Package ‘epivizrData’

April 25, 2017

Type Package

Title Data Management API for epiviz interactive visualization app

Version 1.4.0

URL http://epiviz.github.io

Description Serve data from Bioconductor Objects through a WebSocket connection.

BugReports https://github.com/epiviz/epivizrData/issues

biocViews Infrastructure, Visualization

Depends R (>= 3.4), methods, epivizrServer (>= 1.1.1), Biobase

Imports S4Vectors, GenomicRanges, SummarizedExperiment (>= 0.2.0), OrganismDbi, GenomicFeatures, GenomeInfoDb, IRanges, ensembldb

Suggests testthat, roxygen2, bumphunter, hgu133plus2.db, Mus.musculus, TxDb.Mmuscullus.UCSC.mm10.knownGene, rjson, knitr, rmarkdown, BiocStyle, EnsDb.Mmusculus.v79

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LazyData true

RoxygenNote 6.0.1


VignetteBuilder knitr

NeedsCompilation no

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R topics documented:

as.list.EpivizMeasurement-method ........................................... 2
createMgr ................................................................. 2
EpivizBlockData-class ......................................................... 3
createMgr

Create a data manager for epiviz app

createMgr(server = server)

Arguments

server An object of class EpivizServer

Value

An object of class EpivizDataMgr

as.list,EpivizMeasurement-method

Convert EpivizMeasurement object to list

Description

Convert EpivizMeasurement object to list

Usage

## S4 method for signature 'EpivizMeasurement'

as.list(x)

Arguments

x EpivizMeasurement object to coerce.

Value

a list describing measurement object
`EpivizBlockData-class`  

Data container for interval data.

**Description**

Used to serve data for visualizations of genomic regions only. Wraps `GenomicRanges` objects.

**Methods**

- `get_default_chart_type()` Get name of default chart type for this data type
- `get_measurements()` Get description of measurements served by this object

**See Also**

`EpivizData`

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`EpivizBpData-class`  

Container for basepair level numeric data

**Description**

Used to serve data to genomic line tracks. Wraps `GenomicRanges` objects. Numeric values obtained from `mcols` slot.

**Methods**

- `get_default_chart_type()` Get name of default chart type for this data type
- `get_measurements()` Get description of measurements served by this object

**See Also**

`EpivizData`
EpivizData-class  

**Data container for epiviz data server**

**Description**

Data container for epiviz data server

**Methods**

- `get_default_chart_type()` Get name of default chart type for this data type
- `get_id()` Get id provided by manager EpivizDataMgr-class
- `get_measurements()` Get description of measurements served by this object
- `get_name()` Get datasource name, usually set by manager EpivizDataMgr-class
- `get_rows(query, metadata, useOffset = FALSE)` Get genomic interval information overlapping query <GenomicRanges> region
- `get_source_name()` Get original datasource name provided by manager EpivizDataMgr-class
- `get_values(query, measurement, round = TRUE)` Get measurement values for features overlapping query region <GenomicRanges>
- `parse_measurement(ms_id = NULL)` Parse a measurement description for data served by this object
- `set_id(id)` Set id, used by manager EpivizDataMgr-class
- `set_limits(ylim)` Set plotting limits for continuous data
- `set_mgr(mgr)` Set data manager, EpivizDataMgr-class
- `set_name(name)` Set datasource name, usually set by manager EpivizDataMgr-class
- `set_source_name(source_name)` Set original datasource name, used by manager EpivizDataMgr-class
- `update(new_object, send_request = TRUE)` Update underlying data object with new object

EpivizDataMgr-class  

**Class providing data manager for epiviz app**

**Description**

Class providing data manager for epiviz app

**Methods**

- `add_measurements(obj, datasource_name = NULL, datasource_origin_name = deparse(substitute(obj)), send_request = TRUE)` register measurements in data manager
- `is_ms_connected(ms_obj_or_id)` check if measurement object was properly added to JS app
- `is_server_closed()` Check if underlying server is closed, logical>
- `list_measurements()` make a printable list of registered measurements
- `rm_all_measurements()` remove all registered measurements
- `rm_measurements(ms_obj_or_id)` remove registered measurements from a given data object
- `update_measurements(ms_obj_or_id, new_object, send_request = TRUE)` update the underlying data object for a registered measurement (given by object or id)
EpivizFeatureData-class

Data container for RangedSummarizedExperiment objects

Description

Used to serve general data (used in e.g., scatter plots and heatmaps). Wraps RangedSummarizedExperiment objects. Numeric values obtained from assays slot.

