

# Package ‘epivizrData’

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**Type** Package

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

**Version** 1.4.0

**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

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**LazyData** true

**RoxygenNote** 6.0.1

**Collate** 'epivizrData-package.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'

**VignetteBuilder** knitr

**NeedsCompilation** no

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## R topics documented:

as.list,EpivizMeasurement-method . . . . .	2
createMgr . . . . .	2
EpivizBlockData-class . . . . .	3

EpivizBpData-class . . . . .	3
EpivizData-class . . . . .	4
EpivizDataMgr-class . . . . .	4
EpivizFeatureData-class . . . . .	5
EpivizGeneInfoData-class . . . . .	5
EpivizMeasurement-class . . . . .	5
epivizrData . . . . .	6
register . . . . .	6
show,EpivizMeasurement-method . . . . .	7

<b>Index</b>	<b>9</b>
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as.list,EpivizMeasurement-method  
*Convert [EpivizMeasurement](#) object to list*

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### 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

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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](#)

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EpivizBpData-class *Container for basepair level numeric data*

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**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](#)

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EpivizData-class      *Data container for epiviz data server*

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### 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](#)  
 update(new\_object, send\_request = TRUE) Update underlying data object with new object

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EpivizDataMgr-class      *Class providing data manager for epiviz app*

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### Description

Class providing data manager for epiviz app

### Methods

add\_measurements(obj, datasource\_name = NULL, datasource\_origin\_name = deparse(substitute(obj)), 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](#)

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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.*

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### Description

Class encapsulating a measurement description for epiviz app.

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 epivizrData
 

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*epivizrData*


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### Description

 epivizrData
 

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 register
 

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*Generic method to register data to the data server*


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### 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, ...)

```

### 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

### 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")
```

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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



# Index

as.list,EpivizMeasurement-method, 2  
createMgr, 2  
EnsDb, 7  
EpivizBlockData  
    (EpivizBlockData-class), 3  
EpivizBlockData-class, 3  
EpivizBpData (EpivizBpData-class), 3  
EpivizBpData-class, 3  
EpivizData, 7  
EpivizData (EpivizData-class), 4  
EpivizData-class, 4  
EpivizDataMgr, 2  
EpivizDataMgr (EpivizDataMgr-class), 4  
EpivizDataMgr-class, 4  
EpivizFeatureData  
    (EpivizFeatureData-class), 5  
EpivizFeatureData-class, 5  
EpivizGeneInfoData  
    (EpivizGeneInfoData-class), 5  
EpivizGeneInfoData-class, 5  
EpivizMeasurement, 2, 8  
EpivizMeasurement  
    (EpivizMeasurement-class), 5  
EpivizMeasurement-class, 5  
epivizrData, 6  
epivizrData-package (epivizrData), 6  
EpivizServer, 2  
ExpressionSet, 7  
  
GenomicRanges, 3–5, 7  
  
OrganismDb, 7  
  
RangedSummarizedExperiment, 5, 7  
register, 6  
register, EnsDb-method (register), 6  
register, ExpressionSet-method  
    (register), 6  
register, GenomicRanges-method  
    (register), 6  
register, OrganismDb-method (register), 6  
register, RangedSummarizedExperiment-method  
    (register), 6  
  
register, TxDb-method (register), 6  
show, EpivizMeasurement-method, 7  
  
TxDb, 7