

Package: geneExpressionFromGEO (via r-universe)

September 14, 2024

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, 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/>. More information can be found in the following manuscript: Davide Chicco, ``geneExpressionFromGEO: 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](https://doi.org/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 | <i>Function that returns numeric values with 2 decimal numbers.</i> |
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Description

Function that returns numeric values with 2 decimal numbers.

Usage

```
dec_two(x)
```

Arguments

x input numeric value with N decimal numbers.

Value

a numeric value with 2 decimal numbers.

Examples

```
aaa <- dec_two(8.31232)
```

`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)
```

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)
```

`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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