Package ‘brgedata’

May 14, 2024

Title Exposures, Gene Expression and Methylation data for illustration purposes

Version 1.26.0

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, rmarkdown, rexposome, BiocStyle

biocViews ExperimentData,Homo_sapiens_Data,MicroarrayData,MethylationArrayData

git_url https://git.bioconductor.org/packages/brgedata

git_branch RELEASE_3_19

git_last_commit 5ccd51d

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-05-14

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

Maintainer Dolors Pelegri-Siso <dolors.pelegri@isglobal.org>
Contents

<table>
<thead>
<tr>
<th>Name</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>brgedata</td>
<td>2</td>
</tr>
<tr>
<td>brge_expo</td>
<td>2</td>
</tr>
<tr>
<td>brge_gexp</td>
<td>3</td>
</tr>
<tr>
<td>brge_methy</td>
<td>3</td>
</tr>
<tr>
<td>brge_prot</td>
<td>4</td>
</tr>
</tbody>
</table>

Index

<table>
<thead>
<tr>
<th>Name</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>brgedata</td>
<td></td>
</tr>
</tbody>
</table>

Description

**brgedata**

ExposomeSet for testing purposes

Usage

data("brge_expo")

Format

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

Value

An ExposomeSet object.
**brge_gexp**

| brge_gexp | ExpressionSet for testing purposes |

**Description**

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

**Usage**

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

**Format**

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

**Value**

An ExpressionSet object.

**Examples**

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

---

**brge_methy**

| brge_methy | GenomicRatioSet for testing purposes |

**Description**

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

**Usage**

```r
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 for testing purposes

Description

ExpressionSet with full set of 47 proteins 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, 3
  brge_methy, 3
  brge_prot, 4

brge_expo, 2
brge_gexp, 3
brge_methy, 3
brge_prot, 4
brgedata, 2
brgedata-package (brgedata), 2