

Package ‘MethylMix’

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Title MethylMix: Identifying methylation driven cancer genes

Version 2.41.0

Description MethylMix is an algorithm implemented to identify hyper and hypomethylated genes for a disease. MethylMix is based on a beta mixture model to identify methylation states and compares them with the normal DNA methylation state. MethylMix uses a novel statistic, the Differential Methylation value or DM-value defined as the difference of a methylation state with the normal methylation state. Finally, matched gene expression data is used to identify, besides differential, functional methylation states by focusing on methylation changes that effect gene expression. References:
Gevaert O. MethylMix: an R package for identifying DNA methylation-driven genes. Bioinformatics (Oxford, England). 2015;31(11):1839-41. doi:10.1093/bioinformatics/btv020.
Gevaert O, Tibshirani R, Plevritis SK. Pancancer analysis of DNA methylation-driven genes using MethylMix. Genome Biology. 2015;16(1):17. doi:10.1186/s13059-014-0579-8.

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Author Olivier Gevaert

Maintainer Olivier Gevaert <olivier.gevaert@gmail.com>

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BatchData	<i>BatchData data set</i>
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Description

Data set with batch number for TCGA samples.

betaEst_2	<i>The betaEst_2 function</i>
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Description

Internal. Estimates a beta distribution via Maximum Likelihood. Adapted from RPMM package.

Usage

betaEst_2(Y, w, weights)

Arguments

- Y

data vector.
- w

posterior weights.
- weights

Case weights.

Value

(a,b) parameters.

blc_2	<i>The blc_2 function</i>
-------	---------------------------

Description

Internal. Fits a beta mixture model for any number of classes. Adapted from RPMM package.

Usage

```
blc_2(Y, w, maxiter = 25, tol = 1e-06, weights = NULL, verbose = TRUE)
```

Arguments

Y	Data matrix (n x j) on which to perform clustering.
w	Initial weight matrix (n x k) representing classification.
maxiter	Maximum number of EM iterations.
tol	Convergence tolerance.
weights	Case weights.
verbose	Verbose output.

Value

A list of parameters representing mixture model fit, including posterior weights and log-likelihood.

ClusterProbes	<i>The ClusterProbes function</i>
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Description

This function uses the annotation for Illumina methylation arrays to map each probe to a gene. Then, for each gene, it clusters all its CpG sites using hierarchical clustering and Pearson correlation as distance and complete linkage. If data for normal samples is provided, only overlapping probes between cancer and normal samples are used. Probes with SNPs are removed. This function is prepared to run in parallel if the user registers a parallel structure, otherwise it runs sequentially. This function also cleans up the sample names, converting them to the 12 digit format.

Usage

```
ClusterProbes(MET_Cancer, MET_Normal, CorThreshold = 0.4)
```

Arguments

MET_Cancer	data matrix for cancer samples.
MET_Normal	data matrix for normal samples.
CorThreshold	correlation threshold for cutting the clusters.

Value

List with the clustered data sets and the mapping between probes and genes.

Examples

```
## Not run:

# Optional register cluster to run in parallel
library(doParallel)
cl <- makeCluster(5)
registerDoParallel(cl)

# Methylation data for ovarian cancer
cancerSite <- "OV"
targetDirectory <- paste0(getwd(), "/")

# Downloading methylation data
METdirectories <- Download_DNAMethylation(cancerSite, targetDirectory, TRUE)

# Processing methylation data
METProcessedData <- Preprocess_DNAMethylation(cancerSite, METdirectories)

# Saving methylation processed data
saveRDS(METProcessedData, file = paste0(targetDirectory, "MET_", cancerSite, "_Processed.rds"))

# Clustering methylation data
res <- ClusterProbes(METProcessedData[[1]], METProcessedData[[2]])

# Saving methylation clustered data
toSave <- list(METcancer = res[[1]], METnormal = res[[2]], ProbeMapping = res$ProbeMapping)
saveRDS(toSave, file = paste0(targetDirectory, "MET_", cancerSite, "_Clustered.rds"))

stopCluster(cl)

## End(Not run)
```

ComBat_NoFiles

The ComBat_NoFiles function

Description

Internal. Performs batch correction.

