Package ‘shinyMethyl’

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Title  Interactive visualization for Illumina methylation arrays

Version  1.10.0

Depends  methods, BiocGenerics (>= 0.3.2), shiny (>= 0.13.2), minfi (>= 1.18.2), IlluminaHumanMethylation450kmanifest, matrixStats, R (>= 3.0.0)

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>

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

```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'
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 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 <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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