

# Package ‘shinyMethyl’

February 27, 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** 1.39.1

**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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|                |  |
|----------------|--|
| runShinyMethyl | <i>Run the interactive shinyMethyl session</i> |
|----------------|--|

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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

---

## 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 type 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

This 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](#) on a [RGChannelSet](#) or [GenomicRatioSet](#).

**Examples**

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

---

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

**Examples**

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

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