

Package ‘geneExpressionFromGEO’

December 9, 2025

Encoding UTF-8

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

Version 1.3[illegible]

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

Depends R ($\geq 3.1.0$)

License GPL-3

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

Imports xml2, Biobase, annotate, GEOquery, utils

Suggests knitr, rmarkdown

VignetteBuilder knitr

RoxygenNote 7.3.2

NeedsCompilation no

Author Davide Chicco [aut, cre] (ORCID:
<<https://orcid.org/0000-0001-9655-7142>>)

Maintainer Davide Chicco <davidechicco@davidechicco.it>

Repository CRAN

Date/Publication 2025-12-09 10:10:02 UTC

Contents

dec_two	2
getDatasetFeaturesFromGEOcode	2
getGeneExpressionFromGEO	3
readUrl	4

Index	5
-------	---

dec_two	<i>Function that returns numeric values with 2 decimal numbers.</i>
---------	---

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)

getDatasetFeaturesFromGEOcode	<i>Function that reads in the GEO code of a dataset, and returns the complete gene expression dataframe by printing its features (if requested).</i>
-------------------------------	--

Description

Function that reads in the GEO code of a dataset, and returns the complete gene expression dataframe by printing its features (if requested).

Usage

getDatasetFeaturesFromGEOcode(GSE_code, verbose = FALSE)

Arguments

GSE_code the GEO code of a dataset.
verbose a boolean flag stating if helping messages should be printed or not

Value

a complete gene expression dataset.

Examples

```
# geneExpressionDF <- getDatasetFeaturesFromGEOcode("GSE23906", FALSE)  
geneExpressionDF <- getDatasetFeaturesFromGEOcode(NULL, FALSE)
```

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("GSE23906", FALSE, FALSE)  
geneExpressionDF1 <- getGeneExpressionFromGEO(NULL, FALSE, FALSE)
```

readUrl	<i>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)</i>
---------	---

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")
```

Index

`dec_two`, [2](#)

`getDatasetFeaturesFromGEOcode`, [2](#)

`getGeneExpressionFromGEO`, [3](#)

`readUrl`, [4](#)