

Package ‘epivizrChart’

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Title R interface to epivizr web components

Version 1.2.0

Description This package provides an API for interactive visualization of genomic data using epivizr 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

Suggests testthat, roxygen2, knitr, Biobase, GenomicRanges, S4Vectors, IRanges, SummarizedExperiment, antiProfilesData, hgu133plus2.db, Mus.musculus, BiocStyle, Homo.sapiens

Collate 'utils.R' 'EpivizrChartDataMgr-class.R'
'EpivizrWebComponent-class.R' 'EpivizrViewComponent-class.R'
'EpivizrDataSource-class.R' 'EpivizrEnvironment-class.R'
'EpivizrChart-class.R' 'EpivizrNavigation-class.R'
'EpivizrCharts-classes.R' 'vignette_data.R' 'util-inits.R'

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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

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

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", "Line-Track", "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 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()` 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_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

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()` 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

<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>interactive</code>	(logical) <code>todo</code>
<code>...</code>	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

append_chart(chart) Append chart or navigation to environment

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

remove_all_charts() Remove all charts from environment
 remove_chart(chart) Remove chart from environment
 render_component() Render to html
 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

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, ...)
```

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.
...	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

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

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

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

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")
```

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

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, method = "C")
```

Arguments

x	object to write to json
method	method used to write json

Value

a string with JSON encoding of object

See Also[toJSON](#)**Examples**

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

rand_id	<i>Random ID generator for epiviz charts</i>
---------	--

Description

Random ID generator for epiviz charts

Usage

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

Arguments

prefix prefix for random ID

Value

random ID

tcga_colon_blocks	<i>Example methylation data (blocks) for epivizr vignette.</i>
-------------------	--

Description

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

Usage

```
tcga_colon_blocks
```

Format

A [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

Value

A [GRanges](#) object.

Source

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

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

Description

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

Usage

```
tcga_colon_curves
```

Format

A [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

Value

A [GRanges](#) object.

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 [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

```
tcga_colon_expression
```

Format

A [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`

Value

A [RangedSummarizedExperiment](#) object.

Source

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

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