

Package ‘epivizrChart’

March 25, 2024

Title R interface to epiviz web components

Version 1.24.0

Description This package provides an API for interactive visualization of genomic data using epiviz web components. Objects in R/BioConductor can be used to generate interactive R mark-down/notebook documents or can be visualized in the R Studio's default viewer.

Imports epivizrData (>= 1.5.1), epivizrServer, htmltools, rjson, methods, BiocGenerics

Suggests testthat, roxygen2, knitr, Biobase, GenomicRanges, S4Vectors, IRanges, SummarizedExperiment, antiProfilesData, hgu133plus2.db, Mus.musculus, BiocStyle, Homo.sapiens, shiny, minfi, Rsamtools, rtracklayer, RColorBrewer, magrittr, AnnotationHub

Collate 'utils.R' 'EpivizChartDataMgr-class.R'
'EpivizWebComponent-class.R' 'EpivizViewComponent-class.R'
'EpivizDataSource-class.R' 'EpivizEnvironment-class.R'
'EpivizChart-class.R' 'EpivizNavigation-class.R'
'EpivizCharts-classes.R' 'vignette_data.R' 'util-inits.R'
'generics.R'

VignetteBuilder knitr

Depends R (>= 3.4.0)

License Artistic-2.0

Encoding UTF-8

LazyData true

biocViews Visualization, GUI

RoxygenNote 7.1.0

git_url <https://git.bioconductor.org/packages/epivizrChart>

git_branch RELEASE_3_18

git_last_commit 84bf342

git_last_commit_date 2023-10-24

Repository Bioconductor 3.18

Date/Publication 2024-03-25

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<code>.constructURL</code>	<i>Construct URL for Websocket connection between R and UI</i>
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Description

Construct URL for Websocket connection between R and UI

Usage

```
.constructURL(host = "localhost", port = 7123L, path = "")
```

Arguments

host	host
port	port
path	path

Value

url

<code>.initialize_chart</code>	<i>Initialize Epiviz Chart based on chart type</i>
--------------------------------	----------------------------------------------------

Description

Initialize Epiviz Chart based on chart type

Usage

```
.initialize_chart(chart_type, ...)
```

Arguments

chart_type	Chart type.
...	Arguments for EpivizChart objects.

```
.register_all_the_epiviz_things
```

(taken from epivizr) register epiviz actions

Description

(taken from epivizr) register epiviz actions

Usage

```
.register_all_the_epiviz_things(srv, app)
```

Arguments

srv	epivizrServer object
app	EpivizApp object

```
.settings_as_df
```

(taken from epivizr) print settings in a readable format

Description

(taken from epivizr) print settings in a readable format

Usage

```
.settings_as_df(chart_settings)
```

Arguments

chart_settings chart settings

Value

chart settings as data frame

append_region	<i>Generic method to add navigation regions</i>
---------------	-------------------------------------------------

Description

Generic method to add navigation regions

Usage

```
append_region(x, ...)
```

```
## S4 method for signature 'EpivizEnvironment'
append_region(x, chr, start, end, return_parent = FALSE)
```

Arguments

x	an object of type EpivizEnvironment
...	other parameters
chr	chromosome id. ex. "chr11"
start	genomic region start
end	genomic region end
return_parent	To return the parent or the new navigation element. Defaults to FALSE

bcode_eset	<i>Example expression data from the Gene Expression barcode project</i>
------------	-------------------------------------------------------------------------

Description

See vignette `data_preprocessing` for code to build this object.

Usage

```
data(bcode_eset)
```

Format

An `Biobase::ExpressionSet` object

BlocksTrack	<i>Method to add Blocks Track</i>
-------------	-----------------------------------

Description

Method to add Blocks Track

Usage

```
BlocksTrack(x, y, ...)
```

```
## S4 method for signature 'EpivizEnvironment'  
BlocksTrack(x, y, ...)
```

Arguments

x	an object of type EpivizEnvironment or EpivizNavigation
y	a genomic data object
...	other parameters for the plot method

cgi_gr	<i>Locations of CpG Islands</i>
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Description

Locations of CpG Islands

Usage

```
data(cgi_gr)
```

Format

A `GenomicRanges::GRanges` object with locations of CpG Islands in hg19

chart_default_settings_colors
Get default chart settings and colors

Description

Get default chart settings and colors

Usage

chart_default_settings_colors(chart_type)

Arguments

chart_type chart type

Value

list of settings and colors

EpivizBlocksTrack-class
Data container for an Epiviz Blocks Track.

