

Package: epivizrChart (via r-universe)

September 23, 2026

Title R interface to epiviz web components

Version 1.35.0

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)

License Artistic-2.0

Encoding UTF-8

LazyData true

biocViews Visualization, GUI

RoxygenNote 7.1.0

Config/pak/sysreqs

make libbz2-dev liblzma-dev libpng-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

Repository <https://bioc.r-universe.dev>

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```
.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

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 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
```

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

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

*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	<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

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>
-------------------	--

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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