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, minfi, caret,
IlluminaHumanMethylation450kanno.ilmn12.hg19,
IlluminaHumanMethylation450kmanifest,
IlluminaHumanMethylation27kmanifest,
IlluminaHumanMethylation27kanno.ilmn12.hg19,
IlluminaHumanMethylationEPICanno.ilm10b2.hg19,
IlluminaHumanMethylationEPICmanifest, shinyFiles (>= 0.6.2),
ggplot2 (>= 2.1.0), pathview, ELMER (>= 2.0.0),
clusterProfiler, parallel, TCGAbiolinks (>= 2.5.5), shinyjs (>=
0.7), colourpicker, shinyBS (>= 0.61)

VignetteBuilder knitr

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

RoxygenNote 6.0.1

git_url https://git.bioconductor.org/packages/TCGAbiolinksGUI

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R topics documented:

TCGAbiolinksGUI   *TCGAbiolinksGUI*

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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