Description

Data container for an Epiviz Blocks Track.

Methods

get_component_type() Get component type for prefix of random id generator
get_default_colors() Get default colors
get_default_settings() Get default settings
get_name() Get name of Epiviz Web Component

epivizChart	<i>Initialize an EpivizChart object to visualize in viewer or knit to HTML.</i>
-------------	-------------------------------------------------------------------------------------------------

Description

Initialize an [EpivizChart](#) object to visualize in viewer or knit to HTML.

Usage

```
epivizChart(
  data_obj = NULL,
  measurements = NULL,
  datasource_name = NULL,
  parent = NULL,
  chart = NULL,
  chr = NULL,
  start = NULL,
  end = NULL,
  settings = NULL,
  colors = NULL,
  ...
)
```

Arguments

data_obj	A data object that will register to an EpivizData object.
measurements	An EpivizMeasurement object.
datasource_name	A name for the datasource. For example, "Mean by Sample Type".
parent	An object of class EpivizEnvironment or EpivizNavigation to append the chart within.
chart	The chart type to be visualized: "BlocksTrack", "HeatmapPlot", "LinePlot", "LineTrack", "ScatterPlot", "StackedLinePlot", "StackedLineTrack".
chr	The chromosome to filter on, e.g., chr="chr11".
start	The start location, e.g., start=110800000.
end	The end location, e.g., end=130383180.
settings	List of settings, e.g., list(title="Blocks Chart").
colors	List of colors. When chart is rendered to html this will be converted to a string encoded as JSON
...	Additional arguments passed to epivizrData::register , e.g., type="bp", columns=c("normal, cancer").

Value

An object of class `EpivizChart`.

Examples

```
data(tcga_colon_blocks)
start <- 99800000
end <- 103383180
blocks_track <- epivizChart(tcga_colon_blocks, chr="chr11", start=start, end=end)
# See package vignette for more examples.
```

`EpivizChart-class` *Data container for an Epiviz chart component.*

Description

Data container for an Epiviz chart component.

Fields

`data` (list) Values of an epiviz chart's data attribute.
`colors` (character) Epiviz chart's colors attribute.
`settings` (list) Epiviz chart's settings attribute.
`parent` An object of class `EpivizEnvironment` where chart is appended.

Methods

`get_attributes()` Get attributes for rendering chart
`get_available_settings()` Get available settings
`get_colors()` Get chart colors
`get_data()` Get chart data
`get_parent()` Get parent
`get_settings()` Get chart settings
`navigate(chr, start, end)` Navigate chart to a genomic location
 chr Chromosome
 start Start location
 end End location
`render_component(shiny = FALSE)` Render to html
`revisualize(chart_type)` Revisualize chart as the given chart type
 chart_type The type of chart to be visualized (`BlocksTrack`, `HeatmapPlot`, `LinePlot`, `LineTrack`, `ScatterPlot`, `StackedLinePlot`, `StackedLineTrack`)
`set_colors(colors)` Set chart colors

set_data(data) Set chart data

set_settings(settings) Modify current settings

settings List of new settings. Call get_available_settings for settings available to modify.

EpivizChartDataMgr-class

Class providing data manager for epiviz charts.

Description

Class providing data manager for epiviz charts.

Fields

.ms_list (environment) List of measurement records

.ms_idCounter (integer) Counter for ID generator

Methods

add_genome(genome) Add genome to data manager (for seqInfo)

chr Chromosome

start Start location

end End location

add_measurements(obj, datasource_name = NULL, datasource_obj_name = deparse(substitute(obj)), ...)

Register measurements in data manager

get_data(measurements, chr = NULL, start = NULL, end = NULL) Get data from data mgr based on measurements, chr, start, and end

measurements List of EpivizMeasurements

chr Chromosome

start Start location

end End location

register_shiny_handler(session) Handlers to enable interactions with Shiny session.

session Shiny session object

rm_all_measurements() Remove all registered measurements

rm_measurements(ms_obj_or_id) Remove registered measurements from a given data object

EpivizDataSource-class

Data container for an Epiviz Data Source component.

Description

Data container for an Epiviz Data Source component.

