

Package ‘UCSCXenaShiny’

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Title A Shiny App for UCSC Xena Database

Version 0.3.0

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Description Provides a web app for downloading, analyzing and visualizing datasets from UCSC Xena (<<http://xena.ucsc.edu/>>), which is a collection of UCSC-hosted public databases such as TCGA, ICGC, TARGET, GTEx, CCLE, and others.

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URL <https://github.com/openbioX/XenaShiny>

BugReports <https://github.com/openbioX/XenaShiny/issues>

Depends R (>= 3.5)

Imports dplyr (>= 0.8.3), DT (>= 0.5), ggplot2 (>= 3.2.0), ggpubr (>= 0.2), magrittr (>= 1.5), plotly (>= 4.9.0), RColorBrewer (>= 1.1.2), shiny (>= 1.3.2), shinyBS (>= 0.61), shinyjs (>= 1.0), shinythemes (>= 1.1.2), shinyWidgets (>= 0.4.8), tibble (>= 2.1.3), UCSCXenaTools (>= 1.2.2), utils, zip (>= 2.0.1)

Suggests covr (>= 3.2.1), testthat (>= 2.0.1)

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

NeedsCompilation no

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app_run	<i>Run Xena Shiny App</i>
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Description

Run Xena Shiny App

Usage

```
app_run()
```

Examples

```
app_run()
```

available_hosts	<i>Show available hosts</i>
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Description

Show available hosts

Usage

```
available_hosts()
```

Value

hosts

Examples

```
available_hosts()
```

dat_datasets	<i>Number of datasets in each cohort</i>
--------------	--

Description

Number of datasets in each cohort

Format

A [data.frame](#)

Source

Generate from data-raw

Examples

```
data("dat_datasets")
```

dat_samples	<i>Number of samples in each cohort</i>
-------------	---

Description

Number of samples in each cohort

Format

A [data.frame](#)

Source

Generate from data-raw

Examples

```
data("dat_samples")
```

get_pancan_value	<i>Fetch identifier value from pan-cancer dataset</i>
------------------	---

Description

Identifier includes gene/probe etc.

Usage

```
get_pancan_value(identifier, subtype = NULL, dataset = NULL,
  host = available_hosts(), samples = NULL)
```

```
get_pancan_gene_value(identifier, host = "toilHub")
```

Arguments

identifier	a length-1 character representing a gene symbol, ensembl gene id, or probe id. Gene symbol is highly recommended.
subtype	a length-1 chracter representing a regular expression for matching DataSubtype column of UCSCXenaTools::XenaData .
dataset	a length-1 chracter representing a regular expression for matching XenaDatasets of UCSCXenaTools::XenaData .
host	a length-1 character representing host name, e.g. "toilHub".
samples	a character vector representing samples want to be returned.

Value

a named vector or list

Functions

- get_pancan_value: Fetch identifier value from pan-cancer dataset
- get_pancan_gene_value: Fetch gene expression value from pan-cancer dataset

Examples

```
# Fetch TP53 expression value from pan-cancer dataset
t1 <- get_pancan_value("TP53",
  dataset = "TcgaTargetGtex_rsem_isoform_tpm",
  host = "toilHub"
)
t2 <- get_pancan_gene_value("TP53")
```

ope_toil_gene	<i>Obtain toilHub info for single gene</i>
---------------	--

Description

Obtain toilHub info for single gene

Usage

```
ope_toil_gene(identifier = "TP53")
```

Arguments

identifier a length-1 character representing a gene symbol, ensembl gene id, or probe id. Gene symbol is highly recommended.

Value

a tibble

Examples

```
t <- ope_toil_gene()
t
```

tcga_gtex	<i>Toil Hub: merged TCGA GTEX selected phenotypes</i>
-----------	---

Description

Toil Hub: merged TCGA GTEX selected phenotypes

Format

A [data.frame](#)

Examples

```
data("tcga_gtex_sampleinfo")
```

toil_info

Toil Hub: TCGA TARGET GTEX selected phenotypes

Description

Toil Hub: TCGA TARGET GTEX selected phenotypes

Format

A [data.frame](#)

Source

Generate from data-raw

Examples

```
data("toil_info")
```

toil_surv

Toil Hub: TCGA survival data

Description

Toil Hub: TCGA survival data

Format

A [data.frame](#)

Source

Generate from data-raw

Examples

```
data("toil_surv")
```

UCSCXenaShiny

Xena Shiny App

Description

Xena Shiny App

`vis_toil_gene`*Visualize single gene expression from toil data hub*

Description

Visualize single gene expression from toil data hub

Usage

```
vis_toil_gene(data, x = "primary_site", y = "expression",
  color = "sample_type", palette = "jco", xlab = "Primary site",
  ylab = "Expression", title = NULL, facet.by = NULL, angle.x = 45,
  ...)
```

Arguments

<code>data</code>	a data frame
<code>x</code>	character string containing the name of x variable.
<code>y</code>	character vector containing one or more variables to plot
<code>color</code>	outline color.
<code>palette</code>	the color palette to be used for coloring or filling by groups. Allowed values include "grey" for grey color palettes; brewer palettes e.g. "RdBu", "Blues", ...; or custom color palette e.g. <code>c("blue", "red")</code> ; and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".
<code>xlab</code>	character vector specifying x axis labels. Use <code>xlab = FALSE</code> to hide xlab.
<code>ylab</code>	character vector specifying y axis labels. Use <code>ylab = FALSE</code> to hide ylab.
<code>title</code>	plot main title.
<code>facet.by</code>	character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.
<code>angle.x</code>	angle for x lab
<code>...</code>	other parameters passing to <code>ggpubr::ggboxplot()</code>

Value

a `ggplot` object

 vis_toil_TvsN

Visualize single gene expression from toil data hub

Description

Visualize single gene expression from toil data hub

Usage

```
vis_toil_TvsN(Gene = "TP53", Mode = "Boxplot", Show.P.value = TRUE,
  Show.P.label = TRUE, Method = "wilcox.test", values = c("#DF2020",
  "#DDDF21"))
```

Arguments

Gene	Gene symbol for comparison
Mode	Boxplot or Violinplot to represent data
Show.P.value	TRUE or FALSE whether to count P value
Show.P.label	TRUE or FALSE present p value with number or label '*** **'
Method	default method is wilcox.test
values	the color to fill tumor or normal

Value

a ggplot object

Examples

```
vis_toil_TvsN(Gene = "TP53", Mode = "Violinplot", Show.P.value = F, Show.P.label = F)
vis_toil_TvsN(Gene = "TP53", Mode = "Boxplot", Show.P.value = F, Show.P.label = F)
```

 XenaInfo

Summary info of UCSC Xena

Description

Summary info of UCSC Xena

Format

A [list](#)

XenaInfo

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Source

Generate from data-raw

Examples

```
data("XenaInfo")
```

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