is in correct format. This step captures many common formatting errors. It returns an instance of the `NormalyzerDataset` class representing the unprocessed data. 3: Calculate a range of normalizations for the dataset. The result is provided as a `NormalyzerResults` object containing the resulting data matrices from each normalization. 4: Analyze the normalizations and generate performance measures for each of the normalized datasets. This result is provided as a `NormalyzerEvaluationResults` object. 5: Output the matrices containing the normalized datasets to files. 6: Generate visualizations overviewing the performance measures and write them to a PDF report.

## Value

None

## Examples

```
## Not run:
data_path <- system.file(package="NormalyzerDE", "extdata", "tiny_data.tsv")
design_path <- system.file(package="NormalyzerDE", "extdata", "tiny_design.tsv")
```

```

out_dir <- tempdir()
normalyzer(
  jobName="my_jobname",
  designPath=design_path,
  dataPath=data_path,
  outputDir=out_dir)
normalyzer(
  "my_jobname",
  designMatrix="design.tsv",
  "data.tsv",
  outputDir="path/to/output",
  normalizeRetentionTime=TRUE,
  retentionTimeWindow=2)
normalyzer(
  "my_jobname",
  designMatrix="design.tsv",
  "data.tsv",
  outputDir="path/to/output",
  inputFormat="maxquantprot")

## End(Not run)

```

---

NormalyzerDataset

*Represents raw input data together with basic annotation information*

---

### Description

Takes a job name, a data matrix, a design matrix as well as specification of the group and sample columns in the design matrix. Provides the basic representation of a dataset in the NormalyzerDE normalization part.

### Usage

```

NormalyzerDataset(
  jobName,
  designMatrix,
  rawData,
  annotationData,
  sampleNameCol,
  groupNameCol,
  tinyRunThres = 50,
  quiet = FALSE
)

```

```

NormalyzerDataset(
  jobName,
  designMatrix,
  rawData,
  annotationData,

```

```

    sampleNameCol,
    groupNameCol,
    tinyRunThres = 50,
    quiet = FALSE
  )

```

### Arguments

jobName	Name of the NormalyzerDE processing run
designMatrix	Matrix containing sample conditions
rawData	Matrix containing raw input data
annotationData	Matrix containing annotation information for each input feature. Is expected to contain the same number of rows as the data but can contain any number of features
sampleNameCol	Name of column in design matrix containing sample information
groupNameCol	Name of column in design matrix containing condition information
tinyRunThres	If fewer features than this is present in the input a limited run will be performed to avoid some steps requiring a more extensive number of features.
quiet	If set to TRUE no information messages will be printed

### Value

nds Generated NormalyzerDataset instance

### Slots

jobName Name of the job represented by the dataset.

rawData Matrix with raw values.

sampleNameCol Name column for sample.

groupNameCol Name column for groups.

designMatrix Data frame containing design.

sampleNames Vector containing sample names.

filterrawdata Reduced raw data matrix where low abundance rows are removed

sampleReplicateGroups Vector with sample replicate information

samplesGroupsWithReplicates Vector with replicated sample replicate information

annotationValues Annotation part of original dataframe.

retentionTimes Vector of retention time values.

singleReplicateRun Conditional whether run is single replicate.

---

normalyzerDE	<i>NormalyzerDE differential expression</i>
--------------	---

---

### Description

Performs differential expression analysis on a normalization matrix. This command executes a pipeline processing the data and generates an annotated normalization matrix and a report containing p-value histograms for each of the performed comparisons.

### Usage

```
normalyzerDE(
  jobName,
  comparisons,
  designPath = NULL,
  dataPath = NULL,
  experimentObj = NULL,
  outputDir = ".",
  logTrans = FALSE,
  type = "limma",
  sampleCol = "sample",
  condCol = "group",
  batchCol = NULL,
  techRepCol = NULL,
  leastRepCount = 1,
  quiet = FALSE,
  sigThres = 0.1,
  sigThresType = "fdr",
  log2FoldThres = 0,
  writeReportAsPngs = FALSE
)
```

