

Package ‘yarn’

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Title YARN: Robust Multi-Condition RNA-Seq Preprocessing and Normalization

Version 1.4.0

Description Expedite large RNA-Seq analyses using a combination of previously developed tools. YARN is meant to make it easier for the user in performing basic mis-annotation quality control, filtering, and condition-aware normalization. YARN leverages many Bioconductor tools and statistical techniques to account for the large heterogeneity and sparsity found in very large RNA-seq experiments.

Depends Biobase

License Artistic-2.0

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VignetteBuilder knitr

biocViews Software, QualityControl, GeneExpression, Sequencing, Preprocessing, Normalization, Annotation, Visualization, Clustering

NeedsCompilation no

Author Joseph N Paulson [aut, cre],
Cho-Yi Chen [aut],
Camila Lopes-Ramos [aut],
Marieke Kuijjer [aut],
John Platig [aut],
Abhijeet Sonawane [aut],
Maud Fagny [aut],
Kimberly Glass [aut],
John Quackenbush [aut]

Maintainer Joseph N Paulson <jpaulson@jimmy.harvard.edu>

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annotateFromBiomart *Annotate your Expression Set with biomaRt*

Description

Annotate your Expression Set with biomaRt

Usage

```
annotateFromBiomart(obj, genes = featureNames(obj),
  filters = "ensembl_gene_id", attributes = c("ensembl_gene_id",
  "hgnc_symbol", "chromosome_name", "start_position", "end_position"),
  biomart = "ensembl", dataset = "hsapiens_gene_ensembl", ...)
```

Arguments

| | |
|------------|---|
| obj | ExpressionSet object. |
| genes | Genes or rownames of the ExpressionSet. |
| filters | getBM filter value, see getBM help file. |
| attributes | getBM attributes value, see getBM help file. |
| biomart | BioMart database name you want to connect to. Possible database names can be retrieved with the function listMarts. |
| dataset | Dataset you want to use. To see the different datasets available within a biomaRt you can e.g. do: mart = useMart('ensembl'), followed by listDatasets(mart). |
| ... | Values for useMart, see useMart help file. |

Value

ExpressionSet object with a fuller featureData.

Examples

```
data(skin)
# subsetting and changing column name just for a silly example
skin <- skin[1:10,]
colnames(fData(skin)) = paste("names",1:6)
host<-"dec2013.archive.ensembl.org"; biomart<-"ENSEMBL_MART_ENSEMBL";
genes <- sapply(strsplit(rownames(skin),split="\\."),function(i)i[1])
newskin <-annotateFromBiomart(skin,genes=genes,biomar=biomart,host=host)
head(fData(newskin)[,7:11])
```

bladder

Bladder RNA-seq data from the GTEx consortium

Description

Bladder RNA-seq data from the GTEx consortium. V6 release.

Usage

```
data(bladder)
```

Format

An object of class "ExpressionSet"; see [ExpressionSet](#).

Value

ExpressionSet object

Source

GTEx Portal

References

GTEx Consortium, 2015. The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. *Science*, 348(6235), pp.648-660. ([PubMed](#))

Examples

```
data(bladder);
checkMissAnnotation(bladder);
```

| | |
|--------------------|--|
| checkMisAnnotation | <i>Check for wrong annotation of a sample using classical MDS and control genes.</i> |
|--------------------|--|

Description

Check for wrong annotation of a sample using classical MDS and control genes.

Usage

```
checkMisAnnotation(obj, phenotype, controlGenes = "all",
  columnID = "chromosome_name", plotFlag = TRUE, legendPosition = NULL,
  ...)
```

Arguments

| | |
|----------------|--|
| obj | ExpressionSet object. |
| phenotype | phenotype column name in the phenoData slot to check. |
| controlGenes | Name of controlGenes, ie. 'Y' chromosome. Can specify 'all'. |
| columnID | Column name where controlGenes is defined in the featureData slot if other than 'all'. |
| plotFlag | TRUE/FALSE Whether to plot or not |
| legendPosition | Location for the legend. |
| ... | Extra parameters for plotCMDs function. |

Value

Plots a classical multi-dimensional scaling of the 'controlGenes'. Optionally returns co-ordinates.