Fields

provider_type (character)

provider_id (character)

provider_url (character)

Methods

get_attributes() Get attributes for rendering web component

get_component_type() Get component type for prefix of random id generator

get_name() Get name of Epiviz Web Component

get_provider_id() Get provider id

get_provider_type() Get provider type

get_provider_url() Get provider url

render_component(shiny = FALSE) Render to html

set_provider_url(url) Set provider url

set_provider_id(id) Set provider id

set_provider_type(type) Set provider type

epivizEnv

Initialize an [EpivizEnvironment](#) object.

Description

Initialize an [EpivizEnvironment](#) object.

Usage

```
epivizEnv(chr = NULL, start = NULL, end = NULL, interactive = FALSE, ...)
```

Arguments

chr	The chromosome to filter on, e.g., chr="chr11"
start	The start location, e.g., start=99800000.
end	The end location, e.g., end=130383180.
interactive	(logical) enable if running a websocket/shiny server
...	Additional params to pass to EpivizWebComponent

Value

An object of class [EpivizEnvironment](#)

Examples

```
epiviz <- epivizEnv(chr="chr11", start=99800000, end=103383180)
```

EpivizEnvironment-class

Data container for an Epiviz environment component.

Description

Data container for an Epiviz environment component.

Fields

charts List of class [EpivizViewComponent](#) used to track nested elements.
 interactive Logical value of whether component is interactive with data source component..
 epiviz_ds [EpivizDataSource](#) object for interactive documents.

Methods

add_data(...) Add data to environment's data manager
 ... Arguments for add_measurements and register, e.g., data, datasource_name, datasource_obj_name, type, etc

add_genome(genome, type = "gene_info", datasource_name = NULL) Add a genome to the view, and a genes-track.
genome annotation object. eg. Homo.sapiens

append_chart(chart) Append chart or navigation to environment

append_region(chr = NULL, start = NULL, end = NULL, ...) Add a child Navigation element to the given genomic region

get_charts() Get charts within environment

get_component_type() Get component type for prefix of random id generator

get_measurements() Get measurements
 get_name() Get name of Epiviz Web Component
 get_rows(...) Get row data from environment's data manager
 get_values(...) Get value data from environment's data manager
 init_region(chr = NULL, start = NULL, end = NULL) Initialize navigation based on a genomic region
 chr Chromosome
 start Start location
 end End location
 init_regions(regions) Initialize navigations based on genomic regions
 regions List of named lists of genomic locations, e.g., list(list(chr='chr11', start=99800000, end=103383180))
 is_interactive() Return whether the environment is interactive with a data source
 navigate(chr = NULL, start = NULL, end = NULL) Navigate environment to genomic location
 chr Chromosome
 start Start location
 end End location
 order_charts(ordered_charts) Order the charts within an environment
 charts An ordered list of EpivizViewComponent objects
 plot(...) Plot an EpivizChart within the environment
 ... Arguments for epivizChart
 register_shiny_handler(session) Enable components to interact with Shiny session.
 session Shiny session object
 remove_all_charts() Remove all charts from environment
 remove_chart(chart) Remove chart from environment
 render_component(shiny = FALSE) Render to html
 shiny if rendering component in a shiny environment
 set_charts(charts) Set charts of environment

EpivizGenesTrack-class

Data container for an Epiviz Genes Track.

Description

Data container for an Epiviz Genes Track.

Methods

get_component_type() Get component type for prefix of random id generator
 get_default_colors() Get default colors
 get_default_settings() Get default settings
 get_name() Get name of Epiviz Web Component

EpivizHeatmapPlot-class

Data container for an Epiviz Heatmap Plot.

Description

Data container for an Epiviz Heatmap Plot.

Methods

get_component_type() Get component type for prefix of random id generator

get_default_colors() Get default colors

get_default_settings() Get default settings

get_name() Get name of Epiviz Web Component

EpivizIGVTrack-class *Data container for an Epiviz Genes Track.*

Description

Data container for an Epiviz Genes Track.

Methods

get_attributes() Get attributes for rendering component

get_component_type() Get component type for prefix of random id generator

get_default_colors() Get default colors

get_default_settings() Get default settings

get_name() Get name of Epiviz Web Component

EpivizLinePlot-class *Data container for an Epiviz Line Plot.*

Description

Data container for an Epiviz Line Plot.

Methods

get_component_type() Get component type for prefix of random id generator

get_default_colors() Get default colors

get_default_settings() Get default settings

get_name() Get name of Epiviz Web Component

EpivizLineTrack-class *Data container for an Epiviz Line Track.*

Description

Data container for an Epiviz Line Track.

