Package ‘epivizrData’

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Type  Package
Title  Data Management API for epiviz interactive visualization app
Version  1.30.0
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.Musculus.v79, AnnotationHub, rtracklayer,
  utils, RMySQL, DBI, matrixStats
License  MIT + file LICENSE
LazyData  true
RoxygenNote  7.1.1
Collate  'epivizrData-package.R' 'SparseEpivizMeasurement-class.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_branch  RELEASE_3_18
.emptyEpivizMeasurement

Create empty Epiviz Measurement

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

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(epivizData)
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

## 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
as.list, SparseEpivizMeasurement-method

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

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

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
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 EpivizData 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.
**register**

Generic method to register data to the data server

**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, ...)
```  
## 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
show,EpivizMeasurement-method

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("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

```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
## 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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