

# Package ‘TCGAbiolinksGUI’

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**Title** ``TCGAbiolinksGUI: A Graphical User Interface to analyze cancer molecular and clinical data''

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## Description

``TCGAbiolinksGUI: A Graphical User Interface to analyze cancer molecular and clinical data.  
A demo version of GUI is found in <https://tcgabiolinksgui.shinyapps.io/tcgabiolinks/>''

**License** GPL (>= 3)

**Depends** R (>= 3.3.1), shinydashboard (>= 0.5.3), TCGAbiolinksGUI.data

**Suggests** testthat, dplyr, knitr, roxygen2, devtools, rvest, xml2,  
BiocStyle, animation, pander

**Imports** shiny (>= 0.14.1), downloader (>= 0.4), grid, DT, plotly,  
readr, maftools, stringr (>= 1.1.0), SummarizedExperiment,  
ggrepel, data.table, caret, shinyFiles (>= 0.6.2), ggplot2 (>= 2.1.0), pathview, ELMER (>= 2.0.0), clusterProfiler, parallel,  
TCGAbiolinks (>= 2.5.5), shinyjs (>= 0.7), colourpicker,  
sesame, shinyBS (>= 0.61)

**VignetteBuilder** knitr

**biocViews** Genetics, GUI, DNAMethylation, StatisticalMethod,  
DifferentialMethylation, GeneRegulation, GeneExpression,  
MethylationArray, DifferentialExpression, Sequencing, Pathways,  
Network, DNASEq

**RoxygenNote** 6.1.1

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

**git\_branch** RELEASE\_3\_12

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**R topics documented:**

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**Description**

A Graphical User Interface for integrative analysis of TCGA data  
 Calls UI interface

**Usage**

```
TCGAbiolinksGUI(run = TRUE)
```

**Arguments**

run                    Used to control the examples.

**Details**

The functions you're likely to need from **TCGAbiolinksGUI** are [TCGAbiolinksGUI](#)

**Value**

Open a connection to shiny

**Examples**

```
## Not run:
  TCGAbiolinksGUI()

## End(Not run)
  TCGAbiolinksGUI(run = FALSE)
```

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