Examples

```
data(bladder)
checkMisAnnotation(bladder, 'GENDER', controlGenes='Y', legendPosition='topleft')
```

| | |
|---------------------|--|
| checkTissuesToMerge | <i>Check tissues to merge based on gene expression profile</i> |
|---------------------|--|

Description

Check tissues to merge based on gene expression profile

Usage

```
checkTissuesToMerge(obj, majorGroups, minorGroups, filterFun = NULL,
  plotFlag = TRUE, ...)
```

Arguments

| | |
|-------------|--|
| obj | ExpressionSet object. |
| majorGroups | Column name in the phenoData slot that describes the general body region or site of the sample. |
| minorGroups | Column name in the phenoData slot that describes the specific body region or site of the sample. |
| filterFun | Filter group specific genes that might disrupt PCoA analysis. |
| plotFlag | TRUE/FALSE whether to plot or not |
| ... | Parameters that can go to checkMisAnnotation |

Value

CMDS Plots of the majorGroupss colored by the minorGroupss. Optional matrix of CMDS loadings for each comparison.

See Also

[checkTissuesToMerge](#)

Examples

```
data(skin)
checkTissuesToMerge(skin, 'SMTS', 'SMTSD')
```

downloadGTEX

Download GTEX files and turn them into ExpressionSet object

Description

Downloads the V6 GTEX release and turns it into an ExpressionSet object.

Usage

```
downloadGTEX(type = "genes", file = NULL, ...)
```

Arguments

| | |
|------|---|
| type | Type of counts to download - default genes. |
| file | File path and name to automatically save the downloaded GTEX expression set. Saves as a RDS file. |
| ... | Does nothing currently. |

Value

Organized ExpressionSet set.

Examples

```
# obj <- downloadGTEX(type='genes',file='~/Desktop/gtex.rds')
```

| | |
|---------------|---------------------------------------|
| extractMatrix | <i>Extract the appropriate matrix</i> |
|---------------|---------------------------------------|

Description

This returns the raw counts, log₂-transformed raw counts, or normalized expression. If normalized = TRUE then the log parameter is ignored.

Usage

```
extractMatrix(obj, normalized = FALSE, log = TRUE)
```

Arguments

| | |
|------------|---|
| obj | ExpressionSet object or objrnx. |
| normalized | TRUE / FALSE, use the normalized matrix or raw counts |
| log | TRUE/FALSE log ₂ -transform. |

Value

matrix

Examples

```
data(skin)
head(yarn:::extractMatrix(skin,normalized=FALSE,log=TRUE))
head(yarn:::extractMatrix(skin,normalized=FALSE,log=FALSE))
```

| | |
|-------------|------------------------------|
| filterGenes | <i>Filter specific genes</i> |
|-------------|------------------------------|

Description

The main use case for this function is the removal of sex-chromosome genes. Alternatively, filter genes that are not protein-coding.

Usage

```
filterGenes(obj, labels = c("X", "Y", "MT"),
  featureName = "chromosome_name", keepOnly = FALSE)
```

Arguments

| | |
|-------------|---|
| obj | ExpressionSet object. |
| labels | Labels of genes to filter or keep, eg. X, Y, and MT |
| featureName | FeatureData column name, eg. chr |
| keepOnly | Filter or keep only the genes with those labels |

Value

Filtered ExpressionSet object

Examples

```
data(skin)
filterGenes(skin, labels = c('X', 'Y', 'MT'), featureName='chromosome_name')
filterGenes(skin, labels = 'protein_coding', featureName='gene_biotype', keepOnly=TRUE)
```

| | |
|----------------|--|
| filterLowGenes | <i>Filter genes that have less than a minimum threshold CPM for a given group/tissue</i> |
|----------------|--|

Description

Filter genes that have less than a minimum threshold CPM for a given group/tissue

Usage

```
filterLowGenes(obj, groups, threshold = 1, minSamples = NULL, ...)
```

Arguments

| | |
|------------|--|
| obj | ExpressionSet object. |
| groups | Vector of labels for each sample or a column name of the phenoData slot. for the ids to filter. Default is the column names. |
| threshold | The minimum threshold for calling presence of a gene in a sample. |
| minSamples | Minimum number of samples - defaults to half the minimum group size. |
| ... | Options for cpm . |

Value

Filtered ExpressionSet object

See Also

[cpm](#) function defined in the edgeR package.

