# Package 'minfiData'

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Title Example data for the Illumina Methylation 450k array

**Version** 0.42.0

<b>Description</b> Data from 6 samples across 2 groups from 450k methylation arrays.		
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2 MsetEx

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)
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.

# 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 comparion preprocessed data.

# **Examples**

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

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