Package ‘shinyMethyl’

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Title Interactive visualization for Illumina methylation arrays

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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

NeedsCompilation no

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**shinyMethyl-package**  
*Interactive visualization for Illumina methylation arrays*

**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*

**Description**

Function to run the interactive shinyMethyl session from a shinyMethylSet.

**Usage**

```r
crunShinyMethyl(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

```r
## 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)
```

## Description

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

## Usage

### Constructor

```r
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

```r
## S4 method for signature 'shinyMethylSet'
getM(object)
## 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)
```
## shinyMethylSet-class

### Arguments

- **object**: A shinyMethylSet.
- **sampleNames**: A character vector.
- **phenotype**: A data.frame.
- **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

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

- **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
```r
showClass("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
```r
## 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
```r
if (require(minfiData)){
  library(minfiData)
  summarized.data <- shinySummarize(RGsetEx)
}
```
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