Examples

```
data(skin)
filterLowGenes(skin, 'SMTSD')
```

`filterMissingGenes` *Filter genes not expressed in any sample*

Description

The main use case for this function is the removal of missing genes.

Usage

```
filterMissingGenes(obj, threshold = 0)
```

Arguments

`obj` ExpressionSet object.
`threshold` Minimum sum of gene counts across samples – defaults to zero.

Value

Filtered ExpressionSet object

Examples

```
data(skin)  
filterMissingGenes(skin)
```

`filterSamples` *Filter samples*

Description

Filter samples

Usage

```
filterSamples(obj, ids, groups = colnames(obj), keepOnly = FALSE)
```

Arguments

`obj` ExpressionSet object.
`ids` Names found within the groups labels corresponding to samples to be removed
`groups` Vector of labels for each sample or a column name of the phenoData slot for the
ids to filter. Default is the column names.
`keepOnly` Filter or keep only the samples with those labels.

Value

Filtered ExpressionSet object

Examples

```
data(skin)
filterSamples(skin,ids = "Skin - Not Sun Exposed (Suprapubic)",groups="SMTSD")
filterSamples(skin,ids=c("GTEX-0HPL-0008-SM-4E3I9","GTEX-145MN-1526-SM-5SI9T"))
```

normalizeTissueAware *Normalize in a tissue aware context*

Description

This function provides a wrapper to various normalization methods developed. Currently it only wraps qsmooth and quantile normalization returning a log-transformed normalized matrix. qsmooth is a normalization approach that normalizes samples in a condition aware manner.

Usage

```
normalizeTissueAware(obj, groups, normalizationMethod = c("qsmooth",
  "quantile"), ...)
```

Arguments

| | |
|---------------------|--|
| obj | ExpressionSet object |
| groups | Vector of labels for each sample or a column name of the phenoData slot for the ids to filter. Default is the column names |
| normalizationMethod | Choice of 'qsmooth' or 'quantile' |
| ... | Options for qsmooth function or normalizeQuantiles |

Value

ExpressionSet object with an assayData called normalizedMatrix

Source

The function qsmooth comes from the qsmooth packages currently available on github under user 'kokrah'.

Examples

```
data(skin)
normalizeTissueAware(skin,"SMTSD")
```

| | |
|----------|--------------------------------------|
| plotCMDS | <i>Plot classical MDS of dataset</i> |
|----------|--------------------------------------|

Description

This function plots the MDS coordinates for the "n" features of interest. Potentially uncovering batch effects or feature relationships.

Usage

```
plotCMDS(obj, comp = 1:2, normalized = FALSE, distFun = dist,  
  distMethod = "euclidian", n = NULL, samples = TRUE, log = TRUE,  
  plotFlag = TRUE, ...)
```

Arguments

| | |
|------------|--|
| obj | ExpressionSet object or objrix. |
| comp | Which components to display. |
| normalized | TRUE / FALSE, use the normalized matrix or raw counts. |
| distFun | Distance function, default is dist. |
| distMethod | The distance measure to be used. This must be one of "euclidean", "maximum", "manhattan", "canberra", "binary" or "minkowski". Any unambiguous substring can be given. |
| n | Number of features to make use of in calculating your distances. |
| samples | Perform on samples or genes. |
| log | TRUE/FALSE log2-transform raw counts. |
| plotFlag | TRUE/FALSE whether to plot or not. |
| ... | Additional plot arguments. |

Value

coordinates

Examples

```
data(skin)  
res <- plotCMDS(skin, pch=21, bg=factor(pData(skin)$SMTSD))  
  
# library(calibrate)  
# textxy(X=res[,1], Y=res[,2], labs=rownames(res))
```

| | |
|-------------|---|
| plotDensity | <i>Density plots of columns in a matrix</i> |
|-------------|---|

Description

Plots the density of the columns of a matrix. Wrapper for [matdensity](#).

