Package ‘UCSCXenaShiny’

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Title A Shiny App for UCSC Xena Database

Version 0.5.0

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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 7.1.0

NeedsCompilation no

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R topics documented:

`app_run` *Run Xena Shiny App*

Description

Run Xena Shiny App

Usage

```
app_run()
```

Examples

```
app_run()
```

`available_hosts` *Show available hosts*

Description

Show available hosts

Usage

```
available_hosts()
```

Value

hosts

Examples

```
available_hosts()
```

`dat_datasets` *Number of datasets in each cohort*

Description

Number of datasets in each cohort

Format

A data.frame

Source

Generate from data-raw

Examples

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

`dat_samples` *Number of samples in each cohort*

Description

Number of samples in each cohort

Format

A data.frame

Source

Generate from data-raw

Examples

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

`get_pancan_value` *Fetch identifier value from pan-cancer dataset*

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` *Obtain toilHub info for single gene*

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` *Toil Hub: merged TCGA GTEX selected phenotypes*

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

A Shiny App for UCSC Xena Data Hubs.

`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

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

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 symbal for comparision
`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

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

Source

Generate from data-raw

Examples

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

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