Package 'mCSEA'

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Type Package

Title Methylated CpGs Set Enrichment Analysis

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Description Identification of diferentially methylated regions (DMRs) in predefined regions (promoters, CpG islands...) from the human genome using Illumina's 450K or EPIC microarray data.
Provides methods to rank CpG probes based on linear models and includes plotting functions.

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`mCSEA-package` *Methylated CpGs Set Enrichment Analysis*

Description

Identification of diferentially methylated regions (DMRs) in predefined regions (promoters, CpG islands...) from the human genome using Illumina's 450K or EPIC microarray data. Provides methods to rank CpG probes based on linear models and includes plotting functions.

Author(s)

Jordi Martorell Marugán

Maintainer: Jordi Martorell Marugán<jordi.martorell@genyo.es>

Examples

```
## Not run:
library(mCSEA)
data(mcseadata)
myRank <- rankProbes(betaTest, phenoTest, refGroup = "Control")
myResults <- mCSEATest(myRank, regionsTypes = "promoters", platform = "EPIC")

## End(Not run)
data(precomputedmCSEA)
head(myResults$promoters)
```

`exprTest` *Expression data example*

Description

exprTest is a subset of 100 genes' microarray expression data for 20 bone marrow samples: 10 from Acute Lymphoblastic Leukemia patients and 10 from healthy patients. It is useful to test mCSEAIntegrate function.

Usage

```
data(exprTest)
```

Format

matrix

Source

Obtained from the leukemiasEset data package

`mCSEAIntegrate` *Integrate methylation and expression*

Description

Uses mCSEA methylation analysis results and expression values to search for significant correlations between DMRs methylation and close genes expression.

Usage

```
mCSEAIntegrate(mCSEAResults, exprData, regionType = c("promoters", "genes",
  "CGI", "custom"), geneIDs = "SYMBOL", dmrName = NULL, pcutoff = 0.05,
  minCor = 0.5, minP = 0.05, makePlot = TRUE, folder = ".", nproc = 1)
```

Arguments

`mCSEAResults`	The object generated by mCSEATest function
`exprData`	A matrix or data frame with genes in rows and samples in columns. A SummarizedExperiment object can be used too
`regionType`	The region types to be represented. Must be one or more of "promoters", "genes", "CGI" and "custom"
`geneIDs`	Gene identifiers used in exprData. One of "SYMBOL", "ENSEMBL", "ENTREZID", "GENEID", "REFSEQ" or "UNIGENE"
`dmrName`	The DMR of interest to correlate with expression (e.g. gene name, CGI name...). If NULL (default), all DMRs with P-Value < pcutoff are selected
`pcutoff`	P-Value threshold to select DMRs if dmrName = NULL
`minCor`	Correlation threshold to output the results
`minP`	Correlation P-Value threshold to output the results
`makePlot`	If TRUE, generate corelation and save them in the folder specified by folder parameter
`folder`	Directory to save the correlation plots if makePlot = TRUE
`nproc`	Number of processors to be used

Value

A data.frame with the integration results.

Author(s)

Jordi Martorell Marugán, <jordi.martorell@genyo.es>

See Also

`rankProbes`, `mCSEATest`

Examples

```
data(precomputedmCSEA)
data(exprTest)

resultsInt <- mCSEAIntegrate(myResults, exprTest, "promoters", "ENSEMBL",
                             "GATA2", makePlot = FALSE)

resultsInt
```

---

mCSEAPlot *Plot mCSEA results*

Description

Generate a graphic with the genomic context of the selected DMR, showing methylation status at each CpG site of different samples groups

Usage

```
mCSEAPlot(mCSEAResults, regionType, dmrName, extend = 1000,
  chromosome = TRUE, leadingEdge = TRUE, CGI = FALSE, genes = TRUE,
  transcriptAnnotation = "transcript", makePDF = TRUE,
  col = c("blue", "magenta", "green", "red", "black"))
```

Arguments

mCSEAResults	The object generated by mCSEATest function
regionType	The region type to be represented. Must be one of "promoters", "genes", "CGI" or "custom"
dmrName	The DMR of interest to be represented (e.g. gene name, CGI name...)
extend	The number of base pairs to extend the plot around the DMR of interest (default = 1000 bp)
chromosome	If TRUE, represent the chromosome and genome axis
leadingEdge	If TRUE, represent the bars indicating if each CpG belongs to the mCSEA leading edge (green) or not (red)
CGI	If TRUE, represent the annotated CpG islands
genes	If TRUE, represent the annotated genes
transcriptAnnotation	Labels showed at the genes track. Must be one of "transcript" (default), "symbol", "gene", "exon" or "feature"
makePDF	If TRUE, save the plot in pdf format in the working directory. Otherwise, draw the plot in the active graphics window
col	Vector with colors to plot methylation in different groups

Value

'NULL'

Author(s)

Jordi Martorell Marugán, <jordi.martorell@genyo.es>

See Also

rankProbes, mCSEATest, mCSEAPlotGSEA

Examples

```
library(mCSEAdata)
data(mcseadata)
## Not run:
myRank <- rankProbes(betaTest, phenoTest, refGroup = "Control")
set.seed(123)
myResults <- mCSEATest(myRank, betaTest, phenoTest,
regionsTypes = "promoters", platform = "EPIC")

## End(Not run)
data(precomputedmCSEA)
mCSEAPlot(myResults, "promoters", "CLIC6",
transcriptAnnotation = "symbol", makePDF = FALSE)
```

---

mCSEAPlotGSEA *Plot mCSEA results*

Description

Generate an enrichment plot

Usage

```
mCSEAPlotGSEA(rank, mCSEAResults, regionType, dmrName)
```

Arguments

rank	A named numeric vector with the ranking statistic of each CpG site
mCSEAResults	The object generated by mCSEATest function
regionType	The region type to be represented. Must be one of "promoters", "genes", "CGI" or "custom"
dmrName	The DMR of interest to be represented (e.g. gene name, CGI name...)

