

Package ‘mCSEAdata’

October 24, 2025

Type Package

Title Data package for mCSEA package

Version 1.29.1

Author Jordi Martorell Marugán

Maintainer Jordi Martorell Marugán <jmartorellm@gmail.com>

Description Data objects necessary to some mCSEA package functions.

There are also example data objects to illustrate mCSEA package functionality.

Depends R (>= 3.5)

Imports GenomicRanges

Suggests BiocStyle, knitr, rmarkdown

VignetteBuilder knitr

biocViews Homo_sapiens_Data, MethylationArrayData, MicroarrayData,
ExperimentData

License GPL-2

Encoding UTF-8

LazyData true

LazyDataCompression xz

git_url <https://git.bioconductor.org/packages/mCSEAdata>

git_branch devel

git_last_commit e7fd1eb

git_last_commit_date 2025-10-22

Repository Bioconductor 3.23

Date/Publication 2025-10-24

Contents

mCSEAdata-package	2
bandTable	2
mcseadata	3

Index	4
--------------	----------

`mCSEAdata-package`*Data and examples for mCSEA package*

Description

Association files between Illumina's 450K, EPIC and EPICv2 microarrays probes and promoters, CpG Islands and gene bodies. Annotation for the previous microarrays' probes. There are also sample data from EPIC platform and expression microarrays to test mCSEA functions and a necessary object for mCSEAPlot function.

Author(s)

Jordi Martorell Marugán Raúl López Domínguez

Maintainer: Jordi Martorell Marugán<jordi.martorell@genyo.es>

Examples

```
data(mcseadata)
data(bandTable)
```

`bandTable`*Human chromosomes information*

Description

bandTable contains chromosomes band information and centromer location from hg19 and hg38 genomes. It is used by mCSEAPlot() function to plot the chromosome track.

Usage

```
data(bandTable)
```

Format

```
data.frame
```

Source

Obtained with Gviz's IdeogramTrack() function.

`mcseadata`*Data and examples for mCSEA package*

Description

Association files between Illumina's 450K and EPIC microarrays probes and promoters, CpG Islands and gene bodies. There are also sample data from EPIC platform to test mCSEA functions and annotation for 450K and EPIC probes.

Usage

```
data(mcseadata)
```

Format

matrix (betaTest and exprTest), data.frame (phenoTest), list (assocPromoters450k, assocPromotersEPIC, assocPromotersEPICv2, assocGenes450k, assocGenesEPIC, assocGenesEPICv2, assocCGI450k, assocCGIEPIC) and assocCGIEPICv2; and GRanges (annot450K, annotEPIC and annotEPICv2)

Source

betaTest and phenoTest are simulated data. exprTest was obtained from leukemiasEset package. annot450K, annotEPIC and annotEPICv2 were constructed with minfi package. assocPromoters450k, assocPromotersEPIC, assocPromotersEPICv2, assocGenes450k, assocGenesEPIC, assocGenesEPICv2, assocCGI450k, assocCGIEPIC and assocCGIEPICv2 were constructed from IlluminaHumanMethylation450kanno.ilmn12.hg19, IlluminaHumanMethylationEPICanno.ilm10b2.hg19 and IlluminaHumanMethylationEPICv2anno.20a1.hg38 packages annotation data.

Index

* datasets

- bandTable, [2](#)
- mcseadata, [3](#)
- mCSEAdata-package, [2](#)

- annot450K (mcseadata), [3](#)
- annotEPIC (mcseadata), [3](#)
- annotEPICv2 (mcseadata), [3](#)
- assocCGI450k (mcseadata), [3](#)
- assocCGIEPIC (mcseadata), [3](#)
- assocCGIEPICv2 (mcseadata), [3](#)
- assocGenes450k (mcseadata), [3](#)
- assocGenesEPIC (mcseadata), [3](#)
- assocGenesEPICv2 (mcseadata), [3](#)
- assocPromoters450k (mcseadata), [3](#)
- assocPromotersEPIC (mcseadata), [3](#)
- assocPromotersEPICv2 (mcseadata), [3](#)

- bandTable, [2](#)
- betaTest (mcseadata), [3](#)

- exprTest (mcseadata), [3](#)

- mCSEAdata (mCSEAdata-package), [2](#)
- mcseadata, [3](#)
- mCSEAdata-package, [2](#)

- phenoTest (mcseadata), [3](#)