Methods

`get_component_type()` Get component type for prefix of random id generator

`get_default_colors()` Get default colors

`get_default_settings()` Get default settings

`get_name()` Get name of Epiviz Web Component

<code>epivizNav</code>	<i>Initialize an EpivizNavigation object to visualize in viewer or knit to HTML.</i>
------------------------	------------------------------------------------------------------------------------------------------

Description

Initialize an [EpivizNavigation](#) object to visualize in viewer or knit to HTML.

Usage

```
epivizNav(
  chr = NULL,
  start = NULL,
  end = NULL,
  parent = NULL,
  interactive = FALSE,
  ...
)
```

Arguments

<code>chr</code>	The chromosome to filter on, e.g., <code>chr="chr11"</code> .
<code>start</code>	The start location, e.g., <code>start=99800000</code> .
<code>end</code>	The end location, e.g., <code>end=130383180</code> .
<code>parent</code>	An object of class <code>[EpivizEnvironment]</code> or EpivizNavigation to append the chart within.
<code>interactive</code>	(logical) enable if running a websocket/shiny server
<code>...</code>	Additional arguments for initializing navigation, e.g., <code>gene</code> and <code>geneInRange</code> .

Value

An object of class [EpivizNavigation](#).

Examples

```
epiviz <- epivizNav(chr="chr11", start=99800000, end=103383180)
```

EpivizNavigation-class

Data container for an Epiviz navigation component.

Description

Data container for an Epiviz navigation component.

Fields

gene (character) Gene

geneInRange (character) Nearest Gene in range.

parent An object of class [EpivizEnvironment](#) where navigation is appended.

Methods

add_genome(genome, type = "gene_info", datasource_name = NULL) Add a genome to the view, and a genes-track.

genome annotation object. eg. Homo.sapiens

clone_charts(charts) Clone EpivizCharts and append to navigation. Each chart must already exist in the navigation's data manager, otherwise an error will occur when attempting to initialize using their measurements

charts list of EpivizCharts whose data exists in the navigation's data manager

get_attributes() Get attributes for rendering chart

get_component_type() Get component type for prefix of random id generator

get_gene() Get gene

get_geneInRange() Get gene in range

get_name() Get name of Epiviz Web Component

render_component(shiny = FALSE) Render to html

shiny if rendering component in a shiny environment

set_gene(gene) Set gene

set_geneInRange(gene) Set step ratio

EpivizScatterPlot-class

Data container for an Epiviz Scatter Plot.

Description

Data container for an Epiviz Scatter Plot.

Methods

get_component_type() Get component type for prefix of random id generator

get_default_colors() Get default colors

get_default_settings() Get default settings

get_name() Get name of Epiviz Web Component

EpivizStackedBlocksTrack-class

Data container for an Epiviz Blocks Track.

Description

Data container for an Epiviz Blocks Track.

Methods

get_component_type() Get component type for prefix of random id generator

get_default_colors() Get default colors

get_default_settings() Get default settings

get_name() Get name of Epiviz Web Component

EpivizStackedLinePlot-class

Data container for an Epiviz Stacked Line Plot.

Description

Data container for an Epiviz Stacked Line Plot.

Methods

get_component_type() Get component type for prefix of random id generator

get_default_colors() Get default colors

get_default_settings() Get default settings

get_name() Get name of Epiviz Web Component

EpivizStackedLineTrack-class

Data container for an Epiviz Stacked Line Track.

Description

Data container for an Epiviz Stacked Line Track.

Methods

get_component_type() Get component type for prefix of random id generator

get_default_colors() Get default colors

get_default_settings() Get default settings

get_name() Get name of Epiviz Web Component

EpivizViewComponent-class

Data container for an Epiviz web component.

Description

Data container for an Epiviz web component.

Fields

chr (CharacterOrNULL) Chromosome location.

start (NumericOrNULL) Start location.

end (NumericOrNULL) End location.

measurements (ListOrNULL) list of measurements of class [EpivizMeasurement](#).

Methods

get_attributes() Get attributes for rendering web component

get_chr() Get chromosome

get_end() Get end

get_measurements() Get measurements

get_start() Get start

set_chr(chr) Set the chromosome

set_end(end) Set end

set_measurements(ms) Set measurements

set_start(start) Set start

EpivizWebComponent-class

Data container for an Epiviz Web component.

Description

Data container for an Epiviz Web component.

