Package 'epivizrData'

April 23, 2024

Type Package

Title Data Management API for epiviz interactive visualization app

Version 1.31.0

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, matrixStats

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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_url https://git.bioconductor.org/packages/epivizrData

git_branch devel

git_last_commit d7e37a3

git_last_commit_date 2023-10-24

Repository Bioconductor 3.19

Date/Publication 2024-04-23

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`.emptyEpivizMeasurement`

Create empty Epiviz Measurement

Description

Create empty Epiviz Measurement

Usage

```
.emptyEpivizMeasurement()
```

.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
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

---

as.list,SparseEpivizMeasurement-method *Convert* SparseEpivizMeasurement *object to* list

---

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

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_` 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 measurments 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
...	Additonal 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

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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