Usage

```
ComBat_NoFiles(dat, saminfo, type = "txt", write = F, covariates = "all",
  par.prior = F, filter = F, skip = 0, prior.plots = T)
```

Arguments

<code>dat</code>	<code>dat</code>
<code>saminfo</code>	<code>saminfo</code>
<code>type</code>	currently supports two data file types 'txt' for a tab-delimited text file and 'csv' for an Excel .csv file (sometimes R handles the .csv file better, so use this if you have problems with a .txt file!).
<code>write</code>	if 'T' ComBat writes adjusted data to a file, and if 'F' and ComBat outputs the adjusted data matrix if 'F' (so assign it to an object! i.e. <code>NewData <- ComBat('my expression.xls','Sample info file.txt', write=F)</code>).
<code>covariates</code>	'covariates=all' will use all of the columns in your sample info file in the modeling (except array/sample name), if you only want use a some of the columns in your sample info file, specify these columns here as a vector (you must include the Batch column in this list).
<code>par.prior</code>	if 'T' uses the parametric adjustments, if 'F' uses the nonparametric adjustments— if you are unsure what to use, try the parametric adjustments (they run faster) and check the plots to see if these priors are reasonable.
<code>filter</code>	'filter=value' filters the genes with absent calls in > 1-value of the samples. The default here (as well as in dchip) is .8. Filter if you can as the EB adjustments work better after filtering. Filter must be numeric if your expression index file contains presence/absence calls (but you can set it >1 if you don't want to filter any genes) and must be 'F' if your data doesn't have presence/absence calls;
<code>skip</code>	is the number of columns that contain probe names and gene information, so 'skip=5' implies the first expression values are in column 6
<code>prior.plots</code>	if true will give prior plots with black as a kernel estimate of the empirical batch effect density and red as the parametric estimate.

Value

Results.

`combineForEachOutput` *The combineForEachOutput function*

Description

Internal. Function to combine results from the foreach loop.

Usage

```
combineForEachOutput(out1, out2)
```

Arguments

<code>out1</code>	result from one foreach loop.
<code>out2</code>	result from another foreach loop.

Value

List with the combined results.

Download_DNAmethylation

The Download_DNAmethylation function

Description

Downloads DNA methylation data from TCGA.

Usage

```
Download_DNAmethylation(CancerSite, TargetDirectory, downloadData = TRUE)
```

Arguments

CancerSite	character of length 1 with TCGA cancer code.
TargetDirectory	character with directory where a folder for downloaded files will be created.
downloadData	logical indicating if data should be downloaded (default: TRUE). If false, the url of the desired data is returned.

Value

list with paths to downloaded files for both 27k and 450k methylation data.

Examples

```
## Not run:

# Optional register cluster to run in parallel
library(doParallel)
cl <- makeCluster(5)
registerDoParallel(cl)

# Methylation data for ovarian cancer
cancerSite <- "OV"
targetDirectory <- paste0(getwd(), "/")

# Downloading methylation data
METdirectories <- Download_DNAmethylation(cancerSite, targetDirectory, TRUE)

# Processing methylation data
METProcessedData <- Preprocess_DNAmethylation(cancerSite, METdirectories)

# Saving methylation processed data
saveRDS(METProcessedData, file = paste0(targetDirectory, "MET_", cancerSite, "_Processed.rds"))
```

```
# Clustering methylation data
res <- ClusterProbes(METProcessedData[[1]], METProcessedData[[2]])

# Saving methylation clustered data
toSave <- list(METcancer = res[[1]], METnormal = res[[2]], ProbeMapping = res$ProbeMapping)
saveRDS(toSave, file = paste0(targetDirectory, "MET_", cancerSite, "_Clustered.rds"))

stopCluster(cl)

## End(Not run)
```

Download_GeneExpression

The Download_GeneExpression function

Description

Downloads gene expression data from TCGA.

Usage

```
Download_GeneExpression(CancerSite, TargetDirectory, downloadData = TRUE)
```

Arguments

CancerSite	character of length 1 with TCGA cancer code.
TargetDirectory	character with directory where a folder for downloaded files will be created.
downloadData	logical indicating if data should be downloaded (default: TRUE). If false, the url of the desired data is returned.

Details

This function downloads RNAseq data (file tag "mRNAseq_Preprocess.Level_3"), with the exception for OV and GBM, for which micro array data is downloaded since there is not enough RNAseq data

Value

list with paths to downloaded files for both 27k and 450k methylation data.

Examples

```
## Not run:

# Optional register cluster to run in parallel
library(doParallel)
cl <- makeCluster(5)
registerDoParallel(cl)

# Gene expression data for ovarian cancer
cancerSite <- "OV"
targetDirectory <- paste0(getwd(), "/")

# Downloading gene expression data
GEDirectories <- Download_GeneExpression(cancerSite, targetDirectory, TRUE)

# Processing gene expression data
GEProcessedData <- Preprocess_GeneExpression(cancerSite, GEDirectories)

# Saving gene expression processed data
saveRDS(GEProcessedData, file = paste0(targetDirectory, "GE_", cancerSite, "_Processed.rds"))

stopCluster(cl)

## End(Not run)
```

GEcancer

Cancer Gene expression data of glioblastoma patients from the TCGA project

Description

Cancer Gene expression data of glioblastoma patients from the TCGA project. A set of 14 genes that have been shown in the literature to be involved in differential methylation in glioblastoma were selected as an example to try out MethyLMix.

Usage

```
data(GEcancer)
```

Format

A numeric matrix with 14 rows (genes) and 251 columns (samples).

