

# Package ‘brgedata’

October 12, 2020

**Title** Exposures, Gene Expression and Methylation data for illustration purposes

**Version** 1.10.0

**Description** This package contains several sets of omics data including Gene Expression (ExpressionSet), Methylation (GenomicRatioSet), Proteome and Exposome (ExposomeSet). This data is used in vignettes and examples at MEAL, MultiDataSet and omicRexposome.

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.0.1

**VignetteBuilder** knitr

**Depends** R (>= 3.4), Biobase

**Imports** SummarizedExperiment

**Suggests** minfi, MultiAssayExperiment, knitr, rexposome

**biocViews** ExperimentData,Homo\_sapiens\_Data,MicroarrayData,MethylationArrayData

**git\_url** <https://git.bioconductor.org/packages/brgedata>

**git\_branch** RELEASE\_3\_11

**git\_last\_commit** 6988272

**git\_last\_commit\_date** 2020-04-27

**Date/Publication** 2020-10-12

**Author** Carlos Ruiz-Arenas [aut, cre],  
Carles Hernandez-Ferrer [aut],  
Juan R. Gonzalez [aut]

**Maintainer** Carlos Ruiz-Arenas <carlos.ruiz@isglobal.org>

## R topics documented:

brgedata . . . . .	2
brge_expo . . . . .	2
brge_gexp . . . . .	2
brge_methy . . . . .	3
brge_prot . . . . .	3

<b>Index</b>	<b>4</b>
--------------	----------

---

brgedata	<i>brgedata</i>
----------	-----------------

---

**Description**

brgedata

---

brge_expo	<i>ExposomeSet for testing purposes</i>
-----------	---

---

**Description**

ExposomeSet with full set of 15 exposures grouped in 3 families for 110 individuals.

**Usage**

```
data("brge_expo")
```

**Format**

An object of class `ExposomeSet` of dimension 15 x 110 x 6.

**Value**

An `ExposomeSet` object.

---

brge_gexp	<i>ExpressionSet for testing purposes</i>
-----------	---

---

**Description**

ExpressionSet with full set of 67528 features from Affymetrix HTA 2.0 for 100 simulated samples.

**Usage**

```
data("brge_gexp")
```

**Format**

An object of class `ExpressionSet` with 67528 rows and 100 columns.

**Value**

An `ExpressionSet` object.

**Examples**

```
data("brge_gexp")
dim(brge_gexp)
sampleNames(brge_gexp)
```

---

brge_methy	GenomicRatioSet <i>for testing purposes</i>
------------	---

---

**Description**

GenomicRatioSet with 476946 features from Illumina 450k methylation array and 115 simulated samples.

**Usage**

```
data("brge_methy")
```

**Format**

An object of class GenomicRatioSet with 476946 rows and 20 columns.

**Value**

An GenomicRatioSet object.

**Examples**

```
data("brge_methy")
dim(brge_methy)
sampleNames(brge_methy)
```

---

brge_prot	ExpressionSet <i>for testing purposes</i>
-----------	---

---

**Description**

ExpressionSet with full set of 47 proteines for 90 simulated samples.

**Usage**

```
data("brge_prot")
```

**Format**

An object of class ExpressionSet with 47 rows and 90 columns.

**Value**

An ExpressionSet object.

**Examples**

```
data("brge_prot")
dim(brge_prot)
sampleNames(brge_prot)
```

# Index

## \* datasets

- brge\_expo, [2](#)
- brge\_gexp, [2](#)
- brge\_methy, [3](#)
- brge\_prot, [3](#)

- brge\_expo, [2](#)
- brge\_gexp, [2](#)
- brge\_methy, [3](#)
- brge\_prot, [3](#)
- brgedata, [2](#)
- brgedata-package (brgedata), [2](#)