

# Package: GEOexplorer (via r-universe)

May 31, 2026

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

**Date** 2023/10/31

**Version** 1.18.0

**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/guyphunt/GEOexplorer/>

**BugReports** <https://github.com/guyphunt/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

**PackageStatus** Deprecated

**Config/pak/sysreqs** cmake make libmagick++-dev gsfonts libicu-dev libpng-dev libuv1-dev libxml2-dev libssl-dev perl python3 libx11-dev zlib1g-dev

**Repository** <https://bioc-release.r-universe.dev>

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**RemoteUrl** <https://github.com/bioc/GEOexplorer>

**RemoteRef** RELEASE\_3\_23

**RemoteSha** d9177c24e752a90eefcf4807be16ca14e45ba5ea

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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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