Package ‘epivizrData’

January 21, 2017

Type Package

Title Data Management API for epiviz interactive visualization app

Version 1.2.0

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 (>= 3.3), methods, epivizrServer (>= 1.1.1), Biobase

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

Suggests testthat, roxygen2, bumphunter, hgu133plus2.db, Mus.musculus, TxDb.Mmuseus.ucsc.mm10.knownGene, rjson, knitr, rmarkdown, BiocStyle

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LazyData true

RoxygenNote 5.0.1


VignetteBuilder knitr

NeedsCompilation no

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createMgr

createMgr

Create a data manager for epiviz app

Description
Create a data manager for epiviz app

Usage
createMgr(server = server)

Arguments
server

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

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

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_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.
**Description**

epivizrData

**register**

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
show,EpivizMeasurement-method

**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("chr1", 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")
```

**Description**
Display measurement datasourceId and id

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

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

A string describing measurement
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