### Arguments

jobName	Name of job
comparisons	Character vector containing target contrasts. If comparing condA with condB, then the vector would be c("condA-condB")
designPath	File path to design matrix
dataPath	File path to normalized matrix
experimentObj	SummarizedExperiment object, can be provided as input as alternative to 'designPath' and 'dataPath'
outputDir	Path to output directory
logTrans	Log transform the input (needed if providing non-logged input)
type	Type of statistical comparison, "limma", "limma_intensity" or "welch", where "limma_intensity" allows the prior to be fit according to intensity rather than using a flat prior

sampleCol	Design matrix column header for column containing sample IDs
condCol	Design matrix column header for column containing sample conditions
batchCol	Provide an optional column for inclusion of possible batch variance in the model
techRepCol	Design matrix column header for column containing technical replicates
leastRepCount	Minimum required replicate count
quiet	Omit status messages printed during run
sigThres	Significance threshold use for illustrating significant hits in diagnostic plots
sigThresType	Type of significance threshold, "fdr" or "p". "fdr" is strongly recommended (Benjamini-Hochberg corrected p-values)
log2FoldThres	Fold-size cutoff for being considered significant in diagnostic plots
writeReportAsPngs	Output report as separate PNG files instead of a single PDF

## Details

When executed, it performs the following steps:

- 1: Read the data and the design matrices into dataframes.
- 2: Generate an instance of the NormalyzerStatistics class representing the data and their statistical comparisons.
- 3: Optionally reduce technical replicates in both the data matrix and the design matrix
- 4: Calculate statistical contrasts between supplied groups
- 5: Generate an annotated version of the original dataframe where columns containing statistical key measures have been added
- 6: Write the table to file
- 7: Generate a PDF report displaying p-value histograms for each calculated contrast

## Value

None

## Examples

```
data_path <- system.file(package="NormalyzerDE", "extdata", "tiny_data.tsv")
design_path <- system.file(package="NormalyzerDE", "extdata", "tiny_design.tsv")
out_dir <- tempdir()
normalyzerDE(
  jobName="my_jobname",
  comparisons=c("4-5"),
  designPath=design_path,
  dataPath=data_path,
  outputDir=out_dir,
  condCol="group")
```

---

NormalyzerEvaluationResults

*Representation of evaluation results by calculating performance measures for an an NormalyzerResults instance*

---

### Description

Contains the resulting information from the processing which subsequently can be used to generate the quality assessment report.

### Usage

NormalyzerEvaluationResults(nr)

NormalyzerEvaluationResults(nr)

### Arguments

nr                    NormalyzerResults object

### Value

nds Generated NormalyzerEvaluationResults instance

### Slots

avgcvmem Average coefficient of variance per method

avgcvmempdiff Percentage difference of mean coefficient of variance compared to log2-transformed data

featureCVPerMethod CV calculated per feature and normalization method.

avgmadmem Average median absolute deviation

avgmadmempdiff Percentage difference of median absolute deviation compared to log2-transformed data

avgvarmem Average variance per method

avgvarmempdiff Percentage difference of mean variance compared to log2-transformed data

lowVarFeaturesCVs List of 5 for log2-transformed data

lowVarFeaturesCVsPercDiff Coefficient of variance for least variable entries

anovaP ANOVA calculated p-values

repCorPear Within group Pearson correlations

repCorSpear Within group Spearman correlations

**Examples**

```
data(example_summarized_experiment)
normObj <- getVerifiedNormalyzerObject("job_name", example_summarized_experiment)
normResults <- normMethods(normObj)
normEval <- NormalyzerEvaluationResults(normResults)
```

---

NormalyzerResults	<i>Representation of the results from performing normalization over a dataset</i>
-------------------	---

---

**Description**

It is linked to a NormalyzerDataset instance representing the raw data which has been processed. After performing evaluation it also links to an instance of NormalyzerEvaluationResults representing the results from the evaluation.

**Usage**

```
NormalyzerResults(nds)
```

```
NormalyzerResults(nds)
```

**Arguments**

nds                    NormalyzerDataset object

**Value**

nr Prepared NormalyzerResults object

**Slots**

normalizations SummarizedExperiment object containing calculated normalization results

nds Normalyzer dataset representing run data

ner Normalyzer evaluation results for running extended normalizations

**Examples**

```
data(example_summarized_experiment)
normObj <- getVerifiedNormalyzerObject("job_name", example_summarized_experiment)
emptyNormResults <- NormalyzerResults(normObj)
```

---

NormalizerStatistics *Class representing a dataset for statistical processing in NormalizerDE*

---

### Description

Is initialized with an annotation matrix, a data matrix and a design data frame. This object can subsequently be processed to generate statistical values and in turn used to write a full matrix with additional statistical information as well as a graphical report of the comparisons.

