# Package 'shinyMethyl'

October 17, 2024

**Title** Interactive visualization for Illumina methylation arrays

**Description** Interactive tool for visualizing Illumina methylation array data. Both the 450k and EPIC array are supported.

**Version** 1.40.0

**Imports** Biobase, BiocGenerics, graphics, grDevices, htmltools, MatrixGenerics, methods, minfi, RColorBrewer, shiny, stats, utils

**Suggests** shinyMethylData, minfiData, BiocStyle, knitr, testthat

**URL** <https://github.com/Jfortin1/shinyMethyl>

**BugReports** <https://github.com/Jfortin1/shinyMethyl>

**VignetteBuilder** knitr

**License** Artistic-2.0

**Encoding** UTF-8

**biocViews** DNAMethylation, Microarray, TwoChannel, Preprocessing, QualityControl, MethylationArray

**RoxygenNote** 7.2.1

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# Contents

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runShinyMethyl                  *Run the interactive shinyMethyl session*

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### Description

Function to run the interactive shinyMethyl session from a shinyMethylSet object.

### Usage

```
runShinyMethyl(shinyMethylSet1, shinyMethylSet2 = NULL)
```

### Arguments

shinyMethylSet1

                  shinyMethylSet that must be extracted from an RGChannelSet object.

shinyMethylSet2

                  Optional shinyMethylSet that must be extracted from a GenomicRatioSet.

### Value

No value returned. Instead the shinyMethyl interactive session is launched.

### Author(s)

Jean-Philippe Fortin

### See Also

[shinyMethylSet](#)

### Examples

```
if (interactive()){
library(minfi)
library(minfiData)
baseDir <- system.file("extdata", package = "minfiData")
targets <- read.metharray.sheet(baseDir)
targets$Sample_Plate <- substr(targets$Slide,1,7)
RGSet <- read.metharray.exp(targets=targets)
summarized.data <- shinySummarize(RGSet)
runShinyMethyl(summarized.data)
}
```

---

shinyMethylSet-class     *shinyMethylSet instances*

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## Description

This class holds summarized data from Illumina methylation microarrays for interactive visualization purpose.

## Usage

```
## Constructor


shinyMethylSet(sampleNames = new("character"),
               phenotype = new("data.frame"),
               mQuantiles = new(vector("list",5)),
               betaQuantiles = new(vector("list",5)),
               methQuantiles = new(vector("list",5)),
               unmethQuantiles = new(vector("list",5)),
               cnQuantiles = new(vector("list",5)),
               greenControls = new(vector("list",12)),
               redControls = new(vector("list",12)),
               pca = new("list"),
               originObject = new("character"),
               array = new("character"))

## Data extraction / Accessors


## S4 method for signature 'shinyMethylSet'
getMeth(object)
## S4 method for signature 'shinyMethylSet'
getUnmeth(object)
## S4 method for signature 'shinyMethylSet'
getBeta(object)
## S4 method for signature 'shinyMethylSet'
getM(object)
## S4 method for signature 'shinyMethylSet'
getCN(object)
## S4 method for signature 'shinyMethylSet'
pData(object)
## S4 method for signature 'shinyMethylSet'
sampleNames(object)
```

## Arguments

object          A shinyMethylSet.

| | |
|---|---|
| sampleNames | A character vector |
| phenotype | A `data.frame` object. |
| methQuantiles | A list of 5 matrices containing several quantiles for the methylation values (between zero and infinity) separated by probe tpye and autosomal/sex probes. Each row is a quantile and each column is a sample. |
| unmethQuantiles | |
| | Similar to `Meth` |
| betaQuantiles | Similar to `Meth` but for Beta-values |
| mQuantiles | Similar to `Meth` but for M-values |
| cnQuantiles | Similar to `Meth` but for Copy Number |
| greenControls | A list containing the matrices of different raw control probes intensities in the green channel |
| redControls | Similar to `greenControls` but for the red channel |
| pca | List containing the PCA scores for the 20,000 most variable CpGs and the percentages of variance explained |
| originObject | Name of the minfi object from which the data were extracted |
| array | Name of the Illumina array platform: 450k or EPIC |

## Details

These class is a representation of a `Meth` matrix and a `Unmeth` matrix linked to a `pData` data frame.

A creationMethod slot is present to indicate from which object type the `shinyMethylSet` has been created: either a `RGChannelSet` or `GenomicRatioSet`

A `MethylSet` stores `meth` and `Unmeth`.

## Constructor

Instances are constructed using the `shinyMethylSet` function with the arguments outlined above.

## Accessors

In the following code, `object` is a `shinyMethylSet`.

getMeth(object), getUnmeth(object)  Get the Meth or Unmeth matrix.

getBeta(object)  get Beta, see details.

getM(object)  get M-values, see details.

getCN(object)  get copy number values which are defined as the sum of the methylation and unmethylation channel.

sampleNames(object)  Get the sampleNames

combine(object1,object2)  combine `shinyMethylSet` objects

## Author(s)

Jean-Philippe Fortin

### See Also

Objects of this class are typically created by using the function [shinySummarize](shinySummarize) on a [RGChannelSet](RGChannelSet) or [GenomicRatioSet](GenomicRatioSet).

### Examples

```
showClass("shinyMethylSet")
```

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shinySummarize-methods

*Summarizing a large 450K experiment into a shinyMethylSet*

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### Description

Summarizing methylation data from a RGChannelSet or GenomicRatioSet into a shinyMethylSet needed to launch the interactive interface of shinyMethyl. That works for both the 450k and EPIC arrays.

### Usage

```
## S4 method for signature 'RGChannelSet'
shinySummarize(object)
## S4 method for signature 'GenomicRatioSet'
shinySummarize(object)
```

### Arguments

object        Either a RGChannelSet or a GenomicRatioSet.

### Details

Either a RGChannelSet is transformed into a shinyMethylSet, or a GenomicRatioSet is transformed to a shinyMethylSet

### Author(s)

Jean-Philippe Fortin

### See Also

[shinyMethylSet](shinyMethylSet) for the output object and [RGChannelSet](RGChannelSet) or [GenomicRatioSet](GenomicRatioSet) for the input object.

### Examples

```
if (require(minfiData)){
  library(minfiData)
  summarized.data <- shinySummarize(RGsetEx)
}
```

# Index