

Package ‘TCGAbiolinksGUI’

June 23, 2022

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

Version 1.22.0

Date 2016-10-28

Author Tiago Chedraoui Silva <tiagochst@gmail.com>,
Antonio Colaprico <antonio.colaprico@ulb.ac.be>,
Catharina Olsen <colsen@ulb.ac.be>,
Michele Ceccarelli,
Gianluca Bontempi <gbonte@ulb.ac.be>,
Benjamin P. Berman <Benjamin.Berman@cshs.org>,
Houtan Noushmehr <houtana@gmail.com>

Maintainer Tiago C. Silva <tiagochst@gmail.com>

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, rmarkdown, 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_15

git_last_commit a486d4d

git_last_commit_date 2022-04-26

Date/Publication 2022-06-23

R topics documented:

TCGAbiolinksGUI	2
Index	3

TCGAbiolinksGUI	<i>TCGAbiolinksGUI</i>
-----------------	------------------------

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)
```

Index

TCGAbiolinksGUI, [2](#), [2](#)
TCGAbiolinksGUI-package
 (TCGAbiolinksGUI), [2](#)