### Usage

```
NormalizerStatistics(experimentObj, logTrans = FALSE)
```

```
NormalizerStatistics(experimentObj, logTrans = FALSE)
```

### Arguments

experimentObj Instance of SummarizedExperiment containing matrix and design information as column data

logTrans Whether the input data should be log transformed

### Value

nds Generated NormalizerStatistics instance

### Slots

annotMat Matrix containing annotation information

dataMat Matrix containing (normalized) expression data

filteredDataMat Filtered matrix with low-count rows removed

designDf Data frame containing design conditions

filteringContrast Vector showing which entries are filtered (due to low count)

pairwiseCompsP List with P-values for pairwise comparisons

pairwiseCompsFdr List with FDR-values for pairwise comparisons

pairwiseCompsAve List with average expression values

pairwiseCompsFold List with log<sub>2</sub> fold-change values for pairwise comparisons

contrasts Spot for saving vector of last used contrasts

condCol Column containing last used conditions

batchCol Column containing last used batch conditions

### Examples

```
data(example_stat_summarized_experiment)
nst <- NormalizerStatistics(example_stat_summarized_experiment)
```



---

normMethods	<i>Perform normalizations on Normalyzer dataset</i>
-------------	---

---

**Description**

Perform normalizations on Normalyzer dataset

**Usage**

```
normMethods(
  nds,
  forceAll = FALSE,
  normalizeRetentionTime = TRUE,
  quiet = FALSE,
  rtStepSizeMinutes = 1,
  rtWindowMinCount = 100,
  rtWindowShifts = 1,
  rtWindowMergeMethod = "mean",
  noLogTransform = FALSE
)
```

**Arguments**

nds	Normalyzer dataset object.
forceAll	Force all methods to run despite not qualifying for thresholds.
normalizeRetentionTime	Perform retention time based normalization methods.
quiet	Prevent diagnostic output
rtStepSizeMinutes	Retention time normalization window size.
rtWindowMinCount	Minimum number of datapoints in each retention-time segment.
rtWindowShifts	Number of layered retention time normalized windows.
rtWindowMergeMethod	Merge approach for layered retention time windows.
noLogTransform	Per default NormalyzerDE performs a log-transformation on the input data. If not needed, specify this option

**Value**

Returns Normalyzer results object with performed analyzes assigned as attributes

**Examples**

```
data(example_summarized_experiment)
normObj <- getVerifiedNormalyzerObject("job_name", example_summarized_experiment)
normResults <- normMethods(normObj)
```

performCyclicLoessNormalization  
*Cyclic Loess normalization*

---

**Description**

Log2 transformed data is normalized by Loess method using the function "normalizeCyclicLoess". Further information is available for the function "normalizeCyclicLoess" in the Limma package.

**Usage**

```
performCyclicLoessNormalization(rawMatrix, noLogTransform = FALSE)
```

**Arguments**

rawMatrix      Target matrix to be normalized  
noLogTransform Assumes no need for log transformation

**Value**

Normalized matrix

**Examples**

```
data(example_data_only_values_small)  
normMatrix <- performCyclicLoessNormalization(example_data_only_values)
```

---

performGlobalRLRNormalization  
*Global linear regression normalization*

---

**Description**

Log2 transformed data is normalized by robust linear regression using the function "rlm" from the MASS package.

**Usage**

```
performGlobalRLRNormalization(rawMatrix, noLogTransform = FALSE)
```

**Arguments**

rawMatrix      Target matrix to be normalized  
noLogTransform Assumes no need for log transformation

**Value**

Normalized matrix

**Examples**

```
data(example_data_only_values_small)
normMatrix <- performGlobalRLRNormalization(example_data_only_values)
```

---

`performNoNormalization`

*Do no normalization (For debugging purposes)*

---

**Description**

Do no normalization (For debugging purposes)

**Usage**

```
performNoNormalization(rawMatrix)
```

**Arguments**

`rawMatrix`      Target matrix to be normalized

**Value**

Normalized matrix

---

`performNormalizations`    *Main function for executing normalizations*

---

**Description**

Main function for executing normalizations

**Usage**

```
performNormalizations(
  nr,
  forceAll = FALSE,
  rtNorm = FALSE,
  rtStepSizeMinutes = 1,
  rtWindowMinCount = 100,
  rtWindowShifts = 1,
  rtWindowMergeMethod = "median",
  noLogTransform = FALSE,
```

```

    quiet = FALSE
  )

  ## S4 method for signature 'NormalizerResults'
  performNormalizations(
    nr,
    forceAll = FALSE,
    rtNorm = FALSE,
    rtStepSizeMinutes = 1,
    rtWindowMinCount = 100,
    rtWindowShifts = 1,
    rtWindowMergeMethod = "median",
    noLogTransform = FALSE,
    quiet = FALSE
  )

