Package ‘epivizrData’

May 3, 2024

Type Package
Title Data Management API for epiviz interactive visualization app
Version 1.32.0
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, EnsemblDb.Mmusculus.v79, AnnotationHub, rtracklayer,
utils, RMySQL, DBI, matrixStats
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RoxygenNote 7.1.1
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'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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.emptyEpivizMeasurement

Create empty Epiviz Measurement

Description

Create empty Epiviz Measurement

Usage

.epivyEpivizMeasurement()
emptyEpivizSparseMeasurement

Create empty Epiviz Measurement

Description
Create empty Epiviz Measurement

Usage
emptyEpivizSparseMeasurement()

ahToMySQL
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

```r
roadmap <- "EpigenomeRoadMap"
bisulphite <- "bisulphite"
```

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

```r
collection <- dbConnect(MySQL(), host=host, user=user, password=pass)
db_name="my_database"
```

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

```r
## 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**

```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
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 \texttt{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
**EpivizFeatureData-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  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

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

## S4 method for signature 'GenomicRanges'

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.

## S4 method for signature 'RangedSummarizedExperiment'

assay  Which assay in object to register

## S4 method for signature 'ExpressionSet'

metadata  Additional metadata about features

## S4 method for signature 'OrganismDb'

annotation  Character string indicating platform annotation (only hgu133plus2 supported for now)

## S4 method for signature 'TxDb'

kind  Make gene or transcript annotation (only gene supported for now)

## S4 method for signature 'EnsDb'

keepSeqlevels  character vector indicating seqlevels in object to keep

## S4 method for signature 'ExpressionSet'
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 datasourcId and id

Description

Display measurement datasourcId and id

Usage

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

Arguments

- object: an 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.
Index

.edgeEpivizMeasurement, 2
.edgeEpivizSparseMeasurement, 3

ahToMySQL, 3
as.data.frame,EpivizData-method, 4
as.list,EpivizMeasurement-method, 4
as.list,SparseEpivizMeasurement-method, 5

createMgr, 5
data.frame, 11

EnsDb, 11
EpivizBlockData
  (EpivizBlockData-class), 6
EpivizBlockData-class, 6
EpivizBpData (EpivizBpData-class), 6
EpivizBpData-class, 6
EpivizData, 4, 11
EpivizData (EpivizData-class), 7
EpivizData-class, 7
EpivizDataMgr, 6
EpivizDataMgr (EpivizDataMgr-class), 8
EpivizDataMgr-class, 8
EpivizFeatureData
  (EpivizFeatureData-class), 8
EpivizFeatureData-class, 8
EpivizGeneInfoData
  (EpivizGeneInfoData-class), 9
EpivizGeneInfoData-class, 9
EpivizMeasurement, 4, 5, 11
EpivizMeasurement
  (EpivizMeasurement-class), 9
EpivizMeasurement-class, 9
epivizrData, 9
EpivizServer, 6
ExpressionSet, 11

GenomicRanges, 6, 7, 9–11

OrganismDb, 11
RangedSummarizedExperiment, 8, 11
register, 10
register, data.frame-method (register), 10
register, EnsDb-method (register), 10
register, ExpressionSet-method (register), 10
register, GenomicRanges-method (register), 10
register, OrganismDb-method (register), 10
register, RangedSummarizedExperiment-method (register), 10
register, TxDb-method (register), 10
show, EpivizMeasurement-method, 11
show, SparseEpivizMeasurement-method, 12
SparseEpivizMeasurement, 5, 12
SparseEpivizMeasurement
  (SparseEpivizMeasurement-class), 12
SparseEpivizMeasurement-class, 12
TxDb, 11