Value

'NULL'

Author(s)

Jordi Martorell Marugán, <jordi.martorell@genyo.es>

References

Subramanian, A. et al (2005). *Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles* . PNAS 102, 15545-15550.

See Also

rankProbes, mCSEATest, mCSEAPlot

Examples

```
## Not run:
library(mCSEAdata)
data(mcseadata)
myRank <- rankProbes(betaTest, phenoTest, refGroup = "Control")
set.seed(123)
myResults <- mCSEATest(myRank, regionsTypes = "promoters",
platform = "EPIC")

## End(Not run)
data(precomputedmCSEA)
mCSEAPlotGSEA(myRank, myResults, "promoters", "CLIC6")
```

---

mCSEATest *mCSEA core analysis*

Description

Perform a methylated CpG sites enrichment analysis in predefined genomic regions

Usage

```
mCSEATest(rank, methData, pheno = NULL, column = 1,
  regionsTypes = c("promoters", "genes", "CGI"), customAnnotation = NULL,
  minCpGs = 5, nproc = 1, nperm = NULL, platform = "450k")
```

Arguments

rank	A named numeric vector with the ranking statistic of each CpG site
methData	A data frame or a matrix containing Illumina's CpG probes in rows and samples in columns. A SummarizedExperiment object can be used too
pheno	A data frame or a matrix containing samples in rows and covariates in columns. If NULL (default), pheno is extracted from the SummarizedExperiment object
column	The column name or number from pheno used to split the samples into groups (first column is used by default)
regionsTypes	A character or character vector indicating the predefined regions to be analyzed. NULL to skip this step and use customAnnotation.
customAnnotation	An optional list with the CpGs associated to each feature (default = NULL)
minCpGs	Minimum number of CpGs associated to a region. Regions below this threshold are not tested
nproc	Number of processors to use in GSEA step (default = 1)
nperm	(deprecated) Number of permutations to do in GSEA step in the previous implementation. Now, this parameter is ignored
platform	Platform used to get the methylation data (450k or EPIC)

Value

A list with the results of each of the analyzed regions. For each region type, a data frame with the results and a list with the probes associated to each region are generated. In addition, this list also contains the input methData, pheno and platform objects

Author(s)

Jordi Martorell Marugán, <jordi.martorell@genyo.es>

References

Subramanian, A. et al (2005). *Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles* . PNAS 102, 15545-15550.

See Also

rankProbes, mCSEAPlot, mCSEAPlotGSEA

Examples

```
## Not run:
library(mCSEAdata)
data(mcseadata)
myRank <- rankProbes(betaTest, phenoTest, refGroup = "Control")
set.seed(123)
myResults <- mCSEATest(myRank, betaTest, phenoTest,
regionsTypes = "promoters", platform = "EPIC")

## End(Not run)
data(precomputedmCSEA)
head(myResults[["promoters"]])
head(myResults[["promoters_association"]])
```

---

precomputedmCSEA *Precomputed mCSEA results*

Description

myRank is a result of rankProbes function. myResults is a result of mCSEATest function.

Usage

```
data(precomputedmCSEA)
```

Format

vector (myRank) and list data.frame (myResults)

Source

Both objects were obtained with the example commands in the mCSEA vignette.

rankProbes *Rank CpG probes*

Description

Apply a linear model to Illumina's 450k or EPIC methylation data to get the t-value of each CpG probe

Usage

```
rankProbes(methData, pheno = NULL, paired = FALSE, explanatory = 1,
  covariates = c(), pairColumn = c(), caseGroup = 1, refGroup = 2,
  continuous = NULL, typeInput = "beta", typeAnalysis = "M")
```

Arguments

methData	A data frame or a matrix containing Illumina's CpG probes in rows and samples in columns. A SummarizedExperiment object can be used too
pheno	A data frame or a matrix containing samples in rows and covariates in columns. If NULL (default), pheno is extracted from the SummarizedExperiment object
paired	Perform a paired t-test (default = FALSE)
explanatory	The column name or position from pheno used to perform the comparison between groups (default = first column)
covariates	A list or character vector with column names from pheno used as data covariates in the linear model
pairColumn	Only for paired analysis. The column name or position from pheno used to connect the paired samples (default = NULL)
caseGroup	The group name or position from explanatory variable used as cases to perform the comparison (default = first group)
refGroup	The group name or position from explanatory variable used as reference to perform the comparison (default = second group)
continuous	A list or character vector with columns names from pheno which should be treated as continuous variables (default = none)
typeInput	Type of input methylation data. "beta" for Beta-values and "M" for M-values
typeAnalysis	"M" to use M-values to rank the CpG probes (default). "beta" to use Beta-values instead

Value

A named vector containing the t-values from the linear model for each CpG probe

Author(s)

Jordi Martorell Marugán, <jordi.martorell@genyo.es>

References

Smyth, G. K. (2005). *Limma: linear models for microarray data*. Bioinformatics and Computational Biology Solutions using R and Bioconductor, 397-420.

See Also

mCSEATest

Examples

```
data(mcseadata)
myRank <- rankProbes(betaTest, phenoTest, refGroup = "Control")
head(myRank)
```

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