

# Package ‘epivizrData’

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**Type** Package

**Title** Data Management API for epiviz interactive visualization app

**Version** 1.35.0

**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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---

.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     | <a href="#">EpivizData</a> 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 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\_ 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   |
| type          | Which type of data object to register for a <a href="#">GenomicRanges</a> 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 <- epivizData::register(gr, type="bp", columns="score")

server <- epivizServer::createServer(port=7123L)
data_mgr <- epivizData::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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