

Package ‘TCGAbiolinksGUI’

October 11, 2022

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

Version 1.22.0

Date 2016-10-28

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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, 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 2022-10-11

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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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