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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    TxDb.Mus musculus.UCSC.mm10.knownGene, rjson, knitr, rmarkdown,
    BiocStyle, EnsemblDb.Mus musculus.v79, AnnotationHub, rtracklayer,
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    'createMgr.R' 'EpivizData-class.R' 'EpivizTrackData-class.R'
    'EpivizBlockData-class.R' 'EpivizBpData-class.R'
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git_branch RELEASE_3_18
Description

Create empty Epiviz Measurement

Usage

`.emptyEpivizMeasurement()`
Create empty Epiviz Measurement

Usage

.emptyEpivizSparseMeasurement()

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

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)

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### as.data.frame,EpivizData-method

Generic as.data.frame method for EpivizData objects

**Description**

Generic as.data.frame method for EpivizData objects

**Usage**

```r
## 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

description

Convert SparseEpivizMeasurement object to list

Usage

## S4 method for signature 'SparseEpivizMeasurement'
as.list(x)

Arguments

x SparseEpivizMeasurement object to coerce.

Value

a list describing measurement object

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)), 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

Description

Infrastructure package for the epivizr interactive visualization system in Bioconductor. It provides connections between Bioconductor infrastructure objects and the epivizr visualization framework.
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, ...)

## 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

```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 `datasourcId` and `id`

Usage

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

Arguments

- `object` a `EpivizMeasurement` to display
Value

A string describing measurement

show,SparseEpivizMeasurement-method

Display measurement datasourceId and id

Description

Display measurement datasourceId and id

Usage

```r
## S4 method for signature 'SparseEpivizMeasurement'
show(object)
```

Arguments

- `object`: a `SparseEpivizMeasurement` to display

Value

A string describing measurement

SparseEpivizMeasurement-class

Class encapsulating a measurement description for epiviz app.

Description

Class encapsulating a measurement description for epiviz app.
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