

Package ‘minfiDataEPIC’

June 13, 2024

Version 1.31.0

Title Example data for the Illumina Methylation EPIC array

Description

Data from 3 technical replicates of the cell line GM12878 from the EPIC methylation array.

Author Jean-Philippe Fortin, Kasper Daniel Hansen

Maintainer Kasper Daniel Hansen <kasperdanielhansen@gmail.com>

License Artistic-2.0

Depends R (>= 3.3), minfi (>= 1.21.2),
IlluminaHumanMethylationEPICmanifest,
IlluminaHumanMethylationEPICanno.ilm10b2.hg19

LazyData yes

biocViews Homo_sapiens_Data, MethylationArrayData, MicroarrayData

NeedsCompilation no

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

git_branch devel

git_last_commit e1a8dab

git_last_commit_date 2024-04-30

Repository Bioconductor 3.20

Date/Publication 2024-06-13

Contents

MsetEPIC	2
RGsetEPIC	2
Index	4

MsetEPIC	<i>An example dataset for Illumina's Human Methylation EPIC dataset, after preprocessing.</i>
----------	---

Description

This contains the raw data for 3 technical replicates of the cell line GM12878 from the Illumina's Human Methylation EPIC platform. The data has been preprocessed with preprocessRaw.

Usage

```
data(MsetEPIC)
```

Format

An object of class "MethylSet"

Details

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, [RGsetEPIC](#) for the companion raw data.

Examples

```
data(MsetEPIC)
pData(MsetEPIC)
```

RGsetEPIC	<i>An example dataset for the Illumina's Human Methylation EPIC platform.</i>
-----------	---

Description

This contains the raw data for 3 technical replicates of the cell line GM12878 from the Illumina's Human Methylation EPIC platform.

Usage

```
data(RGsetEPIC)
```

Format

An object of class "RGChannelSet"

Details

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, [MsetEPIC](#) for the comparison preprocessed data.

Examples

```
data(RGsetEPIC)  
pData(RGsetEPIC)
```

Index

* datasets

MsetEPIC, [2](#)

RGsetEPIC, [2](#)

MethylSet, [2](#)

MsetEPIC, [2](#), [3](#)

preprocessRaw, [2](#)

RGChannelSet, [3](#)

RGsetEPIC, [2](#), [2](#)