Package 'geneExpressionFromGEO'

October 13, 2022

```
Encoding UTF-8
```

Title Easily Downloads a Gene Expression Dataset from a GEO Code and Retrieves the Gene Symbols of Its Probesets

Version 0.9

Description A function that reads in the GEO code of a gene expression dataset, retrieves its data from GEO, (optionally) retrieves the gene symbols of the dataset, and returns a simple dataframe table containing all the data. Platforms available: GPL11532, GPL23126, GPL6244, GPL8300, GPL80, GPL96, GPL570, GPL571, GPL20115, GPL1293, GPL6102, Cpression Omnibus. ID: identifier code. The GEO datasets are downloaded from the URL https://ftp.ncbi.nlm.nih.gov/geo/series/. More information can be found in the following manuscript: Davide Chicco, "geneExpressionFrom-GEO: an R package to facilitate data reading from Gene Expression Omnibus (GEO)". Microarray Data Analysis, Methods in Molecular Biology, volume 2401, chapter 12, pages 187-194, Springer Protocols, 2021, doi:10.1007/978-1-0716-1839-4_12.

BugReports https://github.com/davidechicco/geneExpressionFromGEO/issues

Depends R (>= 3.1.0)

License GPL-3

URL https://github.com/davidechicco/geneExpressionFromGEO

Imports BiocManager, xml2, Biobase, annotate, GEOquery, markdown, R.utils

Suggests knitr, rmarkdown

VignetteBuilder knitr

RoxygenNote 7.1.1

NeedsCompilation no

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Repository CRAN

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dec_two

Function that returns numeric values with 2 decimal numbers.

Description

Function that returns numeric values with 2 decimal numbers.

Usage

```
dec_two(x)
```

Arguments

х

input numeric value with N decimal numbers.

Value

a numeric value with 2 decimal numbers.

Examples

```
aaa <- dec_two(8.31232)</pre>
```

getGeneExpressionFromGEO

Function that reads in the GEO code of a dataset, and returns the gene expression dataframe.

Description

Function that reads in the GEO code of a dataset, and returns the gene expression dataframe.

Usage

getGeneExpressionFromGEO(datasetGeoCode, retrieveGeneSymbols, verbose = FALSE)

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Arguments

datasetGeoCode the GEO code of a dataset.

retrieveGeneSymbols

a boolean flag stating if the function should retrieve the gene symbols or not.

verbose

a boolean flag stating if helping messages should be printed or not

Value

a gene expression dataset.

Examples

```
geneExpressionDF1 <- getGeneExpressionFromGEO("GSE3268", FALSE, FALSE)</pre>
```

readUrl

Function that reads in a URL to check and verifies if it exists (function written by Janko Thyson @rappster and taken from https://stackoverflow.com/a/12195574)

Description

Function that reads in a URL to check and verifies if it exists (function written by Janko Thyson @rappster and taken from https://stackoverflow.com/a/12195574)

Usage

```
readUrl(url)
```

Arguments

url

the URL of a webpage

Value

the output of a webpage verification check

Examples

```
y <- \ readUrl("http://stat.ethz.ch/R-manual/R-devel/library/base/html/connections.html") \\
```

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