Fields

data_mgr [EpivizChartDataMgr](#)
name (character) Epiviz chart type (tag name).
class (CharacterOrNULL) Epiviz chart's class attribute.
id (character) Epiviz chart's id attribute.

Methods

get_attributes() Get attributes for rendering web component
get_class() Get class
get_data_mgr() Get data manager
get_id() Get id
get_name() Get name of Epiviz Web Component
set_class(class) Set chart class
set_id(id) Set chart id
set_name(name) Set name

get_available_chart_types

Construct URL for Websocket connection between R and UI

Description

Construct URL for Websocket connection between R and UI

Usage

```
get_available_chart_types()
```

Value

url

```
get_registered_data_types
```

Construct URL for Websocket connection between R and UI

Description

Construct URL for Websocket connection between R and UI

Usage

```
get_registered_data_types()
```

Value

url

```
HeatmapPlot
```

Method to add Heatmap Plot

Description

Method to add Heatmap Plot

Usage

```
HeatmapPlot(x, y, ...)
```

```
## S4 method for signature 'EpivizEnvironment'
```

```
HeatmapPlot(x, y, ...)
```

Arguments

x an object of type [EpivizEnvironment](#) or [EpivizNavigation](#)

y a genomic data object

... other parameters for the plot method

json_parser	<i>JSON parser used by this package</i>
-------------	-----------------------------------------

Description

Currently this just renames [fromJSON](#) in the rjson package.

Usage

```
json_parser(  
  json_str,  
  file,  
  method = "C",  
  unexpected.escape = "error",  
  simplify = TRUE  
)
```

Arguments

json_str	json string to parse
file	file to read json_Str from
method	method used to parse json
unexpected.escape	handling escape characters, one of error, skip, keep
simplify	if TRUE, convert json-encoded lists to vectors

Value

a JSON object

See Also

[fromJSON](#)

Examples

```
json_parser('{"a":true, "b":false, "c":null}')
```

json_writer	<i>JSON writer used by this package</i>
-------------	-----------------------------------------

Description

Currently this just renames [toJSON](#) in the `rjson` package.

Usage

```
json_writer(x, indent = 0, method = "C")
```

Arguments

<code>x</code>	object to write to json
<code>indent</code>	integer specifying how much indentation to use when formatting the JSON object; if 0, no pretty-formatting is used
<code>method</code>	method used to write json

Value

a string with JSON encoding of object

See Also

[toJSON](#)

Examples

```
json_writer(1:10)
```

LinePlot	<i>Method to add Line Plot</i>
----------	--------------------------------

Description

Method to add Line Plot

Usage

```
LinePlot(x, y, ...)

## S4 method for signature 'EpivizEnvironment'
LinePlot(x, y, ...)
```

Arguments

x	an object of type EpivizEnvironment or EpivizNavigation
y	a genomic data object
...	other parameters for the plot method

LineTrack

Method to add Line Track

Description

Method to add Line Track

Usage

```
LineTrack(x, y, ...)
```

```
## S4 method for signature 'EpivizEnvironment'
LineTrack(x, y, ...)
```

Arguments

x	an object of type EpivizEnvironment or EpivizNavigation
y	a genomic data object
...	other parameters for the plot method

plot,EpivizEnvironment,ANY-method

Generic methods to plot charts and add navigation regions

Description

Generic methods to plot charts and add navigation regions

Usage

```
## S4 method for signature 'EpivizEnvironment,ANY'
plot(x, y, ...)
```

Arguments

x	an object of type EpivizEnvironment or EpivizNavigation
y	a genomic data object
...	other parameters for the plot method

Examples

```
## Not run:
library(epivizrChart)
library(Homo.sapiens)
require(magrittr)

# example data set
data(sumexp)
# create an environment element
epivizEnv <- epivizEnv()

# chain and add navigation regions and plots.
epivizEnv %>%
plot(sumexp, datasource_name="sumExp", columns=c("cancer", "normal")) %>%
append_region(chr="chr11", start=118000000, end=121000000) %>%
plot(sumexp, datasource_name="sumExp", columns=c("normal", "cancer"))
epivizEnv

## End(Not run)
```

rand_id

Random ID generator for epiviz charts

Description

Random ID generator for epiviz charts

Usage

```
rand_id(prefix = "")
```

Arguments

prefix prefix for random ID

Value

random ID

ScatterPlot	<i>Method to add Scatter Plot</i>
-------------	-----------------------------------

