

# Package ‘minfiData’

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**Version** 0.30.0

**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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**License** Artistic-2.0

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

**LazyData** yes

**biocViews** Homo\_sapiens\_Data, MethylationArrayData, MicroarrayData

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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)
```

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RGsetEx

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

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**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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