

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)

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

Imports ELMER (>= 2.0.0), pathview, parallel, maftools, shiny (>= 0.14.1), downloader (>= 0.4), grid, DT, plotly, readr, stringr (>= 1.1.0), SummarizedExperiment, ggrepel, data.table, shinyFiles (>= 0.6.2), ggplot2 (>= 2.1.0), clusterProfiler, 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

NeedsCompilation no

R topics documented:

TCGAbiolinksGUI 2

Index**3**

`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)
```

Index

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