

# Package ‘MethylAid’

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**Type** Package

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

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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

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**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)**

mvانيتerson

**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> |
|-----------|---------------------------------------------------------------------------|

---

## 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

lauches 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](#)