Package ‘shinyMethyl’

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Title Interactive visualization for Illumina methylation arrays

Version 1.10.0

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Imports RColorBrewer

Suggests shinyMethylData, minfiData, BioconductorStyle, 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
runShinyMethyl(shinyMethylSet1, shinyMethylSet2 = NULL)
```

Arguments

- `shinyMethylSet1`: shinyMethylSet that must be extracted from an RGChannelSet
- `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`
shinyMethylSet-class

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)

---

shinyMethylSet-class  shinyMethylSet instances

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

## 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

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
```
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
```
## 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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