Package ‘geneExpressionFromGEO’

November 7, 2021

Encoding UTF-8

Title Retrieves Gene Expression Dataset and Gene Symbols from GEO Code

Version 0.8

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, 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/>. 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, Springer Protocols, New York City, New York, USA, 2021. In press.

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

Date/Publication 2021-11-07 00:30:02 UTC
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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**

```r
dec_two(x)
```

**Arguments**

- `x` input numeric value with \(N\) decimal numbers.

**Value**

a numeric value with 2 decimal numbers.

**Examples**

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

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**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**

```r
getGeneExpressionFromGEO(datasetGeoCode, retrieveGeneSymbols, verbose = FALSE)
```
readUrl

**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**

```r
geneExpressionDF1 <- getGeneExpressionFromGEO("GSE3268", FALSE, FALSE)
```

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**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**

```r
readUrl(url)
```

**Arguments**

- **url**  the URL of a webpage

**Value**

the output of a webpage verification check

**Examples**

```r
```
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