

# Package ‘epivizrData’

April 24, 2025

**Type** Package

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

**Version** 1.37.0

**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                |
| <i>Create empty Epiviz Measurement</i> |

---

Description

Create empty Epiviz Measurement

Usage

.emptyEpivizMeasurement()

---

|                                        |
|----------------------------------------|
| .emptyEpivizSparseMeasurement          |
| <i>Create empty Epiviz Measurement</i> |

---

Description

Create empty Epiviz Measurement

Usage

.emptyEpivizSparseMeasurement()

---

|           |                                                                                |
|-----------|--------------------------------------------------------------------------------|
| ahToMySQL | <i>Utility function to import data to a MySQL database from Annotation Hub</i> |
|-----------|--------------------------------------------------------------------------------|

---

## 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 | <a href="#">EpivizMeasurement</a> 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_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 | <i>epivizrData</i> |
|-------------|--------------------|

---

### Description

Infrastructure package for the epivizr interactive visualization system in Bioconductor. It provides connections between Bioconductor infrastructure objects and the epivizr visualization framework.

---

|          |                                                           |
|----------|-----------------------------------------------------------|
| register | <i>Generic method to register data to the data server</i> |
|----------|-----------------------------------------------------------|

---

### 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 <- epivizrServer::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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