

# Package ‘GEOexplorer’

October 17, 2024

**Title** GEOexplorer: a webserver for gene expression analysis and visualisation

**Date** 2023/10/31

**Version** 1.10.0

**Description** GEOexplorer is a webserver and R/Bioconductor package and web application that enables users to perform gene expression 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** false

**Roxygen** list(markdown = TRUE)

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

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

**RoxygenNote** 7.2.3

**biocViews** Software, GeneExpression, mRNAArray, DifferentialExpression, Microarray, MicroRNAArray, Transcriptomics, RNASeq

**Depends** shiny, limma, Biobase, plotly, enrichR, R (>= 4.1.0)

**Imports** DT, XML, httr, sva, xfun, edgeR, htmltools, factoextra, heatmaply, pheatmap, scales, shinyHeatmaply, shinybusy, ggplot2, stringr, umap, GEOquery, impute, grDevices, stats, graphics, markdown, knitr, utils, xml2, R.utils, readxl, shinycssloaders, car

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

**VignetteBuilder** knitr

**Config/testthat/edition** 3

**git\_url** <https://git.bioconductor.org/packages/GEOexplorer>

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**Author** Guy Hunt [aut, cre] (<<https://orcid.org/0000-0002-5217-2678>>),  
 Rafael Henkin [ctb, ths] (<<https://orcid.org/0000-0002-5511-5230>>),  
 Alfredo Iacoangeli [ctb, ths] (<<https://orcid.org/0000-0002-5280-5017>>),  
 Fabrizio Smeraldi [ctb, ths] (<<https://orcid.org/0000-0002-0057-8940>>),  
 Michael Barnes [ctb, ths] (<<https://orcid.org/0000-0001-9097-7381>>)

**Maintainer** Guy Hunt <guy.hunt@kcl.ac.uk>

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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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