

Package ‘MEDIPSData’

December 4, 2025

Type Package
Title Example data for MEDIPS and QSEA packages
Version 1.46.0
Depends R (≥ 3.5)
Suggests MEDIPS, GenomicRanges, qsea
Date 2025-07-28
Author Lukas Chavez
Maintainer Lukas Chavez <lchavez@liai.org>
Description Example data for MEDIPS and QSEA packages,
consisting of chromosome 22 MeDIP and control/Input sample data.
Additionally, the package contains MeDIP seq data from 3 NSCLC samples
and adjacent normal tissue (chr 20-22).
All data has been aligned to human genome hg19.
License GPL (≥ 2)
LazyLoad yes
biocViews ExperimentData, Genome, SequencingData
git_url <https://git.bioconductor.org/packages/MEDIPSData>
git_branch RELEASE_3_22
git_last_commit 1d8e5ae
git_last_commit_date 2025-10-29
Repository Bioconductor 3.22
Date/Publication 2025-12-04

Contents

annotation	2
CS	2
DE_Input	3
DE_MeDIP	3
hESCs_Input	4
hESCs_MeDIP	4
mart_gene	5
NSCLC_dataset	5
resultTable	6
samplesNSCLC	6
tcga_luad_lusc_450kmeth	7

Index**8**

annotation	<i>QSEA example annotation</i>
------------	--------------------------------

Description

This is a list of GRange objects, which contain genomic annotations for hg19 reference, obtained from UCSC table browser.

Usage

```
data(annotation)
```

Examples

```
## Not run:
data(annotation)
library(GenomicRanges)
names(ROIs)
ROIs$'gene body'
names(tfbs)

## End(Not run)
```

CS	<i>COUPLING SET</i>
----	---------------------

Description

This is a CpG coupling set generated by the MEDIPS package based on the human chromosome 22 (hg19) and with a window size of 100bp.

Usage

```
data(CS)
```

Examples

```
## Not run:
data(CS)
library(MEDIPS)
CS

## End(Not run)
```

DE_Input

control data set from definitive endoderm

Description

This is a MEDIPS SET object created from Input-seq control data derived from definitive endoderm as presented by Chavez et al. 2010. The parameter settings are: BSgenome= "BSgenome.Hsapiens.UCSC.hg19" extend= 300 shift= 0 uniq= T ws= 100 chr.select= "chr22"

Usage

```
data(DE_Input)
```

References

Chavez, L., Jozefczuk, J., Grimm, C., Dietrich, J., Timmermann, B., Herwig, R., Adjaye, J. (2010): Computational analysis of genome-wide DNA methylation during the differentiation of human embryonic stem cells along the endodermal lineage, Genome Research. 20(10):1441-50

Examples

```
## Not run:
data(DE_Input)
library(MEDIPS)
DE_Input

## End(Not run)
```

DE_MeDIP

Concatenated set of three MeDIP-seq data sets (replicates) from definitive endoderm

Description

This is a concatenated set of three MEDIPS SET objects created from MeDIP-seq data derived from definitive endoderm as presented by Chavez et al. 2010. The parameter settings are: BSgenome= "BSgenome.Hsapiens.UCSC.hg19" extend= 300 shift= 0 uniq= T ws= 100 chr.select= "chr22"

Usage

```
data(DE_MeDIP)
```

References

Chavez, L., Jozefczuk, J., Grimm, C., Dietrich, J., Timmermann, B., Herwig, R., Adjaye, J. (2010): Computational analysis of genome-wide DNA methylation during the differentiation of human embryonic stem cells along the endodermal lineage, Genome Research. 20(10):1441-50

Examples

```
## Not run:
data(DE_MeDIP)
library(MEDIPS)
DE_MeDIP

## End(Not run)
```

hESCs_Input

control data set from human embryonic stem cells

Description

This is a MEDIPS SET object created from Input-seq control data derived from human embryonic stem cells as presented by Chavez et al. 2010. The parameter settings are: BSgenome="BSgenome.Hsapiens.UCSC.hg19" extend= 300 shift= 0 uniq= T ws= 100 chr.select= "chr22"

Usage

```
data(hESCs_Input)
```

References

Chavez, L., Jozefczuk, J., Grimm, C., Dietrich, J., Timmermann, B., Herwig, R., Adjaye, J. (2010): Computational analysis of genome-wide DNA methylation during the differentiation of human embryonic stem cells along the endodermal lineage, Genome Research. 20(10):1441-50

Examples

```
## Not run:
data(hESCs_Input)
library(MEDIPS)
hESCs_Input

## End(Not run)
```

hESCs_MeDIP

Concatenated set of three MeDIP-seq data sets (replicates) from human embryonic stem cells

