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easyDifferentialGeneCoexpression

Function that computes the differential coexpression of a list of probesets in a specific dataset and returns the most significant pairs

Description

Function that computes the differential coexpression of a list of probesets in a specific dataset and returns the most significant pairs

Usage

```
easyDifferentialGeneCoexpression(
  list_of_probesets_to_select,
  GSE_code,
  featureNameToDiscriminateConditions,
  firstConditionName,
  secondConditionName,
  batchCorrection = TRUE,
  verbose = FALSE
)
```

Arguments

| | |
|-------------------------------------|------------------------------------------------------------------------------------------------------------|
| list_of_probesets_to_select | list of probesets for which the differential coexpression should be computed |
| GSE_code | GEO accession code of the dataset to analyze |
| featureNameToDiscriminateConditions | name of the feature of the dataset that contains the two conditions to investigate |
| firstConditionName | name of the first condition in the feature to discriminate (for example, "healthy") |
| secondConditionName | name of the second condition in the feature to discriminate (for example, "cancer") |
| batchCorrection | says if the script should perform the batch correction with <code>limma::removeBatchEffect()</code> or not |
| verbose | prints all the intermediate message to standard output or not |

Value

a dataframe containing the significantly differentially co-expressed pairs of genes

Examples

```
probesetList <- c("200738_s_at", "217356_s_at", "206686_at")
verboseFlag <- "TRUE"
batchCorrection <- "TRUE"
signDiffCoexpressGenePairs <- easyDifferentialGeneCoexpression(probesetList,
"GSE3268", "description", "Normal", "Tumor", verboseFlag)
```

fromProbesetToGeneSymbol

Function that associates a gene symbol to a probeset for some Affymetrix platforms

Description

Function that associates a gene symbol to a probeset for some Affymetrix platforms

Usage

```
fromProbesetToGeneSymbol(  
  thisProbeset,  
  thisPlatform,  
  this_platform_ann_df,  
  verbose = FALSE  
)
```

Arguments

thisProbeset probeset in input
thisPlatform GEO platform accession code
this_platform_ann_df
annotation dataframe of the platform
verbose prints all the intermediate message to standard output or not

Value

a gene symbol as string

geoDataDownload *Function that downloads gene expression data from GEO, after checking the connection*

Description

Function that downloads gene expression data from GEO, after checking the connection

Usage

```
geoDataDownload(GSE_code, verbose = FALSE)
```

Arguments

GSE_code GEO code dataset
verbose prints all the intermediate message to standard output or not

Value

a gene set gene expression AnnotationDataFrame

geoPlatformAnnotationsDownload
Function that downloads the annotations of a GEO platform

Description

Function that downloads the annotations of a GEO platform

Usage

```
geoPlatformAnnotationsDownload(platformID, verbose = FALSE)
```

Arguments

platformID GEO platform ID
verbose prints all the intermediate message to standard output or not

Value

a dataframe containing the annotations of the GEO platform

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|-------------------|---------------------------------------------------------------------------------------------------------------------------------|
| probesetRetrieval | <i>Function that reads a CSV file of probesets or gene symbols and, in the latter case, it retrieves the original probesets</i> |
|-------------------|---------------------------------------------------------------------------------------------------------------------------------|

Description

Function that reads a CSV file of probesets or gene symbols and, in the latter case, it retrieves the original probesets

Usage

```
probesetRetrieval(  
  probesets_or_gene_symbols,  
  csv_file_name,  
  platformCode,  
  verbose = FALSE  
)
```

Arguments

| | |
|---------------------------|-------------------------------------------------------------------------------------------|
| probesets_or_gene_symbols | flag saying if we're reading probesets or gene symbols |
| csv_file_name | complete name of CSV file containing the probesets or the gene symbols |
| platformCode | code of the microarray platform for which the probeset-gene symbol mapping should be done |
| verbose | prints all the intermediate message to standard output or not |

Value

a vector of probesets

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