References

Cancer Genome Atlas Research Network. Comprehensive genomic characterization defines human glioblastoma genes and core pathways. *Nature*. 2008 Oct 23; 455(7216):1061-8. doi: 10.1038/nature07385. Epub 2008 Sep 4. Erratum in: *Nature*. 2013 Feb 28;494(7438):506. PubMed PMID: 18772890; PubMed Central PMCID: PMC2671642.

See Also

TCGA: The Cancer Genome Atlas: <http://cancergenome.nih.gov/>

 GetData

The GetData function

Description

This function wraps the functions for downloading and pre-processing DNA methylation and gene expression data, as well as for clustering CpG probes.

Usage

```
GetData(cancerSite, targetDirectory)
```

Arguments

`cancerSite` character of length 1 with TCGA cancer code.
`targetDirectory` character with directory where a folder for downloaded files will be created.

Details

Pre-process of DNA methylation data includes eliminating samples and genes with too many NAs, imputing NAs, and doing Batch correction. If there is both 27k and 450k data, and both data sets have more than 50 samples, we combine the data sets, by reducing the 450k data to the probes present in the 27k data, and bath correction is performed again to the combined data set. If there are samples with both 27k and 450k data, the 450k data is used and the 27k data is discarded, before the step mentioned above. If the 27k or the 450k data does not have more than 50 samples, we use the one with the greatest number of samples, we do not combine the data sets.

For gene expression, this function downloads RNAseq data (file tag "mRNAseq_Preprocess.Level_3"), with the exception for OV and GBM, for which micro array data is downloaded since there is not enough RNAseq data. Pre-process of gene expression data includes eliminating samples and genes with too many NAs, imputing NAs, and doing Batch correction.

For the clustering of the CpG probes, this function uses the annotation for Illumina methylation arrays to map each probe to a gene. Then, for each gene, it clusters all its CpG sites using hierarchical clustering and Pearson correlation as distance and complete linkage. If data for normal samples is provided, only overlapping probes between cancer and normal samples are used. Probes with SNPs are removed.

This function is prepared to run in parallel if the user registers a parallel structure, otherwise it runs sequentially.

This function also cleans up the sample names, converting them to the 12 digit format.

Value

The following files will be created in target directory:

- gdac: a folder with the raw data downloaded from TCGA.
- MET_CancerSite_Processed.rds: processed methylation data at the CpG sites level (not clustered).
- GE_CancerSite_Processed.rds: processed gene expression data.
- data_CancerSite.rds: list with both gene expression and methylation data. Methylation data is clustered and presented at the gene level. A matrix with the mapping from CpG sites to genes is included.

Examples

```
## Not run:
# Get data for ovarian cancer
cancerSite <- "OV"
targetDirectory <- paste0(getwd(), "/")
GetData(cancerSite, targetDirectory)

# Optional register cluster to run in parallel
library(doParallel)
cl <- makeCluster(5)
registerDoParallel(cl)

cancerSite <- "OV"
targetDirectory <- paste0(getwd(), "/")
GetData(cancerSite, targetDirectory)

stopCluster(cl)

## End(Not run)
```

get_firehoseData	<i>The get_firehoseData function</i>
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Description

Gets data from TCGA's firehose.

Usage

```
get_firehoseData(downloadData = TRUE, saveDir = "./",
  TCGA_acronym_uppercase = "LUAD", dataType = "stddata",
  dataFileTag = "mRNAseq_Preprocess.Level_3", FFPE = FALSE,
  fileType = "tar.gz", gdacURL = "http://gdac.broadinstitute.org/runs/",
  untarUngzip = TRUE, printDisease_abbr = FALSE)
```

Arguments

- downloadData logical indicating if data should be downloaded (default: TRUE). If false, the url of the desired data is returned.
- saveDir path to directory to save downloaded files.
- TCGA_acronym_uppercase TCGA's cancer site code.
- dataType type of data in TCGA (default: "stddata").
- dataFileTag name of the file to be downloaded (the default is to download RNAseq data, but this can be changed to download other data).
- FFPE logical indicating if FFPE data should be downloaded (default: FALSE).
- fileType type of downloaded file (default: "fileType", other type not admitted at the moment).
- gdacURL gdac url.
- untarUngzip logical indicating if the gzip file downloaded should be untarred (default: TRUE).
- printDisease_abbr if TRUE data is not downloaded but all the possible cancer sites codes are shown (default: FALSE).

Value

DownloadedFile path to directory with downloaded files.

METcancer	<i>DNA methylation data from cancer tissue from glioblastoma patients from the TCGA project</i>
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Description

Cancer Gene expression data of glioblastoma patients from the TCGA project. A set of 14 genes that have been shown in the literature to be involved in differential methylation in glioblastoma were selected as an example to try out MethyLMix.

Usage

data(METcancer)

Format

A numeric matrix with 14 rows (genes) and 251 columns (samples).

