Package ‘epivizrData’

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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.Mmusculus.UCSC.mm10.knownGene, rjson, knitr, rmarkdown, BiocStyle

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LazyData true

RoxygenNote 5.0.1

Collate 'epivizrData-package.R' 'EpivizMeasurement-class.R'
'EpivizDataMgr-class.R' 'createMgr.R' 'EpivizData-class.R'
'EpivizTrackData-class.R' 'EpivizBlockData-class.R'
'EpivizBpData-class.R' 'EpivizGeneInfoData-class.R'
'EpivizFeatureData-class.R' 'make_gene_info_gr.R'
'register-methods.R'

VignetteBuilder knitr

NeedsCompilation no

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createMgr

Description
Create a data manager for epiviz app

Usage
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

Examples

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

**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

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

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.
register

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("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")
```

show,EpivizMeasurement-method

Display measurement datasourceId and id

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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