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.
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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)  
}
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.
shinyMethylSet-class

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

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

```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

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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