# Package ‘mCSEAdata’

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**Type** Package

**Title** Data package for mCSEA package

**Version** 1.30.0

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**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** RELEASE_3_22

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## `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.

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### Examples

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

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## `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.

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`mcseadata` *Data and examples for mCSEA package*

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## 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.

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