Package 'dynamicHeatmap'

July 9, 2019

Title Dynamic Heatmap Viewer

Version 0.2

Description An implementation of the Dynamic Heatmap Viewer tool in BRB-ArrayTools

Depends R (>= 3.5.0)

License Same as BRB-ArrayTools
(https://brb.nci.nih.gov/BRB-ArrayTools/)

Encoding UTF-8

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RoxygenNote 6.1.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

R topics documented:

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dynamicHeatmap | *dynamicHeatmap() function*

Description

Run clustering calculations and show the gene expresion data in the Dynamic Heatmap Viewer.

Usage

```
dynamicHeatmap(exprData, expDesign, geneId, analysisOptions, metric,
  linkage, sortSamplesByClass, sortSamplesClassName,
  useSamplesCenteredCorrelation, projectPath, outputName)
```

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Arguments

`exprData`	A matrix of gene expression data for samples. Rows are genes and columns are arrays. Its column names must be provided.
`expDesign`	A matrix/data frame of sample classes and names.
`geneId`	A matrix/data frame of gene IDs.
`analysisOptions`	
	A character string specifying one of the Hierarchical clustering option: "CenterAndScaleGenes", "CenterGenes", or "None".
`metric`	A character string specifying one of the distance matrix: "1-Correlation", "Euclidean".
`linkage`	A character string specifying one of the linkage: "Average", "Complete", "Single", "Ward".
`sortSamplesByClass`	
	A logical variable. If it is `TRUE`, no sample clustering calculation will be performed, and the heatmap orders the samples in the chosen class. If it is `FALSE`, a sample clustering calculation will be performed, and the heatmap orders the samples according to the clustering result.
`sortSamplesClassName`	
	A character string specifying the sample class name for ordering in the heatmap.
`useSamplesCenteredCorrelation`	
	A logical variable. If it is `TRUE`, the sample clustering calculation uses the "1-Correlation" distances. If it is `FALSE`, the sample clustering calculation uses the uncentered correlation distances.
`projectPath`	A character string specifying the full project path.
`outputName`	A character string specifying the output folder name.

Details

Please see the BRB-ArrayTools manual (https://brb.nci.nih.gov/BRB-ArrayTools/Documentation.html) for details.

Examples

```
dataset<-"Brca"
# Gene IDs
geneId <- read.delim(system.file("extdata", paste0(dataset, "_GENEID.txt")
  , package = "dynamicHeatmap"), as.is = TRUE, colClasses = "character")
# Expression data, and here are log ratio.
x <- read.delim(system.file("extdata", paste0(dataset, "_LOGRAT.TXT")
  , package = "dynamicHeatmap"), header = FALSE)
# Gene filter information, 1 - pass the filter, 0 - filtered
geneFilter <- scan(system.file("extdata", paste0(dataset, "_FILTER.TXT")
  , package = "dynamicHeatmap"), quiet = TRUE)
# Class information
expDesign <- read.delim(system.file("extdata", paste0(dataset, "_EXPDESIGN.txt")
  , package = "dynamicHeatmap"), as.is = TRUE)
# Filter out genes.
geneId <- geneId[geneFilter == 1, ]
x <- x[geneFilter == 1, ]
# Pick the first column as the array IDs.
exprData <- x
```

```
colnames(exprData) <- expDesign[, 1]

projectPath <- tempdir()
outputName = "DynamicHeatmap"
dynamicHeatmap(exprData, expDesign, geneId,
                analysisOptions = "CenterAndScaleGenes",
                  # "CenterAndScaleGenes", "CenterGenes", "None"
                metric = "1-Correlation", # "1-Correlation", "Euclidean"
                linkage = "Average",  # "Average", "Complete", "Single", "Ward"
                sortSamplesByClass = FALSE,
                sortSamplesClassName = "BRCA1.v.notBRCA1",
                useSamplesCenteredCorrelation = FALSE,
                projectPath,
                outputName)
```

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test.dynamicHeatmap   *test.dynamicHeatmap() function*

Description

This function will load a test dataset to run the dynamicHeatmap function.

Usage

```
test.dynamicHeatmap(dataset = c("Brca", "Perou", "Pomeroy"), projectPath,
  outputName = "DynamicHeatmap")
```

Arguments

dataset   A character string specifying one of "Brca", "Perou" or "Pomeroy" datasets.

projectPath   A character string specifying the project path. Default is C:/Users/UserName/Documents/$dataset.

outputName   A character string for the output folder name.

See Also

[dynamicHeatmap](#)

Examples

```
test.dynamicHeatmap("Brca")
```

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