Description

This is a concatenated set of three MEDIPS SET objects created from MeDIP-seq data derived from human embryonic stem cells as presented by Chavez et al. 2010. The parameter settings are: BSgenome= "BSgenome.Hsapiens.UCSC.hg19" extend= 300 shift= 0 uniq= T ws= 100 chr.select= "chr22"

Usage

```
data(hESCs_MeDIP)
```

References

Chavez, L., Jozefczuk, J., Grimm, C., Dietrich, J., Timmermann, B., Herwig, R., Adjaye, J. (2010): Computational analysis of genome-wide DNA methylation during the differentiation of human embryonic stem cells along the endodermal lineage, *Genome Research*. 20(10):1441-50

Examples

```
## Not run:
data(hESCs_MeDIP)
library(MEDIPS)
hESCs_MeDIP

## End(Not run)
```

mart_gene	<i>An annotation object generated by accessing biomaRt using the MEDIPS.getAnnotation function of the MEDIPS package.</i>
-----------	---

Description

This is an annotation object generated by accessing biomaRt using the MEDIPS.getAnnotation function of the MEDIPS package: `mart_gene = MEDIPS.getAnnotation(mart="ensembl", dataset=c("hsapiens_gene_ensembl"), annotation=c("GENE"), chr=22)` The annotation object contains genomic coordinates of human genes on chromosome 22.

Usage

```
data(mart_gene)
```

Examples

```
## Not run:
data(mart_gene)
data(resultTable)
library(MEDIPS)
resultTable = MEDIPS.setAnnotation(regions=resultTable, annotation=mart_gene)

## End(Not run)
```

NSCLC_dataset	<i>QSEA MeDIP-seq lung cancer example dataset</i>
---------------	---

Description

This is a qsea set object 'qseaSet' and a qsa glm object 'qseaGLM' qseaSet contains MeDIP seq data from NSCLC samples and adjacent normal. qseaGLM contains test statistics for the comparison of tumor and normal samples.

Usage

```
data(annotation)
```

Examples

```
## Not run:
data(NSCLC_dataset)
library(qsea)
qseaSet
qseaGLM

## End(Not run)
```

resultTable	<i>A result table as returned by the MEDIPS.meth function of the MEDIPS package</i>
-------------	---

Description

This is a result table as returned by the MEDIPS.meth function using the following command:
 mr.edgeR = MEDIPS.meth(MSet1=hESCs, MSet2=DE, CSet=CS, ISet1=hESCs.Input, ISet2=DE.Input,
 p.adj="bonferroni", diff.method="edgeR", prob.method="poisson", CNV=F, MeDIP=T) where hESCs,
 DE, and CS are data objects included in this data package.

Usage

```
data(resultTable)
```

Examples

```
## Not run:
data(resultTable)
library(MEDIPS)
mr.edgeR.s = MEDIPS.selectSig(results=mr.edgeR, p.value=0.05, adj=T, ratio=NULL, bg.counts=NULL, CNV=F)
mr.edgeR.s

## End(Not run)
```

samplesNSCLC	<i>QSEA lung cancer MeDIP seq sample table</i>
--------------	--

Description

This data set contains a sample table describing the samples of the QSEA lung cancer MeDIP seq example data.

Usage

```
data(samplesNSCLC)
```

Examples

```
## Not run:
data(samplesNSCLC)
samplesNSCLC

## End(Not run)
```

`tcga_luad_lusc_450kmeth`*Lung cancer calibration data*

Description

Calibration data for the lung cancer MeDIP seq example data, taken from TCGA LUAD and LUSC studies.

Usage

```
data(CS)
```

Examples

```
## Not run:  
data(tcga_luad_lusc_450kmeth)  
tcga_luad_lusc_450kmeth  
  
## End(Not run)
```

Index

* datasets

- annotation, [2](#)
- CS, [2](#)
- DE_Input, [3](#)
- DE_MeDIP, [3](#)
- hESCs_Input, [4](#)
- hESCs_MeDIP, [4](#)
- mart_gene, [5](#)
- NSCLC_dataset, [5](#)
- resultTable, [6](#)
- samplesNSCLC, [6](#)
- tcga_luad_lusc_450kmeth, [7](#)

annotation, [2](#)

CS, [2](#)

DE_Input, [3](#)

DE_MeDIP, [3](#)

hESCs_Input, [4](#)

hESCs_MeDIP, [4](#)

mart_gene, [5](#)

NSCLC_dataset, [5](#)

resultTable, [6](#)

samplesNSCLC, [6](#)

tcga_luad_lusc_450kmeth, [7](#)