```

### Arguments

nr	Normalizer results object.
forceAll	Ignore dataset size limits and run all normalizations (only meant for testing purposes)
rtNorm	Perform retention time based normalizations
rtStepSizeMinutes	Retention time normalization window size.
rtWindowMinCount	Minimum number of datapoints in each retention-time segment.
rtWindowShifts	Number of layered retention time normalized windows.
rtWindowMergeMethod	Merge approach for layered retention time windows.
noLogTransform	Prevent log-transforming input
quiet	Don't show regular output messages

### Value

nr NormalizerDE results object

---

performQuantileNormalization

*Quantile normalization is performed by the function "normalize.quantiles" from the package preprocessCore.*

---

### Description

It makes the assumption that the data in different samples should originate from an identical distribution. It does this by generating a reference distribution and then scaling the other samples accordingly.

**Usage**

```
performQuantileNormalization(rawMatrix, noLogTransform = FALSE)
```

**Arguments**

rawMatrix      Target matrix to be normalized  
noLogTransform Assumes no need for log transformation

**Value**

Normalized matrix

**Examples**

```
data(example_data_only_values_small)  
normMatrix <- performQuantileNormalization(example_data_only_values)
```

---

```
performSMADNormalization
```

*Median absolute deviation normalization Normalization subtracts the median and divides the data by the median absolute deviation (MAD).*

---

**Description**

Median absolute deviation normalization Normalization subtracts the median and divides the data by the median absolute deviation (MAD).

**Usage**

```
performSMADNormalization(rawMatrix, noLogTransform = FALSE)
```

**Arguments**

rawMatrix      Target matrix to be normalized  
noLogTransform Assumes no need for log transformation

**Value**

Normalized matrix

**Examples**

```
data(example_data_only_values_small)  
normMatrix <- performSMADNormalization(example_data_only_values)
```

---

performVSNNormalization

*Log2 transformed data is normalized using the function "justvsn" from the VSN package.*

---

### Description

The VSN (Variance Stabilizing Normalization) attempts to transform the data in such a way that the variance remains nearly constant over the intensity spectrum

### Usage

```
performVSNNormalization(rawMatrix)
```

### Arguments

rawMatrix      Target matrix to be normalized

### Value

Normalized matrix

### Examples

```
data(example_data_only_values_small)
normMatrix <- performVSNNormalization(example_data_only_values)
```

---

plotBoxPlot

*Boxplots showing distribution of values after different normalizations*

---

### Description

Boxplots showing distribution of values after different normalizations

### Usage

```
plotBoxPlot(nr, currentLayout, pageno)
```

### Arguments

nr              Normalizer results object.  
currentLayout    Layout used for document.  
pageno          Current page number.

### Value

None

---

plotComparisonVenns    *If multiple comparisons - Show overlap in Venn diagrams*

---

### Description

If multiple comparisons - Show overlap in Venn diagrams

### Usage

```
plotComparisonVenns(  
  nst,  
  jobName,  
  currentLayout,  
  pageno,  
  sigThres = 0.1,  
  sigThresType = "fdr",  
  log2FoldThres = 0,  
  maxContrasts = 4  
)
```

### Arguments

nst	NormalyzerDE statistics object.
jobName	Name of processing run.
currentLayout	Layout used for document.
pageno	Current page number.
sigThres	Cutoff value for significance threshold
sigThresType	Type of significance cutoff
log2FoldThres	Log2-fold based cutoff threshold
maxContrasts	Maximum contrasts to show pairwise comparisons for

### Value

None

---

plotContrastPCA	<i>Show in a PCA plot what samples are compared in statistical contrast This is useful to understand what conditions are compared and for checking for outliers in the contrast</i>
-----------------	---

---

**Description**

Show in a PCA plot what samples are compared in statistical contrast This is useful to understand what conditions are compared and for checking for outliers in the contrast

**Usage**

```
plotContrastPCA(nst, jobName, currentLayout, pageno, pcs = c(1, 2))
```

**Arguments**

nst	NormalyzerDE statistics object.
jobName	Name of processing run.
currentLayout	Layout used for document.
pageno	Current page number.
pcs	Principal components to show.

**Value**

None

---

plotContrastPHists	<i>Takes an NormalyzerStatistics instance and generates and prints a p- value histogram for each onto the viewport</i>
--------------------	--

---

**Description**

Takes an NormalyzerStatistics instance and generates and prints a p-value histogram for each onto the viewport

**Usage**

```
plotContrastPHists(nst, jobName, currentLayout, pageno)
```

**Arguments**

nst	NormalyzerDE statistics object.
jobName	Name of processing run.
currentLayout	Layout used for document.
pageno	Current page number.