References

Cancer Genome Atlas Research Network. Comprehensive genomic characterization defines human glioblastoma genes and core pathways. Nature. 2008 Oct 23; 455(7216):1061-8. doi: 10.1038/nature07385. Epub 2008 Sep 4. Erratum in: Nature. 2013 Feb 28;494(7438):506. PubMed PMID: 18772890; PubMed Central PMCID: PMC2671642.

See Also

TCGA: The Cancer Genome Atlas: <http://cancergenome.nih.gov/>

MethylMix

MethylMix: Mixture model for DNA methylation data in cancer.

Description

MethylMix identifies DNA methylation driven genes by modeling DNA methylation data in cancer vs. normal and looking for homogeneous subpopulations. In addition matched gene expression data (e.g. from microarray technology or RNA sequencing) is used to identify functional DNA methylation events by requiring a negative correlation between methylation and gene expression of a particular gene. See references below.

Usage

```
MethylMix(METcancer, GEcancer, METnormal = NULL, listOfGenes = NULL,
  filter = TRUE, NoNormalMode = FALSE, OutputRoot = "")
```

Arguments

METcancer	Matrix with the methylation data of cancer tissue with genes in rows and samples in columns.
GEcancer	Gene expression data for cancer tissue with genes in rows and samples in columns.
METnormal	Matrix with the normal methylation data of the same genes as in METcancer. Again genes in rows and samples in columns. The samples do not have to match with the cancer data. If this argument is NULL, MethylMix will run without comparing to normal samples.
listOfGenes	Vector with genes names to be evaluated, names must coincide with the names of the rows of METcancer.
filter	Logical indicating if the linear regression to select genes with significant negative relation between methylation and gene expression should be performed (default: TRUE).
NoNormalMode	Logical indicating if the methylation states found in the cancer samples should be compared to the normal samples (default: FALSE).
OutputRoot	Path to store the MethylMix results object.

Value

MethylMixResults is a list with the following components:

MethylationDrivers

Genes identified as transcriptionally predictive and differentially methylated by MethylMix.

NrComponents

The number of methylation states found for each driver gene.

MixtureStates	A list with the DM-values for each driver gene. Differential Methylation values (DM-values) are defined as the difference between the methylation mean in one mixture component of cancer samples and the methylation mean in the normal samples, for a given gene.
MethylationStates	Matrix with DM-values for all driver genes (rows) and all samples (columns).
Classifications	Matrix with integers indicating to which mixture component each cancer sample was assigned to, for each gene.
Models	Beta mixture model parameters for each driver gene.

References

- Gevaert O. **MethylMix: an R package for identifying DNA methylation-driven genes**. Bioinformatics (Oxford, England). 2015;31(11):1839-41. doi:10.1093/bioinformatics/btv020.
- Gevaert O, Tibshirani R, Plevritis SK. **Pancancer analysis of DNA methylation-driven genes using MethylMix**. Genome Biology. 2015;16(1):17. doi:10.1186/s13059-014-0579-8.
- Pierre-Louis Cedoz, Marcos Prunello, Kevin Brennan, Olivier Gevaert; MethylMix 2.0: an R package for identifying DNA methylation genes. Bioinformatics. doi:10.1093/bioinformatics/bty156.

Examples

```
# load the three data sets needed for MethylMix
data(METcancer)
data(METnormal)
data(GEcancer)

# run MethylMix on a small set of example data
MethylMixResults <- MethylMix(METcancer, GEcancer, METnormal)

## Not run:
# run in parallel
library(doParallel)
cl <- makeCluster(5)
registerDoParallel(cl)
MethylMixResults <- MethylMix(METcancer, GEcancer, METnormal)
stopCluster(cl)

## End(Not run)
```

Description

Internal. Prepares all the structures to store the results and calls in a foreach loop a function that fits the mixture model in each gene.

Usage

```
MethylMix_MixtureModel(METcancer, METnormal = NULL, FunctionalGenes,
  NoNormalMode = FALSE)
```

Arguments

METcancer	matrix with methylation data for cancer samples (genes in rows, samples in columns).
METnormal	matrix with methylation data for normal samples (genes in rows, samples in columns). If NULL no comparison to normal samples will be done.
FunctionalGenes	vector with genes names to be considered for the mixture models.
NoNormalMode	logical, if TRUE no comparison to normal samples is performed. Defaults to FALSE.

Value

MethylationStates matrix of DM values, with driver genes in the rows and samples in the columns.

NrComponents matrix with the number of components identified for each driver gene.

Models list with the mixture model fitted for each driver gene.

MethylationDrivers character vector with the genes found by MethylMix as differentially methylated and transcriptionally predictive (driver genes).

MixtureStates a list with a matrix for each driver gene containing the DM values.

Classifications a vector indicating to which component each sample was assigned.

MethylMix_ModelGeneExpression

The MethylMix_ModelGeneExpression function

Description

Model gene expression as a function of gene expression with a simple linear regression model. Genes with a significant negative linear association between DNA methylation and gene expression are returned.

