

Package ‘GEOexplorer’

April 14, 2025

Title GEOexplorer: a webserver for gene expression analysis and visualisation

Date 2023/10/31

Version 1.13.0

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>

git_branch devel

git_last_commit 6e19a44

git_last_commit_date 2024-10-29
Repository Bioconductor 3.21
Date/Publication 2025-04-14
Author Guy Hunt [aut, cre] (ORCID: <<https://orcid.org/0000-0002-5217-2678>>),
Rafael Henkin [ctb, ths] (ORCID:
<<https://orcid.org/0000-0002-5511-5230>>),
Alfredo Iacoangeli [ctb, ths] (ORCID:
<<https://orcid.org/0000-0002-5280-5017>>),
Fabrizio Smeraldi [ctb, ths] (ORCID:
<<https://orcid.org/0000-0002-0057-8940>>),
Michael Barnes [ctb, ths] (ORCID:
<<https://orcid.org/0000-0001-9097-7381>>)
Maintainer Guy Hunt <guy.hunt@kcl.ac.uk>

Contents

loadApp	2
Index	3

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

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()
```

Index

* **GEO**

loadApp, [2](#)

loadApp, [2](#)