**Value**

None

---

plotCorrelation	<i>Visualize within-replicates correlations</i>
-----------------	---

---

**Description**

Visualize within-replicates correlations

**Usage**

```
plotCorrelation(nr, currentLayout, pageno)
```

**Arguments**

nr	Normalyzer results object.
currentLayout	Layout used for document.
pageno	Current page number.

**Value**

None

---

plotCVvsIntensity	<i>Plots page displaying coefficient of variance (CV) against raw intensity for features across the performed normalizations</i>
-------------------	--

---

**Description**

Plots page displaying coefficient of variance (CV) against raw intensity for features across the performed normalizations

**Usage**

```
plotCVvsIntensity(nr, currentLayout, pageno)
```

**Arguments**

nr	Normalyzer results object.
currentLayout	Layout used for document.
pageno	Current page number.

**Value**

None

---

plotDendrograms	<i>Visualize dendrogram grouping of samples</i>
-----------------	---

---

**Description**

Visualize dendrogram grouping of samples

**Usage**

```
plotDendrograms(nr, currentLayout, pageno)
```

**Arguments**

nr	Normalyzer results object.
currentLayout	Layout used for document.
pageno	Current page number.

**Value**

None

---

plotDensity	<i>Density plots showing value distributions after normalizations</i>
-------------	---

---

**Description**

Density plots showing value distributions after normalizations

**Usage**

```
plotDensity(nr, currentLayout, pageno)
```

**Arguments**

nr	Normalyzer results object.
currentLayout	Layout used for document.
pageno	Current page number.

**Value**

None

---

plotFrontPage	<i>Generate first page in output report and write to viewport</i>
---------------	---

---

**Description**

Generate first page in output report and write to viewport

**Usage**

```
plotFrontPage(currentjob, currentFont)
```

**Arguments**

currentjob	Name of current run.
currentFont	Font used for output document.

**Value**

None

---

plotMA	<i>Produces a page containing expression vs. fold-change figures (MA plots) The visualized fold is between the first sample in each group and the average of the replicate to which that sample belongs</i>
--------	---

---

**Description**

Produces a page containing expression vs. fold-change figures (MA plots) The visualized fold is between the first sample in each group and the average of the replicate to which that sample belongs

**Usage**

```
plotMA(nr, currentLayout, pageno)
```

**Arguments**

nr	Normalyzer results object.
currentLayout	Layout used for document.
pageno	Current page number.

**Value**

None

---

plotMDS	<i>MDS plots showing grouping of samples after normalizations</i>
---------	---

---

**Description**

MDS plots showing grouping of samples after normalizations

**Usage**

```
plotMDS(nr, currentLayout, pageno)
```

**Arguments**

nr	Normalyzer results object.
currentLayout	Layout used for document.
pageno	Current page number.

**Value**

None

---

plotMeanSD	<i>Visualize standard deviation over (expression?) for different values</i>
------------	---

---

**Description**

Visualize standard deviation over (expression?) for different values

**Usage**

```
plotMeanSD(nr, currentLayout, pageno)
```

**Arguments**

nr	Normalyzer results object.
currentLayout	Layout used for document.
pageno	Current page number.

**Value**

None

---

plotPHist	<i>Generate P-histograms for ANOVA calculated after each normalization</i>
-----------	--

---

**Description**

Generate P-histograms for ANOVA calculated after each normalization

**Usage**

```
plotPHist(nr, currentLayout, pageno)
```

**Arguments**

nr	Normalyzer results object.
currentLayout	Layout used for document.
pageno	Current page number.

**Value**

None

---

plotQQ	<i>Produces page showing QQ-plots for the first sample for each normalization method. This plot can be used to assess whether the data follows a normal distribution.</i>
--------	---

---

**Description**

Produces page showing QQ-plots for the first sample for each normalization method. This plot can be used to assess whether the data follows a normal distribution.

**Usage**

```
plotQQ(nr, currentLayout, pageno)
```

**Arguments**

nr	Normalyzer results object.
currentLayout	Layout used for document.
pageno	Current page number.

**Value**

None

---

**plotReplicateVarAndStableVariables**

*Write figures displaying pooled coefficient of variance, median absolute deviation and pooled estimate of variance percentage compared to log2-transformed and stable variables plot displaying CV of stable variables against pooled CV measure. The stable variables are calculated by an ANOVA comparison across sample conditions and selecting features with the least clear difference.*

---

**Description**

Write figures displaying pooled coefficient of variance, median absolute deviation and pooled estimate of variance percentage compared to log2-transformed and stable variables plot displaying CV of stable variables against pooled CV measure. The stable variables are calculated by an ANOVA comparison across sample conditions and selecting features with the least clear difference.