Usage

```
MethylMix_ModelGeneExpression(METcancer, GECancer, CovariateData = NULL)
```

Arguments

METcancer	matrix with methylation data for cancer samples (genes in rows, samples in columns).
GEcancer	matrix with gene expression data for cancer samples (genes in rows, samples in columns).
CovariateData	vector (numeric or character) indicating a covariate to be included in the model to adjust for it. Not used in an standard run of MethylMix. It can be used if samples can from different tissue type, for example.

Value

vector with the names of the genes for which there is a significant linear and negative association between methylation and gene expression.

Examples

```
# load data sets
data(METcancer)
data(GEcancer)

# model gene expression
MethylMixResults <- MethylMix_ModelGeneExpression(METcancer, GEcancer)
```

MethylMix_ModelSingleGene

The MethylMix_ModelSingleGene function

Description

Internal. For a given gene, this function fits the mixture model, selects the number of components and defines the respective methylation states.

Usage

```
MethylMix_ModelSingleGene(GeneName, METdataVector, METdataNormalVector = NULL,
  NoNormalMode = FALSE, maxComp = 3, PvalueThreshold = 0.01,
  MeanDifferenceTreshold = 0.1, minSamplesPerGroup = 1)
```

Arguments

GeneName	character string with the name of the gene to model
METdataVector	vector with methylation data for cancer samples.
METdataNormalVector	vector with methylation data for normal samples. It can be NULL and then no normal mode will be used.

NoNormalMode	logical, if TRUE no comparison to normal samples is performed. Defaults to FALSE.
maxComp	maximum number of mixture components admitted in the model (3 by default).
PvalueThreshold	threshold to consider results significant.
MeanDifferenceTreshold	threshold in beta value scale from which two methylation means are considered different.
minSamplesPerGroup	minimum number of samples required to belong to a new mixture component in order to accept it. Default is 1 (not used). If -1, each component has to have at least 5% of all cancer samples.

Details

maxComp, PvalueThreshold, METDiffThreshold, minSamplesPerGroup are arguments for this function but are fixed in their default values for the user because they are not available in the main MethylMix function, to keep it simple. It would be easy to make them available to the user if we want to.

Value

NrComponents number of components identified.
 Models an object with the parameters of the model fitted.
 MethylationStates vector with DM values for each sample.
 MixtureStates vector with DMvalues for each component.
 Classifications a vector indicating to which component each sample was assigned.
 FlipOverState FlipOverState

MethylMix_PlotModel	<i>The MethylMix_PlotModel function.</i>
---------------------	--

Description

Produces plots to represent MethylMix's output.

Usage

```
MethylMix_PlotModel(GeneName, MixtureModelResults, METcancer, GEcancer = NULL,
  METnormal = NULL)
```

Arguments

GeneName	Name of the gene for which to create a MethylMix plot.
MixtureModelResults	List returned by MethylMix function.
METcancer	Matrix with the methylation data of cancer tissue with genes in rows and samples in columns.
GEcancer	Gene expression data for cancer tissue with genes in rows and samples in columns (optional).
METnormal	Matrix with the normal methylation data of the same genes as in METcancer (optional). Again genes in rows and samples in columns.

Value

a list with MethylMix plots, a histogram of the methylation data (MixtureModelPlot) and a scatter-plot between DNA methylation and gene expression (CorrelationPlot, is NULL if gene expression data is not provided). Both plots show the different mixture components identified.

Examples

```
# Load the three data sets needed for MethylMix
data(METcancer)
data(METnormal)
data(GEcancer)

# Run methylmix on a small set of example data
MethylMixResults <- MethylMix(METcancer, GEcancer, METnormal)

# Plot the most famous methylated gene for glioblastoma
MethylMix_PlotModel("MGMT", MethylMixResults, METcancer)

# Plot MGMT also with its normal methylation variation
MethylMix_PlotModel("MGMT", MethylMixResults, METcancer, METnormal = METnormal)

# Plot a MethylMix model for another gene
MethylMix_PlotModel("ZNF217", MethylMixResults, METcancer, METnormal = METnormal)

# Also plot the inverse correlation with gene expression (creates two separate plots)
MethylMix_PlotModel("MGMT", MethylMixResults, METcancer, GEcancer, METnormal)

# Plot all functional and differential genes
for (gene in MethylMixResults$MethylationDrivers) {
  MethylMix_PlotModel(gene, MethylMixResults, METcancer, METnormal = METnormal)
}
```

MethylMix_Predict	<i>The MethylMix_Predict function</i>
-------------------	---------------------------------------

Description

Given a new data set with methylation data, this function predicts the mixture component for each new sample and driver gene. Predictions are based on posterior probabilities calculated with MethylMix's fitted mixture model.

