Package: yarn (via r-universe)

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

Version 1.40.0

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

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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 teh 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)
biomart<-"ENSEMBL_MART_ENSEMBL";
genes <- sapply(strsplit(rownames(skin),split="\\."),function(i)i[1])
newskin <-annotateFromBiomart(skin,genes=genes,biomar=biomart)
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 *Check for wrong annotation of a sample using classical MDS and control genes.*

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 *Check tissues to merge based on gene expression profile*

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 *Extract the appropriate matrix*

Description

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

Usage

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

Arguments

obj	ExpressionSet object or objrix.
normalized	TRUE / FALSE, use the normalized matrix or raw counts
log	TRUE/FALSE log2-transform.

Value

matrix

Examples

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

`filterGenes` *Filter specific genes*

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

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-OHPL-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 *Plot classical MDS of dataset*

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 *Density plots of columns in a matrix*

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 *Plot heatmap of most variable genes*

Description

This function plots a heatmap of the gene expressions forthe "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 log2(raw counts + 1)), for MA use log2(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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