Package ‘MethylAidData’

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Type Package

Title MethylAid-summarized data for 2800 Illumina 450k array samples and 2620 EPIC array samples

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Author Davy Cats, Tyler J. Gorrie-Stone, Bastiaan T. Heijmans, John W. Holloway, BIOS Consortium, Maarten van Iterson, Faisal I. Rezwam, Leonard Schalkwyk

Maintainer M. van Iterson `<mviterson@gmail.com>`

Description A data package containing summarized Illumina 450k array data on 2800 samples and summarized EPIC data for 2620 samples. The data can be use as a background data set in the interactive application.

License GPL (>= 2)

VignetteBuilder knitr

biocViews ExperimentData, TechnologyData, MicroarrayData, MethylationArrayData

Depends MethylAid, R (>= 3.2)

Suggests BiocParallel, BiocStyle, knitr, minfiData, minfiDataEPIC

NeedsCompilation no

RoxygenNote 6.0.1

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Contents

`exampleDataLarge` *summarizedData object on 2800 450k Human Methylation samples*

Description

Summarized 450K dataon 2800 samples. The data can be use as a background data set in the interactive application.

Usage

```
exampleDataLarge
```

Format

summarizedData-object

Value

Pre-summarizedData object on 2800 450k Human Methylation samples.

Examples

```
library(MethylAid)
data(exampleDataLarge)
data(exampleData)
## Not run: visualize(exampleData, background=exampleDataLarge)
library(minfiData)
baseDir <- system.file("extdata", package="minfiData")
targets <- read.metharray.sheet(baseDir)
data <- summarize(targets)
## Not run: visualize(data, background=exampleDataLarge)
```

`MethylAidDataEPIC` *summarizedData object for 2620 EPIC Human Methylation samples*

Description

Summarized EPIC data for 2620 samples. The data can be use as a background data set in the interactive application.

Usage

```
MethylAidDataEPIC
```

Format

summarizedData-object

Value

Pre-summarizedData object for 2620 EPIC Human Methylation samples.

Examples

```
data(MethylAidDataEPIC)
library(minfiDataEPIC)
baseDir <- system.file("extdata", package="minfiDataEPIC")
targets <- read.metharray.sheet(baseDir)
data <- summarize(targets)
## Not run: visualize(data, background=MethylAidDataEPIC)
```

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