

Package ‘epivizrData’

December 11, 2018

Type Package

Title Data Management API for epiviz interactive visualization app

Version 1.10.0

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.Mmusculus.UCSC.mm10.knownGene, rjson, knitr, rmarkdown, BiocStyle, EnsDb.Mmusculus.v79, AnnotationHub, rtracklayer, utils, RMySQL, DBI

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LazyData true

RoxygenNote 6.1.0

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' 'utils.R'

VignetteBuilder knitr

NeedsCompilation no

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git_url <https://git.bioconductor.org/packages/epivizrData>

git_branch RELEASE_3_8

git_last_commit 1d39e16

git_last_commit_date 2018-10-30

Date/Publication 2018-12-10

R topics documented:

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| ahToMySQL | <i>Utility function to import data to a MySQL database from Annotation Hub</i> |
|-----------|--|

Description

Utility function to import data to a MySQL database from Annotation Hub

Usage

```
ahToMySQL(ah, annotations = list(), ...)
```

Arguments

| | |
|-------------|---|
| ah | AnnotationHub object with records to add to database. |
| annotations | A named list of lists (key/value pairs). Keys must be the AH ID for the corresponding record and the value is a named list representing an annotation. An annotation is automatically inferred by the record's metadata. Any annotation that is passed for a particular record is concatenated to its inferred annotation. If the annotation has a subtype column, it is used to name the data object being added to the db, otherwise the record's tags is used. |
| ... | arguments for toMySQL (connection, db_name, batch, index) |

Examples

```
## Not run:
library(epivizrData)
library(AnnotationHub)
library(DBI)
library(RMySQL)

ah <- AnnotationHub()
db_annotations <- list()
```

```

# Query Patterns
roadmap <- "EpigenomeRoadMap"
bisulphite <- "bisulphite"

esophagus <- query(ah, c("esophagus", "roadmap", "bisulphite"))
eso_anno <- list(tissue="Digestive", subtype="Esophagus")
eso_id <- names(esophagus)
db_annotations[[eso_id]] <- eso_anno

connection <- dbConnect(MySQL(), host=host, user=user, password=pass)
db_name="my_database"

ahToMySQL(ah=record, annotations=db_annotations,
          connection=connection, db_name=db_name)

## End(Not run)

```

as.data.frame,EpivizData-method

Generic as.data.frame method for EpivizData objects

Description

Generic as.data.frame method for EpivizData objects

Usage

```

## S4 method for signature 'EpivizData'
as.data.frame(x, query = NULL, ...)

```

Arguments

| | |
|-------|--|
| x | EpivizData object to coerce. |
| query | GRanges object |
| ... | other param to send to data.frame |

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

| | |
|-----------|---|
| createMgr | <i>Create a data manager for epiviz app</i> |
|-----------|---|

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](#)

Examples

```
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](#)

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](#)

`toMySQL(connection, db_name, annotation = NULL, batch = 50, index = TRUE)` Send Epiviz-Data to a MySQL Database

connection DBIConnection to a database

db_name Name of MySQL database

annotation Annotation for index table

batch Batch size for data sent to the MySQL database

index Insert into respective index table

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)),
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 un-
derlying 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 | <i>Generic method to register data to the data server</i> |
|----------|---|

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, ...)

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

## S4 method for signature 'data.frame'
register(object, columns = 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
- EnsDb: Register an [EnsDb](#) object
- data.frame: Register an [data.frame](#)

Examples

```
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

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show,EpivizMeasurement-method

Value

A string describing measurement

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