Package ‘epivizrData’

January 14, 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.MmuscusLCSC.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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R topics documented:

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as.list,EpivizMeasurement-method

ConvertEpivizMeasurementobjecttolist

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

createMgr

Create a data manager for epiviz app

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
EpivizBlockData-class

Examples

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

---

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_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

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, ...)
```

### Arguments

- **object**
  - The object to register to the 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

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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