Usage

```
plotDensity(obj, groups = NULL, normalized = FALSE, legendPos = NULL, ...)
```

Arguments

| | |
|------------|---|
| obj | ExpressionSet object |
| groups | Vector of labels for each sample or a column name of the phenoData slot for the ids to filter. Default is the column names. |
| normalized | TRUE / FALSE, use the normalized matrix or log2-transformed raw counts |
| legendPos | Legend title position. If null, does not create legend by default. |
| ... | Extra parameters for matdensity . |

Value

A density plot for each column in the ExpressionSet object colored by groups

Examples

```
data(skin)
filtData <- filterLowGenes(skin, "SMTSD")
plotDensity(filtData, groups="SMTSD", legendPos="topleft")
# to remove the legend
plotDensity(filtData, groups="SMTSD")
```

| | |
|-------------|--|
| plotHeatmap | <i>Plot heatmap of most variable genes</i> |
|-------------|--|

Description

This function plots a heatmap of the gene expressions for the "n" features of interest.

Usage

```
plotHeatmap(obj, n = NULL, fun = stats::sd, normalized = TRUE,
  log = TRUE, ...)
```

Arguments

| | |
|------------|---|
| obj | ExpressionSet object or objrix. |
| n | Number of features to make use of in plotting heatmap. |
| fun | Function to sort genes by, default sd . |
| normalized | TRUE / FALSE, use the normalized matrix or raw counts. |
| log | TRUE/FALSE log2-transform raw counts. |
| ... | Additional plot arguments for heatmap.2 . |

Value

coordinates

Examples

```
data(skin)
tissues <- pData(skin)$SMTSD
plotHeatmap(skin,normalized=FALSE,log=TRUE,trace="none",n=10)
# Even prettier

# library(RColorBrewer)
data(skin)
tissues <- pData(skin)$SMTSD
heatmapColColors <- brewer.pal(12,"Set3")[as.integer(factor(tissues))]
heatmapCols <- colorRampPalette(brewer.pal(9, "RdBu"))(50)
plotHeatmap(skin,normalized=FALSE,log=TRUE,trace="none",n=10,
  col = heatmapCols,ColSideColors = heatmapColColors,cexRow = 0.6,cexCol = 0.6)
```

qsmooth

Quantile shrinkage normalization

Description

This function was modified from github user kokrah.

Usage

```
qsmooth(obj, groups, norm.factors = NULL, plot = FALSE, window = 0.05,
  log = TRUE)
```

Arguments

| | |
|--------------|---|
| obj | for counts use log2(raw counts + 1)), for MA use log2(raw intensities) |
| groups | groups to which samples belong (character vector) |
| norm.factors | scaling normalization factors |
| plot | plot weights? (default=FALSE) |
| window | window size for running median (a fraction of the number of rows of exprs) |
| log | Whether or not the data should be log transformed before normalization, TRUE = YES. |

Value

Normalized expression

Source

[Kwame Okrah's qsmooth R package](#)

Examples

```
data(skin)
head(yarn:::qsmooth(skin, groups=pData(skin)$SMTSD))
```

qstats

Compute quantile statistics

Description

This function was directly borrowed from github user kokrah.

Usage

```
qstats(exprs, groups, window)
```

Arguments

| | |
|--------|--|
| exprs | for counts use $\log_2(\text{raw counts} + 1)$, for MA use $\log_2(\text{raw intensities})$ |
| groups | groups to which samples belong (character vector) |
| window | window size for running median as a fraction on the number of rows of exprs |

Value

list of statistics

Source

[Kwame Okrah's qsmooth R package](#) Compute quantile statistics

skin

Skin RNA-seq data from the GTEx consortium

Description

Skin RNA-seq data from the GTEx consortium. V6 release. Random selection of 20 skin samples. 13 of the samples are fibroblast cells, 5 Skin sun exposed, 2 sun unexposed.

Usage

```
data(skin)
```

Format

An object of class "ExpressionSet"; see [ExpressionSet](#).

Value

ExpressionSet object

Source

GTEx Portal

References

GTEx Consortium, 2015. The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. *Science*, 348(6235), pp.648-660. ([PubMed](#))

Examples

```
data(skin);  
checkMissAnnotation(skin, "GENDER");
```

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