

# Package ‘MethylAid’

April 7, 2026

**Type** Package

**Title** Visual and interactive quality control of large Illumina DNA Methylation array data sets

**Version** 1.45.0

**Date** 2019-10-07

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**Description** A visual and interactive web application using RStudio's shiny package. Bad quality samples are detected using sample-dependent and sample-independent controls present on the array and user adjustable thresholds. In depth exploration of bad quality samples can be performed using several interactive diagnostic plots of the quality control probes present on the array. Furthermore, the impact of any batch effect provided by the user can be explored.

**License** GPL (>= 2)

**VignetteBuilder** knitr

**biocViews** DNAMethylation, MethylationArray, Microarray, TwoChannel, QualityControl, BatchEffect, Visualization, GUI

**Depends** R (>= 3.4)

**Imports** Biobase, BiocParallel, BiocGenerics, ggplot2, grid, gridBase, grDevices, graphics, hexbin, matrixStats, minfi (>= 1.22.0), methods, RColorBrewer, shiny, stats, SummarizedExperiment, utils

**Suggests** BiocStyle, knitr, MethylAidData, minfiData, minfiDataEPIC, RUnit

**RoxygenNote** 6.0.1

**git\_url** <https://git.bioconductor.org/packages/MethylAid>

**git\_branch** devel

**git\_last\_commit** 4bb83e1

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.23

**Date/Publication** 2026-04-06

## Contents

as.background . . . . .	2
combine,summarizedData,ANY-method . . . . .	3
exampleData . . . . .	3
show,summarizedData-method . . . . .	4
summarize . . . . .	4
summarizedData-class . . . . .	5
visualize . . . . .	6
<b>Index</b>	<b>8</b>

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as.background	<i>generate background data</i>
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## Description

Generate background data from a summarizedData-object

## Usage

```
as.background(object)
```

```
## S4 method for signature 'summarizedData'
as.background(object)
```

## Arguments

object summarizedData-object

## Details

Generates a background dataset can be used in the filter plots

## Value

list with background data for the filter plots

## Author(s)

mvaniterson

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combine, summarizedData, ANY-method  
*concatenates two summarizedData objects into one object*

---

### Description

Concatenates two summarizedData objects into one object

### Usage

```
## S4 method for signature 'summarizedData,ANY'  
combine(x, y, by = c("identical", "overlap"))
```

### Arguments

x	summarizedData-object
y	summarizedData-object
by	argument indicating how the targets information should be combined

### Value

one summarizedData object

### Examples

```
data(exampleData)  
combine(exampleData, exampleData)
```

---

exampleData                    *summarizedData object on 500 450k Human Methylation samples*

---

### Description

Pre-summarizedData object on 500 450k Human Methylation samples. Can be used as input for visualize

### Usage

```
exampleData
```

### Format

summarizedData-object

**Value**

Pre-summarizedData object on 500 450k Human Methylation samples.

**Examples**

```
data(exampleData)
## Not run: visualize(exampleData)
```

---

```
show, summarizedData-method
```

*show method for Illumina Human DNA Methylation array data*

---

**Description**

show method for summarized Illumina Human DNA Methylation array data

**Usage**

```
## S4 method for signature 'summarizedData'
show(object)
```

**Arguments**

object                    summarizedData object

**Value**

print short summary summarizedData object

**Examples**

```
data(exampleData)
exampleData
```

---

```
summarize
```

*summarization of Illumina Human DNA Methylation array data*

---

**Description**

summarize is the main function when called all samples in the targets file will be summarized

**Usage**

```
summarize(targets, batchSize = -1, BPPARAM = NULL, rp.zero = TRUE,
  verbose = TRUE, file = NULL, ...)
```

**Arguments**

targets	valid minfi targets file
batchSize	the size of each the batch
BPPARAM	see bpparam()
rp.zero	Default TRUE replaces zero intensity values with NA's
verbose	default is TRUE
file	if given summarized data is stored as RData object
...	optional arguments to read.metharray.exp, i.e. force=TRUE

**Details**

By default the summarization is performed on all data at once. Optionally the data can be summarized in batches using the batchSize option. Summarization of data can be performed in parallel as well see the MethyLAid vignette for examples.

**Value**

summarized data is saved optionally returned

**Author(s)**

mvaniterson

**Examples**

```
library(minfiData)
baseDir <- system.file("extdata", package="minfiData")
targets <- read.metharray.sheet(baseDir)
data <- summarize(targets)
```

---

summarizedData-class *container for summarized Illumina Human DNA Methylation array data*

---

**Description**

container for summarized Illumina Human DNA Methylation array data

**Slots**

**targets:** Object of class "data.frame" containing targets information.  
**controls:** Object of class "data.frame" containing quality control probe information.  
**Rcontrols:** Object of class "matrix" containing quality control probe intensities for the Red channel.

**Gcontrols:** Object of class "matrix" containing quality control probe intensities for the Grn channel.

**DPfreq:** Object of class "vector" containing frequencies of probes above background.

**MU:** Object of class "matrix" containing Methylated and Unmethylated intensities.

**plotdata:** Object of class "list" containing data to make plotting efficient.

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visualize	<i>visualize the summarized Illumina Human DNA Methylation array data</i>
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## Description

launch a shiny app for visualization of the summarized Illumina Human DNA Methylation array data

## Usage

```
visualize(object, thresholds = list(hm450k = list(MU = 10.5, OP = 11.75, BS =
  12.75, HC = 13.25, DP = 0.95), epic = list(MU = 10, OP = 12, BS = 11.75, HC =
  12.75, DP = 0.95)), background = NULL, ...)
```

```
## S4 method for signature 'summarizedData'
visualize(object, thresholds = list(hm450k =
  list(MU = 10.5, OP = 11.75, BS = 12.75, HC = 13.25, DP = 0.95), epic = list(MU
  = 10, OP = 12, BS = 11.75, HC = 12.75, DP = 0.95)), background = NULL, ...)
```

## Arguments

object	summarizedData object
thresholds	default thresholds
background	optional summarizedData-object used as background in filter control plots
...	for future use

## Details

Outliers are detected based on a set of default thresholds. To use a use-defined set of thresholds use the thresholds argument.

## Value

launches a web browser with the shiny application and returns a data.frame with detected outliers

**Examples**

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

## End(Not run)
```

# Index

## \* datasets

- exampleData, 3
- as.background, 2
- as.background, summarizedData-method  
(as.background), 2
- combine, summarizedData, ANY-method, 3
- exampleData, 3
- show, summarizedData-method, 4
- summarize, 4
- summarizedData-class, 5
- visualize, 6
- visualize, summarizedData-method  
(visualize), 6