Usage

```
MethylMix_Predict(newBetaValuesMatrix, MethylMixResult)
```

Arguments

`newBetaValuesMatrix`

Matrix with new observations for prediction, genes/cpg sites in rows, samples in columns. Although this new matrix can have a different number of genes/cpg sites than the one provided as METcancer when running MethylMix, naming of genes/cpg sites should be the same.

`MethylMixResult`

Output object from MethylMix

Value

A matrix with predictions (indices of mixture component), driver genes in rows, new samples in columns

Examples

```
# load the three data sets needed for MethylMix
data(METcancer)
data(METnormal)
data(GEcancer)

# run MethylMix on a small set of example data
MethylMixResults <- MethylMix(METcancer, GEcancer, METnormal)
# toy example new data, of same dimension of original METcancer data
newMETData <- matrix(runif(length(METcancer)), nrow = nrow(METcancer))
rownames(newMETData) <- rownames(METcancer)
colnames(newMETData) <- paste0("sample", 1:ncol(METcancer))
predictions <- MethylMix_Predict(newMETData, MethylMixResults)
```

MethylMix_RemoveFlipOver

The MethylMix_RemoveFlipOver function

Description

Internal. The estimated densities for each beta component can overlap, generating samples that look like being separated from their group. This function re classifies such samples.

Usage

```
MethylMix_RemoveFlipOver(OrigOrder, MethylationState, classification,
  METdataVector, NrComponents, UseTrainedFlipOver = FALSE,
  FlipOverState = 0)
```

Arguments

OrigOrder	order of sorted values in the methylation vector.
MethylationState	methylation states for this gene.
classification	vector with integers indicating to wich component each sample was classified into.
METdataVector	vector with methylation values from the cancer samples.
NrComponents	number of components in this gene.
UseTrainedFlipOver	.
FlipOverState	.

Value

Corrected vectors with methylation states and classification.

METnormal

DNA methylation data from normal tissue from glioblastoma patients

Description

Normal tissue DNA methylation data of glioblastoma patients. These normal tissue samples were run on the same platform and are described in the publication referenced below.

Usage

```
data(METnormal)
```

Format

A numeric matrix with 14 rows (genes) and 4 columns (samples).

References

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predictOneGene	<i>The predictOneGene function</i>
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Description

Auxiliar function. Given a new vector of beta values, this function calculates a matrix with posterior prob of belonging to each mixture component (columns) for each new beta value (rows), and return the number of the mixture component with highest posterior probabilit

Usage

```
predictOneGene(newVector, mixtureModel)
```

Arguments

newVector	vector with new beta values
mixtureModel	beta mixture model object for the gene being evaluated.

Value

A matrix with predictions (indices of mixture component), driver genes in rows, new samples in columns

`Preprocess_CancerSite_Methylation27k`*The Preprocess_CancerSite_Methylation27k function*

Description

Internal. Pre-processes DNA methylation data from TCGA from Illymina 27k arrays.

Usage

```
Preprocess_CancerSite_Methylation27k(CancerSite, METdirectory,  
  MissingValueThreshold = 0.2)
```

Arguments

<code>CancerSite</code>	character of length 1 with TCGA cancer code.
<code>METdirectory</code>	character with directory where a folder for downloaded files will be created. Can be the object returned by the <code>Download_DNAMethylation</code> function.
<code>MissingValueThreshold</code>	threshold for removing samples or genes with missing values.

Value

List with pre processed methylation data for cancer and normal samples.

`Preprocess_CancerSite_Methylation450k`*The Preprocess_CancerSite_Methylation450k function*

Description

Internal. Pre-processes DNA methylation data from TCGA from Illymina 450k arrays.

Usage

```
Preprocess_CancerSite_Methylation450k(CancerSite, METdirectory,  
  MissingValueThreshold = 0.2)
```

Arguments

<code>CancerSite</code>	character of length 1 with TCGA cancer code.
<code>METdirectory</code>	character with directory where a folder for downloaded files will be created. Can be the object returned by the <code>Download_DNAMethylation</code> function.
<code>MissingValueThreshold</code>	threshold for removing samples or genes with missing values.

Value

List with pre processed methylation data for cancer and normal samples.

Preprocess_DNAmethylation

The Preprocess_DNAmethylation function

Description

Pre-processes DNA methylation data from TCGA.

Usage

```
Preprocess_DNAmethylation(CancerSite, METdirectories,  
  MissingValueThreshold = 0.2)
```

Arguments

CancerSite character of length 1 with TCGA cancer code.

METdirectories character vector with directories with the downloaded data. It can be the object returned by the Download_DNAmethylation function.

MissingValueThreshold
 threshold for removing samples or genes with missing values.

Details

Pre-process includes eliminating samples and genes with too many NAs, imputing NAs, and doing Batch correction. If there is both 27k and 450k data, and both data sets have more than 50 samples, we combine the data sets, by reducing the 450k data to the probes present in the 27k data, and bath correction is performed again to the combined data set. If there are samples with both 27k and 450k data, the 450k data is used and the 27k data is discarded, before the step mentioned above. If the 27k or the 450k data does not have more than 50 samples, we use the one with the greatest number of samples, we do not combine the data sets.

