Package ‘shinyMethyl’

April 15, 2017

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, BioStyle, 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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R topics documented:

shinyMethyl-package ......................................................... 2
runShinyMethyl ............................................................ 2
shinyMethylSet-class .................................................... 3
shinySummarize-methods ............................................... 5

Index 6
**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 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

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'
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)
```
## 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.

- \texttt{getMeth(object)} \texttt{getUnmeth(object)} Get the Meth or Unmeth matrix.
- \texttt{getBeta(object)} Get Beta, see details.
- \texttt{getM(object)} Get M-values, see details.
- \texttt{getCN(object)} Get copy number values which are defined as the sum of the methylation and unmethylation channel.
- \texttt{sampleNames(object)} Get the sampleNames
- \texttt{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")

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 <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)
}
Index

*Topic methods
  shinySummarize-methods, 5
*Topic package
  shinyMethyl-package, 2

combine (shinyMethylSet-class), 3
combine, shinyMethylSet, shinyMethylSet-method (shinyMethylSet-class), 3

GenomicRatioSet, 5
getBeta (shinyMethylSet-class), 3
getBeta, shinyMethylSet-method (shinyMethylSet-class), 3
getCN (shinyMethylSet-class), 3
getCN, shinyMethylSet-method (shinyMethylSet-class), 3
getGreenControls (shinyMethylSet-class), 3
getM (shinyMethylSet-class), 3
getM, shinyMethylSet-method (shinyMethylSet-class), 3
getMeth (shinyMethylSet-class), 3
getMeth, shinyMethylSet-method (shinyMethylSet-class), 3
getPCA (shinyMethylSet-class), 3
getRedControls (shinyMethylSet-class), 3
getUnmeth (shinyMethylSet-class), 3
getUnmeth, shinyMethylSet-method (shinyMethylSet-class), 3

orderByName (shinyMethylSet-class), 3

pData (shinyMethylSet-class), 3
pData, shinyMethylSet-method (shinyMethylSet-class), 3

RGChannelSet, 5
runShinyMethyl, 2

sampleNames (shinyMethylSet-class), 3
sampleNames, shinyMethylSet-method (shinyMethylSet-class), 3
shinyMethyl (shinyMethyl-package), 2
shinyMethyl-package, 2
shinyMethylSet, 2, 5

shinyMethylSet (shinyMethylSet-class), 3
shinyMethylSet-class, 3
shinySummarize, 5
shinySummarize (shinySummarize-methods), 5
shinySummarize, GenomicRatioSet-method (shinySummarize-methods), 5
shinySummarize, RGChannelSet-method (shinySummarize-methods), 5
shinySummarize-methods, 5
show, shinyMethylSet-method (shinyMethylSet-class), 3