Package 'shinyMethyl'

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Title Interactive visualization for Illumina methylation arrays

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

Version 1.48.0

Imports Biobase, BiocGenerics, graphics, grDevices, htmltools, MatrixGenerics, methods, minfi, RColorBrewer, shiny, stats, utils

Suggests shinyMethylData, minfiData, BiocStyle, knitr, testthat

URL https://github.com/Jfortin1/shinyMethyl

BugReports https://github.com/Jfortin1/shinyMethyl

VignetteBuilder knitr

License Artistic-2.0

Encoding UTF-8

biocViews DNAMethylation, Microarray, TwoChannel, Preprocessing, QualityControl, MethylationArray

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`runShinyMethyl` *Run the interactive shinyMethyl session*

Description

Function to run the interactive shinyMethyl session from a shinyMethylSet object.

Usage

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

Arguments

`shinyMethylSet1`	`shinyMethylSet` that must be extracted from an `RGChannelSet` object.
`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`

Examples

```
if (interactive()){
library(minfi)
library(minfiData)
baseDir <- system.file("extdata", package = "minfiData")
targets <- read.metharray.sheet(baseDir)
targets$Sample_Plate <- substr(targets$Slide,1,7)
RGSet <- read.metharray.exp(targets=targets)
summarized.data <- shinySummarize(RGSet)
runShinyMethyl(summarized.data)
}
```

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"),
               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 tpye 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

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

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

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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