

# Package ‘shinyMethyl’

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**Title** Interactive visualization for Illumina's 450k methylation arrays

**Version** 1.0.2

**Depends** methods, BiocGenerics (>= 0.3.2), shiny (>= 0.9.1), minfi (>= 1.6.0), IlluminaHumanMethylation450kmanifest, matrixStats, R (>= 3.0.0)

**Imports** RColorBrewer

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

**Description** Interactive tool for visualizing Illumina's 450k array data

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

**VignetteBuilder** knitr

**License** Artistic-2.0

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

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shinyMethyl-package     *Interactive visualization for Illumina's 450k methylation arrays*

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**Description**

Interactive tool for visualizing Illumina's 450k array data

**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*

---

**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"))

## 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

### 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](#).

## 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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