Package ‘MEDIPSData’

March 23, 2017

**Type** Package

**Title** Example data for MEDIPS and QSEA packages

**Version** 1.10.0

**Depends** R (>= 2.15.0)

**Date** 2016-07-27

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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

**NeedsCompilation** no

**R topics documented:**

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annotation

**QSEA example annotation**

### Description

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

### Usage

data(annotation)

### Examples

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

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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

```r
## 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


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

## hESCs_MeDIP

### Examples

```r
## 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

```r
data(hESCs_Input)
```

### References


### Examples

```r
## 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

```r
data(hESCs_MeDIP)
```
References


Examples

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

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**mart_gene**

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

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**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**

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

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**NSCLC_dataset**

QSEA MeDIP-seq lung cancer example dataset

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

## End(Not run)

resultTable  
An *result table* as returned 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:

```r
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

```r
data(resultTable)
```

### Examples

```r
## 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)
```

## Not run:
data(samplesNSCLC)
samplesNSCLC

## End(Not run)

### Description

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

### Usage

```r
data(samplesNSCLC)
```

### Examples

```r
## 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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