Package 'bsseqData'

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Title Example whole genome bisulfite data for the bsseq package

Description Example whole genome bisulfite data for the bsseq package

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BS.cancer.ex *WGBS for colon cancer, chr 21 and 22*

Description

Whole-genome bisulfite sequencing data (WGBS) for colon cancer on chromosome 21 and 22. 3 patients were sequenced and the data contains matched colon cancer and normal colon.

Usage

```
data(BS.cancer.ex)
```

Format

The data is stored as an object of class "BSseq".

Details

The file 'scripts/create_BS.cancer.R' (see example for location) is a script that generates all data objects in this package from the raw alignment output, contained in the directory 'umtab' (see example for location). The raw alignment output is the output from the BSmooth alignment suite, using an old (legacy) format.

This dataset BS.cancer.ex.fit is the same basic data, but it also contains smoothed methylation values.

References

Hansen, K. D. et al. (2011) *Increased methylation variation in epigenetic domains across cancer types*. Nature Genetics 43, 768-775.

See Also

BS.cancer.ex.fit, BS.cancer.ex.tstat (t-statistics for this dataset) and keepLoci.ex for related datasets and the "BSseq" class. Also see the vignette(s) in the **bsseq** package.

Examples

```
data(BS.cancer.ex)
BS.cancer.ex

script <- system.file("scripts", "create_BS.cancer.R",
                      package = "bsseqData")
script
readLines(script)
system.file("umtab", package = "bsseqData")
```

BS.cancer.ex.fit *WGBS for colon cancer, chr 21 and 22, including smoothed methylation values*

Description

Whole-genome bisulfite sequencing data (WGBS) for colon cancer on chromosome 21 and 22. 3 patients were sequenced and the data contains matched colon cancer and normal colon. This dataset includes smoothed methylation values.

Usage

```
data(BS.cancer.ex.fit)
```

Format

The data is stored as an object of class "BSseq".

Details

The file 'scripts/create_BS.cancer.R' (see example for location) is a script that generates all data objects in this package from the raw alignment output, contained in the directory 'umtab' (see example for location). The raw alignment output is the output from the BSmooth alignment suite, using an old (legacy) format.

This dataset is exactly like BS.cancer.ex except it also contains smoothed methylation values.

References

Hansen, K. D. et al. (2011) *Increased methylation variation in epigenetic domains across cancer types*. Nature Genetics 43, 768-775.

See Also

BS.cancer.ex, BS.cancer.ex.tstat (t-statistics for this dataset) and keepLoci.ex for related datasets as well as the "BSseq" class and the BSmooth function. Also see the vignette(s) in the **bsseq** package.

Examples

```
data(BS.cancer.ex.fit)
BS.cancer.ex.fit

script <- system.file("scripts", "create_BS.cancer.R",
                      package = "bsseqData")
script
readLines(script)
system.file("umtab", package = "bsseqData")
```

BS.cancer.ex.tstat *T-statistics for WGBS data for colon cancer, chr 21 and 22*

Description

T-statistics produced by the BSmooth.tstat function, run on the BS.cancer.ex.fit object subsetted by keepLoci.ex.

Usage

```
data(BS.cancer.ex.tstat)
```

Format

The data is stored as an object of class "BSseqTstat".

Details

See below for the script creating this object.

References

Hansen, K. D. et al. (2011) *Increased methylation variation in epigenetic domains across cancer types*. Nature Genetics 43, 768-775.

See Also

BS.cancer.ex.fit (data used to produce the t-statistics) and keepLoci.ex (used for subsetting) as well as the "BSseqTstat" class and BSmooth.tstat. Also see the vignette(s) in the **bsseq** package.

Examples

```
data(BS.cancer.ex.tstat)
BS.cancer.ex.tstat
## This script shows how the object was created
script <- system.file("scripts", "create_BS.cancer.R",
                      package = "bsseqData")
script
readLines(script)
```

keepLoci.ex *Which methylation loci were included in an analysis of BS.cancer.ex.*

Description

This object describes which methylation loci were kept, when t-statistics were generated from BS.cancer.fit.ex using the function BSmooth.tstat.

Usage

```
data(keepLoci.ex)
```

Format

A vector of indices into BS.cancer.fit.ex.

Details

See below how this object was created and used.

See Also

BS.cancer.ex.fit (this is the data the subsetting index works on) and BS.cancer.ex.tstat and the BSmooth.tstat function . Also see the vignette(s) in the **bsseq** package.

Examples

```
data(keepLoci.ex)
## This script shows how the object was created
script <- system.file("scripts", "create_BS.cancer.R",
                      package = "bsseqData")
script
readLines(script)
```

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