Value

List with the pre-processed data matrix for cancer and normal samples.

Examples

```
## Not run:  
  
# Optional register cluster to run in parallel  
library(doParallel)  
cl <- makeCluster(5)  
registerDoParallel(cl)
```

```

# Methylation data for ovarian cancer
cancerSite <- "OV"
targetDirectory <- paste0(getwd(), "/")

# Downloading methylation data
METdirectories <- Download_DNAMethylation(cancerSite, targetDirectory, TRUE)

# Processing methylation data
METProcessedData <- Preprocess_DNAMethylation(cancerSite, METdirectories)

# Saving methylation processed data
saveRDS(METProcessedData, file = paste0(targetDirectory, "MET_", cancerSite, "_Processed.rds"))

# Clustering methylation data
res <- ClusterProbes(METProcessedData[[1]], METProcessedData[[2]])

# Saving methylation clustered data
toSave <- list(METcancer = res[[1]], METnormal = res[[2]], ProbeMapping = res$ProbeMapping)
saveRDS(toSave, file = paste0(targetDirectory, "MET_", cancerSite, "_Clustered.rds"))

stopCluster(cl)

## End(Not run)

```

Preprocess_GeneExpression

The Preprocess_GeneExpression function

Description

Pre-processes gene expression data from TCGA.

Usage

```

Preprocess_GeneExpression(CancerSite, MAdirectories,
  MissingValueThresholdGene = 0.3, MissingValueThresholdSample = 0.1)

```

Arguments

CancerSite	character of length 1 with TCGA cancer code.
MAdirectories	character vector with directories with the downloaded data. It can be the object returned by the Download_DNAMethylation function.
MissingValueThresholdGene	threshold for missing values per gene. Genes with a percentage of NAs greater than this threshold are removed. Default is 0.3.
MissingValueThresholdSample	threshold for missing values per sample. Samples with a percentage of NAs greater than this threshold are removed. Default is 0.1.

Details

Pre-process includes eliminating samples and genes with too many NAs, imputing NAs, and doing Batch correction.

Value

List with the pre-processed data matrix for cancer and normal samples.

Examples

```
## Not run:

# Optional register cluster to run in parallel
library(doParallel)
cl <- makeCluster(5)
registerDoParallel(cl)

# Gene expression data for ovarian cancer
cancerSite <- "OV"
targetDirectory <- paste0(getwd(), "/")

# Downloading gene expression data
GEDirectories <- Download_GeneExpression(cancerSite, targetDirectory, TRUE)

# Processing gene expression data
GEProcessedData <- Preprocess_GeneExpression(cancerSite, GEDirectories)

# Saving gene expression processed data
saveRDS(GEProcessedData, file = paste0(targetDirectory, "GE_", cancerSite, "_Processed.rds"))

stopCluster(cl)

## End(Not run)
```

Preprocess_MAdata_Cancer

The Preprocess_MAdata_Cancer function

Description

Internal. Pre-process gene expression data for cancer samples.

Usage

```
Preprocess_MAdata_Cancer(CancerSite, Directory, File,
  MissingValueThresholdGene = 0.3, MissingValueThresholdSample = 0.1)
```

Arguments

CancerSite	TCGA code for the cancer site.
Directory	Directory.
File	File.
MissingValueThresholdGene	threshold for missing values per gene. Genes with a percentage of NAs greater than this threshold are removed. Default is 0.3.
MissingValueThresholdSample	threshold for missing values per sample. Samples with a percentage of NAs greater than this threshold are removed. Default is 0.1.

Value

The data matrix.

Preprocess_MAdata_Normal

The Preprocess_MAdata_Normal function

Description

Internal. Pre-process gene expression data for normal samples.

Usage

```
Preprocess_MAdata_Normal(CancerSite, Directory, File,
  MissingValueThresholdGene = 0.3, MissingValueThresholdSample = 0.1)
```

Arguments

CancerSite	TCGA code for the cancer site.
Directory	Directory.
File	File.
MissingValueThresholdGene	threshold for missing values per gene. Genes with a percentage of NAs greater than this threshold are removed. Default is 0.3.
MissingValueThresholdSample	threshold for missing values per sample. Samples with a percentage of NAs greater than this threshold are removed. Default is 0.1.

Value

The data matrix.

ProbeAnnotation	<i>ProbeAnnotation data set</i>
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Description

Data set with annotation from Illumina methylatin arrays mapping CpG sites to genes.

SNPprobes	<i>SNPprobes data set</i>
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Description

Vector with probes with SNPs.

TCGA_BatchCorrection_MolecularData	<i>The TCGA_BatchCorrection_MolecularData function</i>
------------------------------------	--

Description

Internal. Wrapper to perform batch correction.

