

Package ‘minfiData’

February 25, 2021

Version 0.36.0

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 (>= 3.3.0), minfi (>= 1.21.2),
IlluminaHumanMethylation450kmanifest,
IlluminaHumanMethylation450kanno.ilmn12.hg19

LazyData yes

biocViews Homo_sapiens_Data, MethylationArrayData, MicroarrayData

git_url <https://git.bioconductor.org/packages/minfiData>

git_branch RELEASE_3_12

git_last_commit fa2879d

git_last_commit_date 2020-10-27

Date/Publication 2021-02-25

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|--------|---|
| MsetEx | <i>An example dataset for Illumina’s Human Methylation 450k dataset, after preprocessing.</i> |
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Description

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

Usage

```
data(MsetEx)
data(MsetEx.sub)
```

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`.

The `MsetEx.sub` is a subset with 600 CpGs (200 of Type II, 200 of Type I - Red and 200 of Type II - Green), used for examples.

Value

An object of class "MethylSet"

See Also

[MethylSet](#) for the class definition, [preprocessRaw](#) for the preprocessing function, [RGsetEx](#) for the companion raw data.

Examples

```
data(MsetEx)
data(MsetEx.sub)
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)
data(RGsetEx.sub)
```

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 `RGsetEx.sub` is a subset with 600 CpGs (200 of Type II, 200 of Type I - Red and 200 of Type II - Green), used for examples.

Value

An object of class "RGChannelSet"

See Also

[RGChannelSet](#) for the class definition, [MsetEx](#) for the comparison preprocessed data.

Examples

```
data(RGsetEx)
data(RGsetEx.sub)
pData(RGsetEx)
```

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