**Usage**

```
plotReplicateVarAndStableVariables(nr, currentLayout, pageno)
```

**Arguments**

nr	Normalizer results object.
currentLayout	Layout used for document.
pageno	Current page number.

**Value**

None

---

**plotReplicateVariance** *Generate normalization replicate variance summary by displaying CV (coefficient of variance), MAD (mean of intragroup median absolute deviation) and PEV (Pooled Estimate of Variance) as mean of intragroups*

---

**Description**

Generate normalization replicate variance summary by displaying CV (coefficient of variance), MAD (mean of intragroup median absolute deviation) and PEV (Pooled Estimate of Variance) as mean of intragroups

**Usage**

```
plotReplicateVariance(nr, currentLayout, pageno)
```

**Arguments**

nr	Normalyzer results object.
currentLayout	Layout used for document.
pageno	Current page number.

**Value**

None

---

plotRLE	<i>Boxplots showing relative log expression after normalizations</i>
---------	--

---

**Description**

Boxplots showing relative log expression after normalizations

**Usage**

```
plotRLE(nr, currentLayout, pageno)
```

**Arguments**

nr	Normalyzer results object.
currentLayout	Layout used for document.
pageno	Current page number.

**Value**

None

---

plotSampleMappingPage	<i>Write page with sample mapping</i>
-----------------------	---------------------------------------

---

**Description**

Write page with sample mapping

**Usage**

```
plotSampleMappingPage(nr, currentFont, currentLayout, currentjob, pageno)
```

**Arguments**

nr	Normalyzer results object.
currentLayout	Layout used for document.
pageno	Current page number.

**Value**

None

plotSampleOutlierSummary

*Write page containing sample summary of intensities, missing values and MDS plot to the viewport*

**Description**

Write page containing sample summary of intensities, missing values and MDS plot to the viewport

**Usage**

```
plotSampleOutlierSummary(nr, currentLayout, pageno)
```

**Arguments**

nr	Normalyzer results object.
currentLayout	Layout used for document.
pageno	Current page number.

**Value**

None

plotScatter

*Produces page containing scatter plot plotting the first two samples from each dataset against each other for each normalization method*

**Description**

Produces page containing scatter plot plotting the first two samples from each dataset against each other for each normalization method

**Usage**

```
plotScatter(nr, currentLayout, pageno)
```



**Arguments**

nr	Normalyzer results object.
currentLayout	Layout used for document.
pageno	Current page number.

**Value**

None

---

plotSigScatter	<i>Takes an NormalyzerStatistics instance and generates and prints a volcano plot</i>
----------------	---

---

**Description**

Takes an NormalyzerStatistics instance and generates and prints a volcano plot

**Usage**

```
plotSigScatter(
  nst,
  jobName,
  currentLayout,
  pageno,
  type = "Volcano",
  sigThres = 0.1,
  sigThresType = "fdr",
  log2FoldThres = 0
)
```

**Arguments**

nst	NormalyzerDE statistics object.
jobName	Name of processing run.
currentLayout	Layout used for document.
pageno	Current page number.
type	Specify whether to plot 'Volcano' or 'MA'.
sigThres	FDR threshold for DE coloring.

**Value**

None

---

```
preprocessData      Replace empty values (0 or empty field) with NA in input data
```

---

**Description**

Replace empty values (0 or empty field) with NA in input data

**Usage**

```
preprocessData(dataMatrix, quiet = FALSE)
```

**Arguments**

```
dataMatrix      Matrix with raw data.
quiet           Don't show diagnostic messages
```

**Value**

Parsed rawdata where 0 values are replaced with NA

---

```
printMeta      Print meta information for Normalyzer plot page ! Needs refactoring
                to reduce redundancy in code ! Needs double check of functionality
```

---

**Description**

Print meta information for Normalyzer plot page ! Needs refactoring to reduce redundancy in code ! Needs double check of functionality

**Usage**

```
printMeta(plotname, pageno, jobname, currentLayout)
```

**Arguments**

```
plotname      Name of current plot.
pageno        Current page number.
jobname       Name of ongoing job.
currentLayout Custom viewport layout.
```

**Value**

None

---

printPlots                      *Generate PDF grid page filling it with provided list of plots*

---

**Description**

Generate PDF grid page filling it with provided list of plots

**Usage**

```
printPlots(plotlist, plotname, pageno, jobname, currentLayout)
```

**Arguments**

plotlist	List of target plots to display.
plotname	List of names corresponding to the provided plot list.
pageno	Current page number.
jobname	Name of ongoing job.
currentLayout	Custom viewport layout.

