Package ‘MEDIPSData’

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Type Package

Title Example data for MEDIPS and QSEA packages

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Depends R (>= 3.5)

Suggests MEDIPS, GenomicRanges, qsea

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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

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Contents

`annotation` *QSEA example annotation*

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` *COUPLING SET*

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_ens
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` *QSEA MeDIP-seq lung cancer example dataset*

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 *A result table as returnced by the MEDIPS.meth function of the MEDIPS package*

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)
```

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