Title
````
``TCGAbiolinksGUI: A Graphical User Interface to analyze cancer molecular and clinical data``
````
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1.0.0
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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, knitr, roxygen2, devtools, rvest, xml2, BiocStyle, animation, pander
Imports
shiny (>= 0.14.1), downloader (>= 0.4), grid, googleVis, readr, stringr (>= 1.1.0), SummarizedExperiment, ggrepel, data.table, shinyFiles (>= 0.6.2), ggplot2 (>= 2.1.0), pathview, ELMER (>= 1.2.1), clusterProfiler, parallel, plotly, TCGAbiolinks (>= 2.2.4), shinyjs (>= 0.7), colourpicker, shinyBS (>= 0.61)
VignetteBuilder
knitr
biocViews
Genetics, GUI, DNA Methylation, Statistical Method, Differential Methylation, Gene Regulation, Gene Expression, Methylation Array, Differential Expression, Sequencing, Pathways, Network, DNA Seq
RoxygenNote
6.0.1
NeedsCompilation
no

R topics documented:
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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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