Usage

TCGA_BatchCorrection_MolecularData(GEN_Data, BatchData, MinInBatch)

Arguments

- | | |
|------------|---|
| GEN_Data | matrix with data to be corrected for batch effects. |
| BatchData | Batch data. |
| MinInBatch | minimum number of samples per batch. |

Value

The corrected data matrix.

TCGA_GENERIC_BatchCorrection

The TCGA_GENERIC_BatchCorrection function

Description

Internal. Performs batch correction.

Usage

TCGA_GENERIC_BatchCorrection(GEN_Data, BatchData)

Arguments

GEN_Data	matrix with data to be corrected for batch effects.
BatchData	Batch data.

Value

The corrected data matrix.

TCGA_GENERIC_CheckBatchEffect

The TCGA_GENERIC_CheckBatchEffect function

Description

Internal. Checks if batch correction is needed.

Usage

TCGA_GENERIC_CheckBatchEffect(GEN_Data, BatchData)

Arguments

GEN_Data	matrix with data to be corrected for batch effects.
BatchData	Batch data.

Value

list with results.

`TCGA_GENERIC_CleanUpSampleNames`*The TCGA_GENERIC_CleanUpSampleNames function*

Description

Internal. Cleans the samples IDs into the 12 digit format and removes doubles.

Usage

```
TCGA_GENERIC_CleanUpSampleNames(GEN_Data, IDlength = 12)
```

Arguments

<code>GEN_Data</code>	data matrix.
<code>IDlength</code>	length of samples ID.

Value

data matrix with cleaned sample names.

`TCGA_GENERIC_GetSampleGroups`*The TCGA_GENERIC_GetSampleGroups function*

Description

Internal. Looks for the group of the samples (normal/cancer).

Usage

```
TCGA_GENERIC_GetSampleGroups(SampleNames)
```

Arguments

<code>SampleNames</code>	vector with sample names.
--------------------------	---------------------------

Value

a list.

`TCGA_GENERIC_LoadIlluminaMethylationData`*The TCGA_GENERIC_LoadIlluminaMethylationData function*

Description

Internal. Read in an illumina methylation file with the following format: header row with sample labels, 2nd header row with 4 columns per sample: beta-value, geneSymbol, chromosome and GenomicCoordinate. The first column has the probe names.

Usage

```
TCGA_GENERIC_LoadIlluminaMethylationData(Filename)
```

Arguments

Filename name of the file with the data.

Value

methylation data.

`TCGA_GENERIC_MergeData`*The TCGA_GENERIC_MergeData function*

Description

Internal.

Usage

```
TCGA_GENERIC_MergeData(NewIDListUnique, DataMatrix)
```

Arguments

NewIDListUnique unique rownames of data.

DataMatrix data matrix.

Value

data matrix.

`TCGA_GENERIC_MET_ClusterProbes_Helper_ClusterGenes_with_hclust`*The TCGA_GENERIC_MET_ClusterProbes_Helper_ClusterGenes_with_hclust function*

Description

Internal. Cluster probes into genes.

Usage

```
TCGA_GENERIC_MET_ClusterProbes_Helper_ClusterGenes_with_hclust(Gene,  
  ProbeAnnotation, MET_Cancer, MET_Normal = NULL, CorThreshold = 0.4)
```

Arguments

Gene	gene.
ProbeAnnotation	data set matching probes to genes.
MET_Cancer	data matrix for cancer samples.
MET_Normal	data matrix for normal samples.
CorThreshold	correlation threshold for cutting the clusters.

Value

List with the clustered data sets and the mapping between probes and genes.

`TCGA_Load_MolecularData`*The TCGA_Load_MolecularData function*

Description

Internal. Reads in gene expression data. Deletes samples and genes with more NAs than the respective thresholds. Imputes other NAs values.

Usage

```
TCGA_Load_MolecularData(Filename, MissingValueThresholdGene = 0.3,  
  MissingValueThresholdSample = 0.1)
```

Arguments

Filename name of the file with the data.

MissingValueThresholdGene threshold for missing values per gene. Genes with a percentage of NAs greater than this threshold are removed. Default is 0.3.

MissingValueThresholdSample threshold for missing values per sample. Samples with a percentage of NAs greater than this threshold are removed. Default is 0.1.

Value

gene expression data.

TCGA_Process_EstimateMissingValues

The TCGA_Process_EstimateMissingValues function

Description

Internal. Removes patients and genes with more missing values than the MissingValueThreshold, and imputes remaining missing values using Tibshirani's KNN method.

Usage

```
TCGA_Process_EstimateMissingValues(MET_Data, MissingValueThreshold = 0.2)
```

Arguments

MET_Data data matrix.

MissingValueThreshold threshold for removing samples and genes with too many missing values.

Value

the data set with imputed values and possibly some genes or samples deleted.

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