Package ‘epivizrData’

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Type Package
Title Data Management API for epiviz interactive visualization app
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Description Serve data from Bioconductor Objects through a WebSocket connection.

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BiocStyle
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  'EpivizDataMgr-class.R' 'createMgr.R' 'EpivizData-class.R'
  'EpivizTrackData-class.R' 'EpivizBlockData-class.R'
  'EpivizBpData-class.R' 'EpivizGeneInfoData-class.R'
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Author Hector Corrada Bravo [aut, cre], Florin Chelaru [aut]
Maintainer Hector Corrada Bravo <hcorrada@gmail.com>

R topics documented:

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as.list, EpivizMeasurement-method

Convert EpivizMeasurement object to list

Description
Convert EpivizMeasurement object to list

Usage
```r
## S4 method for signature 'EpivizMeasurement'
as.list(x)
```

Arguments
- `x` EpivizMeasurement object to coerce.

Value
- a list describing measurement object

createMgr

Create a data manager for epiviz app

Description
Create a data manager for epiviz app

Usage
```r
createMgr(server = server)
```

Arguments
- `server` An object of class `EpivizServer`

Value
- An object of class `EpivizDataMgr`
**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

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```r
server <- epivizrServer::createServer(port=7123L)
data_mgr <- epivizrData::createMgr(server)
```
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_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
- `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, 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.
epivizrData  epivizrData

Description

epivizrData

register  Generic method to register data to the data server

Description

Generic method to register data to the data server

Usage

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, ...)

Arguments

object  The object to register to data server
columns  Name of columns containing data to register
...  Additional arguments passed to object constructors
type  Which type of data object to register for a GenomicRanges object. block: only region data, bp base-pair resolution quantitative data (see columns argument), geneInfo information about gene location.
assay  Which assay in object to register
metadata  Additional metadata about features
annotation  Character string indicating platform annotation (only hgu133plus2 supported for now)
kind  Make gene or transcript annotation (only gene supported for now)
keepSeqlevels  character vector indicating seqlevels in object to keep

Value
Object inheriting from `EpivizData` class

Methods (by class)
- GenomicRanges: Register a `GenomicRanges` object
- RangedSummarizedExperiment: Register a `RangedSummarizedExperiment` object
- ExpressionSet: Register an `ExpressionSet` object
- OrganismDb: Register an `OrganismDb` object
- TxDb: Register a `TxDb` object

Examples
```r
library(GenomicRanges)
# create an example GRanges object
gr <- GRanges("chr10", IRanges(start=1:1000, width=100), score=rnorm(1000))
# this returns an EpivizData object without adding to data manager
# this is not the preferred way of creating these object, but is shown
# here for completeness.
ms_obj <- epivizrData:::register(gr, type="bp", columns="score")

server <- epivizrServer::createServer(port=7123L)
data_mgr <- epivizrData::createMgr(server)

# This adds a data object to the data manager
data_mgr$add_measurements(gr, "example_gr", type="bp", columns="score")
```

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**show,EpivizMeasurement-method**

*Display measurement datasourceId and id*

**Description**
Display measurement datasourceId and id

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

**Arguments**
- `object`  a `EpivizMeasurement` to display
Value

A string describing measurement
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