

Package ‘epivizrChart’

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Title R interface to epiviz web components

Version 1.31.0

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 markdown/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)

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Contents

.constructURL	3
.initialize_chart	3
.register_all_the_epiviz_things	4
.settings_as_df	4
append_region	5
bcode_eset	5
BlocksTrack	6
cgi_gr	6
chart_default_settings_colors	7
EpivizBlocksTrack-class	7
epivizChart	8
EpivizChart-class	9
EpivizChartDataMgr-class	10
EpivizDataSource-class	10
epivizEnv	11
EpivizEnvironment-class	12
EpivizGenesTrack-class	13
EpivizHeatmapPlot-class	13
EpivizIGVTrack-class	14
EpivizLinePlot-class	14
EpivizLineTrack-class	14
epivizNav	15
EpivizNavigation-class	15
EpivizScatterPlot-class	16
EpivizStackedBlocksTrack-class	17
EpivizStackedLinePlot-class	17
EpivizStackedLineTrack-class	17
EpivizViewComponent-class	18
EpivizWebComponent-class	18
get_available_chart_types	19
get_registered_data_types	19
HeatmapPlot	20
json_parser	20
json_writer	21
LinePlot	22
LineTrack	22
plot,EpivizEnvironment,ANY-method	23
rand_id	23
ScatterPlot	24
StackedBlocksTrack	24
StackedLinePlot	25
StackedLineTrack	25
sumexp	26
tcga_colon_blocks	26
tcga_colon_curves	27
tcga_colon_expression	27

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

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

.initialize_chart	<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>
--------	---------------------------------

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	<i>Data container for an Epiviz chart component.</i>
-------------------	--

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 measurment 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	<i>Initialize an EpivizEnvironment object.</i>
-----------	--

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 componenet is interactive with data source componenet..

`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

epivizNav	<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

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.
parent	An object of class [EpivizEnvironment] or EpivizNavigation to append the chart within.
interactive	(logical) enable if running a websocket/shiny server
...	Additional arguments for initializing navigation, e.g., gene and geneInRange.

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	<i>Method to add Heatmap Plot</i>
-------------	-----------------------------------

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

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

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

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	<i>Method to add Stacked Line Track</i>
------------------	---

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	<i>Example exon-level RNAseq data from TCGA project for epivizr vignette.</i>
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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/>

Index

`.constructURL`, [3](#)
`.initialize_chart`, [3](#)
`.register_all_the_epiviz_things`, [4](#)
`.settings_as_df`, [4](#)

`append_region`, [5](#)
`append_region`, `EpivizEnvironment`-method
 (`append_region`), [5](#)

`bcode_eset`, [5](#)
`BlocksTrack`, [6](#)
`BlocksTrack`, `EpivizEnvironment`-method
 (`BlocksTrack`), [6](#)

`cgi_gr`, [6](#)
`chart_default_settings_colors`, [7](#)

`EpivizBlocksTrack`
 (`EpivizBlocksTrack`-class), [7](#)
`EpivizBlocksTrack`-class, [7](#)
`EpivizChart`, [3](#), [8](#)
`EpivizChart` (`EpivizChart`-class), [9](#)
`epivizChart`, [8](#)
`EpivizChart`-class, [9](#)
`EpivizChartDataMgr`, [18](#)
`EpivizChartDataMgr`
 (`EpivizChartDataMgr`-class), [10](#)
`EpivizChartDataMgr`-class, [10](#)
`EpivizData`, [8](#)
`EpivizDataSource`, [12](#)
`EpivizDataSource`
 (`EpivizDataSource`-class), [10](#)
`EpivizDataSource`-class, [10](#)
`epivizEnv`, [11](#)
`EpivizEnvironment`, [5](#), [6](#), [8](#), [9](#), [11](#), [16](#), [20](#),
 [22–25](#)
`EpivizEnvironment`
 (`EpivizEnvironment`-class), [12](#)
`EpivizEnvironment`-class, [12](#)
`EpivizGenesTrack`
 (`EpivizGenesTrack`-class), [13](#)
`EpivizGenesTrack`-class, [13](#)
`EpivizHeatmapPlot`
 (`EpivizHeatmapPlot`-class), [13](#)

`EpivizHeatmapPlot`-class, [13](#)
`EpivizIGVTrack` (`EpivizIGVTrack`-class),
 [14](#)
`EpivizIGVTrack`-class, [14](#)
`EpivizLinePlot` (`EpivizLinePlot`-class),
 [14](#)
`EpivizLinePlot`-class, [14](#)
`EpivizLineTrack`
 (`EpivizLineTrack`-class), [14](#)
`EpivizLineTrack`-class, [14](#)
`EpivizMeasurement`, [8](#), [18](#)
`epivizNav`, [15](#)
`EpivizNavigation`, [6](#), [8](#), [15](#), [20](#), [22–25](#)
`EpivizNavigation`
 (`EpivizNavigation`-class), [15](#)
`EpivizNavigation`-class, [15](#)
`epivizrData::register`, [8](#)
`EpivizScatterPlot`
 (`EpivizScatterPlot`-class), [16](#)
`EpivizScatterPlot`-class, [16](#)
`EpivizStackedBlocksTrack`
 (`EpivizStackedBlocksTrack`-class),
 [17](#)
`EpivizStackedBlocksTrack`-class, [17](#)
`EpivizStackedLinePlot`
 (`EpivizStackedLinePlot`-class),
 [17](#)
`EpivizStackedLinePlot`-class, [17](#)
`EpivizStackedLineTrack`
 (`EpivizStackedLineTrack`-class),
 [17](#)
`EpivizStackedLineTrack`-class, [17](#)
`EpivizViewComponent`, [12](#)
`EpivizViewComponent`
 (`EpivizViewComponent`-class), [18](#)
`EpivizViewComponent`-class, [18](#)
`EpivizWebComponent`, [11](#)
`EpivizWebComponent`
 (`EpivizWebComponent`-class), [18](#)
`EpivizWebComponent`-class, [18](#)

`fromJSON`, [20](#), [21](#)

`get_available_chart_types`, [19](#)

`get_registered_data_types`, [19](#)

`HeatmapPlot`, [20](#)
`HeatmapPlot`, `EpivizEnvironment`-method
 (`HeatmapPlot`), [20](#)

`json_parser`, [20](#)
`json_writer`, [21](#)

`LinePlot`, [22](#)
`LinePlot`, `EpivizEnvironment`-method
 (`LinePlot`), [22](#)
`LineTrack`, [22](#)
`LineTrack`, `EpivizEnvironment`-method
 (`LineTrack`), [22](#)

`minfi::blockFinder()`, [26](#), [27](#)

`plot`, `EpivizEnvironment`, ANY-method, [23](#)

`rand_id`, [23](#)

`ScatterPlot`, [24](#)
`ScatterPlot`, `EpivizEnvironment`-method
 (`ScatterPlot`), [24](#)
`StackedBlocksTrack`, [24](#)
`StackedBlocksTrack`, `EpivizEnvironment`-method
 (`StackedBlocksTrack`), [24](#)
`StackedLinePlot`, [25](#)
`StackedLinePlot`, `EpivizEnvironment`-method
 (`StackedLinePlot`), [25](#)
`StackedLineTrack`, [25](#)
`StackedLineTrack`, `EpivizEnvironment`-method
 (`StackedLineTrack`), [25](#)

`sumexp`, [26](#)

`tcga_colon_blocks`, [26](#)
`tcga_colon_curves`, [27](#)
`tcga_colon_expression`, [27](#)
`toJSON`, [21](#)