Package ‘MethylAid’

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Type Package

Title Visual and interactive quality control of large Illumina 450k 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.

URL `http://shiny.bioexp.nl/MethylAid`

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VignetteBuilder knitr

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

Depends R (>= 3.0)

Imports Biobase, BiocParallel, BiocGenerics, FDb.InfiniumMethylation.hg19, ggplot2, grid, gridBase, hexbin, IlluminaHumanMethylation450kmanifest, matrixStats, minfi, methods, RColorBrewer, shiny

Suggests BiocStyle, knitr, MethylAidData, minfiData, RUnit

NeedsCompilation no

R topics documented:

`as.background` *generate background data*

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

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

Description

concatenate 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 summarized 450k Illumina Human Methylation data*

Description

show method for summarized 450k Illumina Human Methylation 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 the human methylation 450k samples*

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

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.450k.sheet(baseDir)
data <- summarize(targets)
```

`summarizedData-class` *container for summarized 450k Illumina Human Methylation data*

Description

container for summarized 450k Illumina Human Methylation 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 internsities.
- **`plotdata`:** Object of class `"list"` containing data to make plotting efficient.

`visualize` *visualize the summarized 450k data*

Description

launch a shiny app for visualization of the summarized 450k data

Usage

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

## S4 method for signature 'summarizedData'
visualize(object, thresholds = list(MU = 10.5, OP =
  11.75, BS = 12.75, HC = 13.25, 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.450k.sheet(baseDir)
data <- summarize(targets)
## Not run:
visualize(data)

## End(Not run)
```

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