

# Package ‘geneExpressionFromGEO’

April 24, 2021

**Encoding** UTF-8

**Title** Retrieves Gene Expression Dataset and Gene Symbols from GEO Code

**Version** 0.6

**Description** A function that reads in the GEO code of a gene expression dataset, retrieves its data from GEO, (optional) 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, GPL expression Omnibus. ID: identifier code. The GEO datasets are downloaded from the URL <<https://ftp.ncbi.nlm.nih.gov/geo/series/>>.

**BugReports** <https://stackoverflow.com/questions/tagged/geneExpressionFromGEO>

**Depends** R (>= 3.1.0)

**License** GPL-3

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

**Imports** xml2, Biobase, annotate, GEOquery

**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.*

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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)
```

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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**

```
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)
```

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readUrl	<i>Function that reads in a URL to check and verifies if it exists (function written by Janko Thyson @rappster and taken from <a href="https://stackoverflow.com/a/12195574">https://stackoverflow.com/a/12195574</a> )</i>
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**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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