

# Package ‘shinyMethyl’

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**Title** Interactive visualization for Illumina methylation arrays

**Version** 1.26.0

**Depends** methods, BiocGenerics (>= 0.3.2), shiny (>= 0.13.2), minfi (>= 1.18.2), IlluminaHumanMethylation450kmanifest, matrixStats, R (>= 3.0.0)

**Imports** RColorBrewer

**Suggests** shinyMethylData, minfiData, BiocStyle, RUnit, digest, knitr

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

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

**VignetteBuilder** knitr

**License** Artistic-2.0

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

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

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shinyMethyl-package     *Interactive visualization for Illumina methylation arrays*

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**Description**

Interactive tool for visualizing Illumina methylation array data (450k and EPIC arrays).

**Author(s)**

Jean-Philippe Fortin <jfortin@jhsph.edu>

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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.

**Usage**

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

**Arguments**

shinyMethylSet1  
                                shinyMethylSet that must be extracted from an RGChannelSet

shinyMethylSet2  
                                optional shinyMethylSet that must be extracted from an GenomicRatioSet

**Value**

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

**Author(s)**

Jean-Philippe Fortin

**See Also**

[shinyMethylSet](#)

**Examples**

```
## Not run:
if (require(minfiData)){
  baseDir <- system.file("extdata", package = "minfiData")
  targets <- read.450k.sheet(baseDir)
  targets$Sample_Plate <- substr(targets$Slide,1,7)
  RGSet <- read.450k.exp(base = baseDir, targets = targets)

  summarized.data <- shinySummarize(RGSet)
  runShinyMethyl(summarized.data)
}

## End(Not run)
```

---

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 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 <jfortin@jhsph.edu>

**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*

---

**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 <jfortin@jhsph.edu>

**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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