

# Package ‘GEOexplorer’

October 16, 2022

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

**Date** 2021/10/15

**Version** 1.2.0

**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>

**git\_branch** RELEASE\_3\_15

**git\_last\_commit** 3158786

**git\_last\_commit\_date** 2022-04-26

**Date/Publication** 2022-10-16

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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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