

Package ‘MEDIPSData’

April 17, 2025

Type Package

Title Example data for MEDIPS and QSEA packages

Version 1.44.0

Depends R (>= 2.15.0)

Date 2021-11-21

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_21

git_last_commit 00ebad4

git_last_commit_date 2025-04-15

Repository Bioconductor 3.21

Date/Publication 2025-04-17

Contents

annotation	2
CS	2
DE_Input	3
DE_MeDIP	3
hESCs_Input	4
hESCs_MeDIP	5

2

CS

mart_gene

NSCLC_dataset

resultTable

samplesNSCLC

tcga_luad_lusc_450kmeth

Index

5

6

6

7

7

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

An annotation object generated by accessing biomaRt using the MEDIPS.getAnnotation function of the MEDIPS package.

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

*QSEA lung cancer MeDIP seq sample table***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, [5](#)
- mart_gene, [5](#)
- NSCLC_dataset, [6](#)
- resultTable, [6](#)
- samplesNSCLC, [7](#)
- tcga_luad_lusc_450kmeth, [7](#)

annotation, [2](#)

CS, [2](#)

DE_Input, [3](#)

DE_MeDIP, [3](#)

hESCs_Input, [4](#)

hESCs_MeDIP, [5](#)

mart_gene, [5](#)

NSCLC_dataset, [6](#)

resultTable, [6](#)

samplesNSCLC, [7](#)

tcga_luad_lusc_450kmeth, [7](#)