# Package ‘epivizrChart’

April 11, 2018

**Title** R interface to epiviz web components

**Version** 1.0.0

**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

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

**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'

**VignetteBuilder** knitr

**Depends** R (>= 3.4.0)

**License** Artistic-2.0

**Encoding** UTF-8

**LazyData** true

**biocViews** Visualization, GUI

**RoxygenNote** 6.0.1

**NeedsCompilation** no

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## R topics documented:

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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

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## `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", "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 `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 measurment 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_provder_url(url)` | Set provider url |
| `set_provider_id(id)` | Set provider id |
| `set_provider_type(type)` | Set provider type |

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## `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) todo |
| `...` | 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

`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 |

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## `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` *Initialize an `EpivizNavigation` object to visualize in viewer or knit to HTML.*

---

### 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 intialize 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` *JSON parser used by this package*

---

### 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` *JSON writer used by this package*

---

### 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` *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

---

## `tcga_colon_blocks` *Example methylation data (blocks) for epivizr vignette.*

### 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` *Example methylation data (smoothed methylation levels) for epivizr vignette*

## 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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