**Value**

None

---

reduceTechnicalReplicates  
*Remove technical replicates from data and design*

---

**Description**

Collapses sample values into their average. If only one value is present due to NA-values in other technical replicates, then that value is used.

**Usage**

```
reduceTechnicalReplicates(se, techRepColName, sampleColName)
```

**Arguments**

se	Summarized experiment where the assay contains the data to be reduced, and the colData the data frame
techRepColName	Technical replicates column name in colData
sampleColName	Sample names column name in colData

**Details**

Takes a SummarizedExperiment where the data is present as the assay and the colData contains the design conditions. In the design conditions there should be one column with the technical replicate groups and one column containing the sample names

**Value**

reducedSe Summarized experiment with reduced data

**Examples**

```
testData <- as.matrix(data.frame(
  c(1,1,1),
  c(1,2,1),
  c(7,7,7),
  c(7,9,7)))
colnames(testData) <- c("a1", "a2", "b1", "b2")
designDf <- data.frame(
  sample=c("a1", "a2", "b1", "b2"),
  techrep=c("a", "a", "b", "b"))
se <- SummarizedExperiment::SummarizedExperiment(
  assay=testData,
  colData=designDf
)
statObj <- reduceTechnicalReplicates(se, "techrep", "sample")
```

---

setupJobDir

*Create empty directory for run*

---

**Description**

Creates a directory at provided path named to the jobname.

**Usage**

```
setupJobDir(jobName, outputDir)
```

**Arguments**

jobName	Name of the run.
outputDir	Path to directory where to create the output directory.

**Value**

Path to newly created directory.

**Examples**

```
setupJobDir("job_name", "path/to/outdir")
```

---

setupPlotting	<i>Setup PDF report settings by initializing the color palette, format for the PDF report and the graphical device</i>
---------------	--

---

**Description**

Setup PDF report settings by initializing the color palette, format for the PDF report and the graphical device

**Usage**

```
setupPlotting(currentJob, jobDir, suffix)
```

**Arguments**

currentJob	Name of current run.
jobDir	Path to output directory for run.
suffix	Text to add to output filename.

**Value**

None

---

setupRawContrastObject	<i>Prepare SummarizedExperiment object for statistics data</i>
------------------------	--

---

**Description**

Prepare SummarizedExperiment object for statistics data

**Usage**

```
setupRawContrastObject(dataPath, designPath, sampleColName)
```

**Arguments**

dataPath	Path to raw data matrix
designPath	Path to design matrix
sampleColName	Name for column in design matrix containing sample names

**Value**

experimentObj Prepared instance of SummarizedExperiment

**Examples**

```
data_path <- system.file(package="NormalyzerDE", "extdata", "tiny_data.tsv")
design_path <- system.file(package="NormalyzerDE", "extdata", "tiny_design.tsv")
sumExpObj <- setupRawContrastObject(data_path, design_path, "sample")
```

---

setupRawDataObject	<i>Prepare SummarizedExperiment object for raw data to be normalized containing data, design and annotation information</i>
--------------------	---

---

**Description**

Prepare SummarizedExperiment object for raw data to be normalized containing data, design and annotation information

**Usage**

```
setupRawDataObject(
  dataPath,
  designPath,
  inputFormat = "default",
  zeroToNA = FALSE,
  sampleColName = "sample",
  groupColName = "group"
)
```

**Arguments**

dataPath	File path to data matrix.
designPath	File path to design matrix.
inputFormat	Type of matrix for data, can be either 'default', 'proteios', 'maxquantprot' or 'maxquantpep'
zeroToNA	If TRUE zeroes in the data is automatically converted to NA values
sampleColName	Column name for column containing sample names
groupColName	Column name for column containing condition levels

**Value**

experimentObj SummarizedExperiment object loaded with the data

**Examples**

```
data_path <- system.file(package="NormalyzerDE", "extdata", "tiny_data.tsv")
design_path <- system.file(package="NormalyzerDE", "extdata", "tiny_design.tsv")
df <- setupRawDataObject(data_path, design_path)
```

---

setupTestData	<i>Generate a random test dataset with features, sample values and retention times</i>
---------------	--

