

Package ‘healthyControlsPresenceChecker’

August 28, 2025

Encoding UTF-8

Title Downloads A Gene Expression Dataset From GEO And Checks If It
Contains Data Of Healthy Controls Or Not

Version 1.13.0

Description A function that reads in the GEO accession code of a gene expression dataset, retrieves its data from GEO, and checks if data of healthy controls are present in the dataset. It returns true if healthy controls data are found, and false otherwise. GEO: Gene Expression Omnibus. ID: identifier code. The GEO datasets are downloaded from the URL <https://ftp.ncbi.nlm.nih.gov/geo/series/>.

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

Depends R (>= 4.0.0)

License GPL-3

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

biocViews GEO, RepositoryData, ExpressionData

Imports xml2, GEOquery, geneExpressionFromGEO, magrittr

Suggests RUnit, BiocGenerics, markdown, BiocStyle, knitr, rmarkdown

VignetteBuilder knitr

RoxygenNote 7.1.1

git_url <https://git.bioconductor.org/packages/healthyControlsPresenceChecker>

git_branch devel

git_last_commit 18ed549

git_last_commit_date 2025-04-15

Repository Bioconductor 3.22

Date/Publication 2025-08-28

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Description

Function that reads in the GEO code of a dataset, and returns true if there's at least a feature containing the healthy controls.

Usage

```
healthyControlsCheck(datasetGeoCode, verbose = FALSE)
```

Arguments

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

Value

a boolean value

Examples

```
healthyControlsCheckOutcome <- healthyControlsCheck("GSE3268", FALSE)
```

healthyControlsChecker	<i>healthyControlsChecker: A package for verifying the presence of healthy controls in a GEO dataset</i>
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Description

The healthyControlsChecker package provides one relevant function: healthyControlsCheck()

healthyControlsCheck() function

The healthyControlsCheck() function reads in the GEO code of a dataset, and returns true if there's at least a feature containing the healthy controls.

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