Package ‘epivizrData’

January 25, 2024

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.Mmuseusculus.ucsc.mm10.knownGene, rjson, knitr, rmarkdown,

BiocStyle, EnDb.Mmuseusculus.v79, AnnotationHub, rtracklayer,

utils, RMySQL, DBI, matrixStats

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LazyData true

RoxygenNote 7.1.1

Collate 'epivizrData-package.R' 'SparseEpivizMeasurement-class.R'

'EpivizMeasurement-class.R' 'EpivizrDataMgr-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

**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**

```r
## 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**

```r
## 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**

```r
## 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**

```r
createMgr(server = server)
```
EpivizBpData-class

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 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

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**EpivizMeasurement-class**

*Class encapsulating a measurement description for epiviz app.*

**Description**

Class encapsulating a measurement description for epiviz app.

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**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 = NULL, 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("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 datasourceId and id

Usage

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

Arguments

- object: a EpivizMeasurement to display
SparseEpivizMeasurement-class

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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