

Package: easyDifferentialGeneCoexpression (via r-universe)

February 13, 2025

Encoding UTF-8

Title Easily Performs Differential Coexpression Analysis

Version 1.4

Description A function that reads in the GEO code of a list of probesets or gene symbols, a gene expression dataset GEO accession code, the name of the dataset feature discriminating the two conditions for the differential coexpression, and the values of the two different conditions for the differential coexpression, and returns the significant pairs of genes/probesets with highest differential coexpression (p-value < 0.005). If the input gene list is made of gene symbols, this package associates the probesets to these gene symbols, if found. Platforms available: GPL80, GPL8300, GPL80, GPL96, GPL570, GPL571, GPL20115, GPL1293, GPL6102, GPL6104, GPL6883, GPL6884, GPL13497, GPL14550, GPL17077, GPL6480. GEO: Gene Expression Omnibus. ID: identifier code. The GEO datasets are downloaded from the URL
<<https://ftp.ncbi.nlm.nih.gov/geo/series/>>.

BugReports <https://github.com/davidechicco/easyDifferentialGeneCoexpression/issues>

Depends R (>= 4.0.0)

License GPL-3

URL <https://github.com/davidechicco/easyDifferentialGeneCoexpression>

Imports annotate, Biobase, diffcoexp, geneExpressionFromGEO, GEOquery, jetset, limma, magrittr, xml2

Suggests knitr, rmarkdown

VignetteBuilder knitr

RoxygenNote 7.1.2

NeedsCompilation no

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Date/Publication 2024-02-05 11:40:02 UTC

Additional_repositories <https://cranhaven.r-universe.dev>

Config/pak/sysreqs libglpk-dev make libicu-dev libpng-dev libxml2-dev
libssl-dev libx11-dev

Repository <https://cranhaven.r-universe.dev>

RemoteUrl <https://github.com/cranhaven/cranhaven.r-universe.dev>

RemoteRef package/easyDifferentialGeneCoexpression

RemoteSha 05a49c08db378f6fd634cdf3f7744c979100a012

RemoteSubdir easyDifferentialGeneCoexpression

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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 `limma::removeBatchEffect()` 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

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

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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