Methods

get_default_chart_type() Get name of default chart type for this data type
get_measurements() Get description of measurements served by this object

See Also

EpivizData

EpivizGeneInfoData-class

Container for gene annotation data

Description

Used to serve data to gene annotation tracks. Wraps GenomicRanges objects. Annotation obtained from columns Gene (gene symbols) and Exons (exon start and end locations).

Methods

get_default_chart_type() Get name of default chart type for this data type
get_measurements() Get description of measurements served by this object
get_rows(query, metadata, useOffset = FALSE) Get genomic interval information overlapping query <GenomicRanges> region

See Also

EpivizData
register,OrganismDb

EpivizMeasurement-class

Class encapsulating a measurement description for epiviz app.

Description

Class encapsulating a measurement description for epiviz app.
**register**

**Description**

Generic method to register data to the data server

**Usage**

```r
register(object, columns = NULL, ...

## S4 method for signature 'GenomicRanges'
register(object, columns, type = c("block", "bp", "gene_info"), ...)

## S4 method for signature 'RangedSummarizedExperiment'
register(object, columns = NULL,
          assay = 1, metadata = NULL)

## S4 method for signature 'ExpressionSet'
register(object, columns, annotation = NULL,
          assay = "exprs")

## S4 method for signature 'OrganismDb'
register(object, kind = c("gene", "tx"),
          keepSeqlevels = NULL, ...)

## S4 method for signature 'TxDb'
register(object, kind = c("gene", "tx"),
          keepSeqlevels = NULL, ...)

## S4 method for signature 'EnsDb'
register(object, kind = c("gene", "tx"),
          keepSeqlevels = NULL, ...)
```

**Arguments**

- `object` The object to register to data server
- `columns` Name of columns containing data to register
- `...` Additional arguments passed to object constructors
show,EpivizMeasurement-method

Display measurement datasourceId and id

Description

Display measurement datasourceId and id
show, EpivizMeasurement-method

Usage

```r
## S4 method for signature 'EpivizMeasurement'
show(object)
```

Arguments

- **object**: an `EpivizMeasurement` to display

Value

A string describing measurement
Index

as.list,EpivizMeasurement-method, 2
createMgr, 2
EnsDb, 7
EpivizBlockData
  (EpivizBlockData-class), 3
  EpivizBlockData-class, 3
EpivizBpData (EpivizBpData-class), 3
  EpivizBpData-class, 3
EpivizData, 7
  EpivizData-EpivizData-class), 4
  EpivizData-class, 4
EpivizDataMgr, 2
  EpivizDataMgr-EpivizDataMgr-class), 4
  EpivizDataMgr-class, 4
EpivizFeatureData
  (EpivizFeatureData-class), 5
EpivizFeatureData-class, 5
EpivizGeneInfoData
  (EpivizGeneInfoData-class), 5
  EpivizGeneInfoData-class, 5
EpivizMeasurement, 2, 8
  EpivizMeasurement-class, 5
epivizrData, 6
epivizrData-package (epivizrData), 6
EpivizServer, 2
ExpressionSet, 7
GenomicRanges, 3–5, 7
OrganismDb, 7
RangedSummarizedExperiment, 5, 7
  register, 6
  register,EnsDb-method (register), 6
  register,ExpressionSet-method (register), 6
  register,GenomicRanges-method (register), 6
  register,OrganismDb-method (register), 6
  register,RangedSummarizedExperiment-method (register), 6

register,TxDB-method (register), 6
show,EpivizMeasurement-method, 7
TxDb, 7