

Package ‘GEOexplorer’

May 22, 2022

Title GEOexplorer: an R/Bioconductor package for gene expression analysis and visualisation

Date 2021/10/15

Version 1.3.0

Description GEOexplorer is a Shiny app that enables exploratory data analysis and differential gene expression of gene expression analysis on microarray gene expression datasets held on the GEO database. The outputs are interactive graphs that enable users to explore the results of the analysis. The development of GEOexplorer was made possible because of the excellent code provided by GEO2R (<https://www.ncbi.nlm.nih.gov/geo/geo2r/>).

License GPL-3

Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

URL <https://github.com/guypwhunt/GEOexplorer/>

BugReports <https://github.com/guypwhunt/GEOexplorer/issues>

RoxygenNote 7.1.1.9001

biocViews Software, GeneExpression, mRNAMicroarray, DifferentialExpression, Microarray, MicroRNAArray

Depends shiny, limma, Biobase, plotly, shinyBS

Imports DT, htmltools, factoextra, heatmaply, maptools, pheatmap, scales, shinyHeatmaply, shinybusy, ggplot2, stringr, umap, GEOquery, impute, grDevices, stats, graphics, utils

Suggests rmarkdown, knitr, usethis, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

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

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loadApp	<i>A Function to Load the GEOexplorer Shiny App</i>
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Description

This function loads the GEOexplorer Shiny App. The GEOexplorer Shiny App extends GEO2R's functionalities by enabling a richer set of analysis and graphics to be performed/generated from the gene expression data.

Usage

```
loadApp()
```

Value

Large Shiny App

Author(s)

Guy Hunt

Examples

```
app <- loadApp()
```

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