Package 'minfiData'

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Title Example data for the Illumina Methylation 450k array

Description Data from 6 samples across 2 groups from 450k methylation arrays

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Depends R (>= 2.13.0), minfi, IlluminaHumanMethylation450kmanifest, IlluminaHumanMethylation450kanno.ilmn12.hg19

LazyData yes

biocViews Homo_sapiens_Data, MethylationArrayData

NeedsCompilation no

R topics documented:

MsetEx   *An example dataset for Illumina's Human Methylation 450k dataset, after preprocessing.*

Description

This contains the raw data for 6 samples from Illumina's Human Methylation 450k dataset. The data has been preprocessed.

Usage

```
data(MsetEx)
```

Format

An object of class "MethylSet"

Details

Currently, the pheno data for these 6 samples are masked. Scripts for creating the object is found in the scripts directory of the package and extdata contains the IDAT files. The data has been preprocessed using preprocessRaw.

See Also

MethylSet for the class definition, preprocessRaw for the preprocessing function, RGsetEx for the companion raw data.

Examples

```
data(MsetEx)
pData(MsetEx)
```

RGsetEx   *An example dataset for Illumina's Human Methylation 450k dataset.*

Description

This contains the raw data for 6 samples from Illumina's Human Methylation 450k dataset.

Usage

```
data(RGsetEx)
```

Format

An object of class "RGChannelSet"

Details

Currently, the pheno data for these 6 samples are masked. Scripts for creating the object is found in the scripts directory of the package and extdata contains the IDAT files.

See Also

RGChannelSet for the class definition, MsetEx for the comparion preprocessed data.

Examples

```
data(RGsetEx)
pData(RGsetEx)
```

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