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)
```

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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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