---

**Description**

Generate a random test dataset with features, sample values and retention times

**Usage**

```
setupTestData(nSamples, nFeatures, rtMin = 40, rtMax = 80, mean = 20, sd = 4)
```

**Arguments**

nSamples	Number of samples
nFeatures	Number of features
rtMin	Minimum retention time
rtMax	Maximum retention time
mean	Mean value for sample intensities
sd	Standard deviation for sample intensities

**Value**

Test dataset

**Examples**

```
df <- setupTestData(6, 20)
df <- setupTestData(6, 20, mean=15, sd=1)
```

---

validateSampleReplication	<i>Check whether all samples have replicates</i>
---------------------------	--

---

**Description**

Check whether all samples have replicates

**Usage**

```
validateSampleReplication(  
  dataMatrix,  
  groups,  
  requireReplicates = TRUE,  
  quiet = FALSE  
)
```

**Arguments**

dataMatrix	Prepared matrix containing expression data.
groups	Vector containing condition levels
requireReplicates	By default stops processing if not all samples have replicates

**Value**

None

---

verifyContrasts	<i>Check that a given contrast string is valid given a particular design matrix. Each level tested for in the contrast should be present in the condition column for the design matrix.</i>
-----------------	---

---

**Description**

Mainly meant to verify strings received during server usage.

**Usage**

```
verifyContrasts(designLevels, contrasts)
```

**Arguments**

designLevels	Vector containing condition levels present in design
contrasts	A string containing one or several (comma delimited) strings for which contrasts should be performed

**Value**

None

---

verifyDesignMatrix	<i>Verify that design matrix setup matches the data matrix</i>
--------------------	--

---

**Description**

Verify that design matrix setup matches the data matrix

**Usage**

```
verifyDesignMatrix(fullMatrix, designMatrix, sampleCol)
```



**Arguments**

fullMatrix      Dataframe with input data.  
designMatrix    Dataframe with design setup.  
sampleCol       Column in design matrix containing sample IDs.

**Value**

None

---

verifyMultipleSamplesPresent  
*Check whether more than one sample is present*

---

**Description**

Check whether more than one sample is present

**Usage**

```
verifyMultipleSamplesPresent(  
  dataMatrix,  
  groups,  
  requireReplicates = TRUE,  
  quiet = FALSE  
)
```

**Arguments**

dataMatrix      Prepared dataframe.  
groups           Vector containing condition levels  
requireReplicates  
                  By default stops processing if not all samples have replicates

**Value**

None

---

`verifySummarizedExperiment`*Verify that design matrix setup matches the data matrix*

---

**Description**

Verify that design matrix setup matches the data matrix

**Usage**

```
verifySummarizedExperiment(summarizedExp, sampleCol)
```

**Arguments**

<code>sampleCol</code>	Column in design matrix containing sample IDs.
<code>fullMatrix</code>	Dataframe with input data.
<code>designMatrix</code>	Dataframe with design setup.

**Value**

None

---

`verifyValidNumbers`*Verify that input fields conform to the expected formats*

---

**Description**

Verify that input fields conform to the expected formats

**Usage**

```
verifyValidNumbers(rawDataOnly, groups, noLogTransform = FALSE, quiet = FALSE)
```

**Arguments**

<code>rawDataOnly</code>	Dataframe with input data.
<code>groups</code>	Condition levels for comparisons.

**Value**

None

---

`writeNormalizedDatasets`*Write normalization matrices to file*

---

### Description

Outputs each of the normalized datasets to the specified directory.

### Usage

```
writeNormalizedDatasets(  
  nr,  
  jobdir,  
  includePairwiseComparisons = FALSE,  
  includeCvCol = FALSE,  
  includeAnovaP = FALSE,  
  normSuffix = "-normalized.txt",  
  rawdataName = "submitted_rawdata.txt"  
)
```

### Arguments

<code>nr</code>	Results object.
<code>jobdir</code>	Path to output directory.
<code>includePairwiseComparisons</code>	Include p-values for pairwise comparisons.
<code>includeCvCol</code>	Include CV column in output.
<code>includeAnovaP</code>	Include ANOVA p-value in output.
<code>normSuffix</code>	String used to name output together with normalization names.
<code>rawdataName</code>	Name of output raw data file.

### Value

None

### Examples

```
data(example_summarized_experiment)  
normObj <- getVerifiedNormalizerObject("job_name", example_summarized_experiment)  
normResults <- normMethods(normObj)  
normResultsWithEval <- analyzeNormalizations(normResults)  
outputDir <- tempdir()  
writeNormalizedDatasets(normResultsWithEval, outputDir)
```

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