Description

Method to add Scatter Plot

Usage

```
ScatterPlot(x, y, ...)
```

```
## S4 method for signature 'EpivizEnvironment'  
ScatterPlot(x, y, ...)
```

Arguments

x	an object of type EpivizEnvironment or EpivizNavigation
y	a genomic data object
...	other parameters for the plot method

StackedBlocksTrack	<i>Method to add Stacked Blocks Track</i>
--------------------	-------------------------------------------

Description

Method to add Stacked Blocks Track

Usage

```
StackedBlocksTrack(x, y, ...)
```

```
## S4 method for signature 'EpivizEnvironment'  
StackedBlocksTrack(x, y, ...)
```

Arguments

x	an object of type EpivizEnvironment or EpivizNavigation
y	a genomic data object
...	other parameters for the plot method

StackedLinePlot *Method to add Stacked Line Plot*

Description

Method to add Stacked Line Plot

Usage

```
StackedLinePlot(x, y, ...)
```

```
## S4 method for signature 'EpivizEnvironment'
StackedLinePlot(x, y, ...)
```

Arguments

x	an object of type EpivizEnvironment or EpivizNavigation
y	a genomic data object
...	other parameters for the plot method

StackedLineTrack *Method to add Stacked Line Track*

Description

Method to add Stacked Line Track

Usage

```
StackedLineTrack(x, y, ...)
```

```
## S4 method for signature 'EpivizEnvironment'
StackedLineTrack(x, y, ...)
```

Arguments

x	an object of type EpivizEnvironment or EpivizNavigation
y	a genomic data object
...	other parameters for the plot method

sumexp

Example SummarizedExperiment for epivizr vignette

Description

Example SummarizedExperiment for epivizr vignette

Usage

```
data(sumexp)
```

Format

A SummarizedExperiment::RangedSummarizedExperiment object.

tcga_colon_blocks

Example methylation data (blocks) for epivizr vignette.

Description

Example results from methylation analysis of human chromosome 11 using the minfi package of TCGA 450k beadarray samples. This object contains large regions of methylation difference between tumor and normal samples obtained from `minfi::blockFinder()`.

Usage

```
data(tcga_colon_blocks)
```

Format

A GenomicRanges::GRanges object with 129 and mcols:

value average smooth methylation difference within block

area block area estimate (abs(value) * length)

cluster id of cluster blockgroup within which block occurs

indexStart index of first cluster in block

indexEnd index of last cluster in block

L number of clusters in block

clusterL number of probes in block

p.value permutation p.value based on difference conditioned on length

fwer family-wise error rate estimate based on difference conditioned on length

p.valueArea permutation p.value based on area

fwerArea family-wise error rate estimate based on area

Source

TCGA project: <https://tcga-data.nci.nih.gov/tcga/>

tcga_colon_curves	<i>Example methylation data (smoothed methylation levels) for epivizr vignette</i>
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Description

Example results from methylation analysis of human chromosome 11 using the `minfi` package of TCGA 450k beadarray samples. This object contains probe cluster level methylation estimates from `minfi::blockFinder()`.

Usage

```
data(tcga_colon_curves)
```

Format

A `GenomicRanges::GRanges` object with 7135 ranges and `mcols`:

`id` probe cluster id

`type` probe cluster type

`blockgroup` probe cluster block group

`diff` raw methylation percentage difference between normal and tumor

`smooth` smooth methylation percentage difference between normal and tumor

`normalMean` mean methylation estimate for normal samples

`cancerMean` mean methylation estimate for cancer samples

Source

TCGA project: <https://tcga-data.nci.nih.gov/tcga/>

tcga_colon_expression *Example exon-level RNAseq data from TCGA project for epivizr vignette.*

Description

A `SummarizedExperiment::RangedSummarizedExperiment` object containing exon-level counts from RNAseq data for colon tumor and normal tissue from the TCGA project. Only exons in human chromosome 11 are included.

Usage

```
data(tcga_colon_expression)
```

Format

A `SummarizedExperiment::RangedSummarizedExperiment` object with 12,800 rows (exons) and 40 samples.

`assay(tcga_colon_expression)` exon-level count matrix

`colData(tcga_colon_expression)` a `DataFrame` containing sample information. Normal/Tumor status is given in column `sample_type`

Source

TCGA project: <https://tcga-data.nci.nih.gov/tcga/>

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