

# Package ‘minfiData’

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**Version** 0.44.0

**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

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## R topics documented:

MsetEx . . . . .	2
RGsetEx . . . . .	3
<b>Index</b>	<b>4</b>

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MsetEx

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

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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)
```

# Index

## \* datasets

MsetEx, [2](#)

RGsetEx, [3](#)

MethylSet, [2](#)

MsetEx, [2, 3](#)

preprocessRaw, [2](#)

RGChannelSet, [3](#)

RGsetEx, [2, 3](#)