

Package ‘shinyMethyl’

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Title Interactive visualization for Illumina's 450k methylation arrays

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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

NeedsCompilation no

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

Description

Interactive tool for visualizing Illumina's 450k array data

Author(s)

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runShinyMethyl *Run the interactive shinyMethyl session*

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

<code>object</code>	A shinyMethylSet.
<code>sampleNames</code>	A character vector
<code>phenotype</code>	A data.frame object.
<code>methQuantiles</code>	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.
<code>unmethQuantiles</code>	Similar to Meth
<code>betaQuantiles</code>	Similar to Meth but for Beta-values
<code>mQuantiles</code>	Similar to Meth but for M-values
<code>cnQuantiles</code>	Similar to Meth but for Copy Number
<code>greenControls</code>	A list containing the matrices of different raw control probes intensities in the green channel
<code>redControls</code>	Similar to greenControls but for the red channel
<code>pca</code>	List containing the PCA scores for the 20,000 most variable CpGs and the percentages of variance explained
<code>originObject</code>	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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