

Package ‘healthyControlsPresenceChecker’

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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, re-trieves its data from GEO, and checks if data of healthy controls are present in the dataset. It re-returns true if healthy controls data are found, and false otherwise. GEO: Gene Expression Om-nibus. ID: identifier code. The GEO datasets are down-loaded 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

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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

healthyControlsChecker: A package for verifying the presence of healthy controls in a GEO dataset

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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