Package: TCGAgistic (via r-universe)

October 27, 2024

Title Easily access TCGA gistic data

Version 0.0.0.9000

Description Streams TCGA GISTIC2 copynumber data into the R session.

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Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.1

Imports maftools, pingr, rlang

URL `https://github.com/CCICB/TCGAgistic`

BugReports `https://github.com/CCICB/TCGAgistic/issues`

Repository https://ccicb.r-universe.dev

RemoteUrl https://github.com/CCICB/TCGAgistic

RemoteRef HEAD

RemoteSha adf0782554c2d7916169cf81f69d19247047b7eb

Contents

`tcga_gistic_available` *List Available Datasets*

Description

List Available Datasets

Usage

```
tcga_gistic_available()
```

Value

a dataframe listing available datasets

Examples

```
tcga_gistic_available()
```

`tcga_gistic_load` *Load TCGA GISTIC data*

Description

Load TCGA GISTIC objects into R. Streams data from TCGAgisticDB repo.

Usage

```
tcga_gistic_load(
  cohort,
  source = "Firehose",
  cnLevel = c("all", "deep", "shallow"),
  verbose = TRUE
)
```

Arguments

`cohort`	abbreviation of TCGA cohort See `tcga_gistic_available()` for valid values (string)
`source`	source of the data (currently we only support ’Firehose’ data (string)
`cnLevel`	level of CN changes to use. Can be ’all’, ’deep’ or ’shallow’. Default uses all i.e, genes with both ’shallow’ or ’deep’ CN changes
`verbose`	verbosity (flag)

Value

A maftools & CRUX-compatible list of summarized data.

Examples

```
# Load libraries
library(TCGAgistic)
library(maftools)

# Load dataset
gistic <- tcga_gistic_load("ACC", source = "Firehose", cnLevel = "all")

# Visualise results
gisticChromPlot(gistic)
```

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