

Package ‘MethylAidData’

July 8, 2025

Type Package

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

Version 1.41.0

Date 2018-03-24

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

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

git_branch devel

git_last_commit 3e6302d

git_last_commit_date 2025-04-15

Repository Bioconductor 3.22

Date/Publication 2025-07-08

Contents

exampleDataLarge	2
MethylAidDataEPIC	2
Index	4

exampleDataLarge	<i>summarizedData object on 2800 450k Human Methylation samples</i>
------------------	---

Description

Summarized 450K data on 2800 samples. The data can be used 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	<i>summarizedData object for 2620 EPIC Human Methylation samples</i>
-------------------	--

Description

Summarized EPIC data for 2620 samples. The data can be used 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)
```

Index

* **datasets**

exampleDataLarge, [2](#)

MethylAidDataEPIC, [2](#)

exampleDataLarge, [2](#)

MethylAidDataEPIC, [2](#)