Package ‘ELMER’

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Title Inferring Regulatory Element Landscapes and Transcription Factor Networks Using Cancer Methylomes

Version 2.26.0

Maintainer Tiago Chedraoui Silva <tiagochst@gmail.com>

Description ELMER is designed to use DNA methylation and gene expression from a large number of samples to infer regulatory element landscape and transcription factor network in primary tissue.

Depends R (>= 3.4.0), ELMER.data (>= 2.9.3)

License GPL-3

LazyData true

VignetteBuilder knitr

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Author  Tiago Chedraoui Silva [aut, cre],
        Lijing Yao [aut],
        Simon Coetzee [aut],
        Nicole Gull [ctb],
        Hui Shen [ctb],
        Peter Laird [ctb],
        Peggy Farnham [aut],
        Dechen Li [ctb],
        Benjamin Berman [aut]

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addDistNearestTSS

**Description**

Calculate the distance between probe and gene TSS

**Usage**

```r
addDistNearestTSS(data, NearGenes, genome, met.platform, cores = 1)
```

**Arguments**

- `data`: A multi Assay Experiment with both DNA methylation and gene Expression objects
- `NearGenes`: A list or a data frame with the pairs gene probes
- `genome`: Which genome build will be used: hg38 (default) or hg19.
- `met.platform`: DNA methylation platform to retrieve data from: EPIC or 450K (default)
- `cores`: Number of cores to be used. Default: 1
addMutCol

Adds mutation information to MAE

Description

Adds mutation information to MAE

Usage

addMutCol(
  data,
  disease,
  genes,
  mutant_variant_classification = c("Frame_Shift_Del", "Frame_Shift_Ins",
                                   "Missense_Mutation", "Nonsense_Mutation", "Splice_Site", "In_Frame_Del",
                                   "In_Frame_Ins", "Translation_Start_Site", "Nonstop_Mutation")
)

Arguments

data MAE object
disease TCGA disease (LUSC, GBM, etc)
genes list of genes to add information
mutant_variant_classification

Examples

## Not run:
data <- ELMER:::getData("elmer.data.example") # Get data from ELMER.data
data <- ELMER:::addMutCol(data, "LUSC","TP53")

## End(Not run)
**calcDistNearestTSS**

*Calculate distance from region to nearest TSS*

**Description**

Idea: For a given region R linked to X genes G merge R with nearest TSS for G (multiple) this will increase nb of lines i.e R1 - G1 - TSS1 - DIST1 R1 - G1 - TSS2 - DIST2 To vectorize the code: make a granges from left and one from right and find distance collapse the results keeping min distance for equals values.

**Usage**

```r
calcDistNearestTSS(links, TRange, tssAnnot)
```

**Arguments**

- **links**: Links to calculate the distance
- **TRange**: Genomic coordinates for Target region
- **tssAnnot**: TSS annotation

**Author(s)**

Tiago C. Silva

**Examples**

```r
## Not run:
data <- ELMER:::getdata("elmer.data.example")
NearbyGenes <- GetNearGenes(
data = data,
probes = c("cg15924102", "cg24741609"),
umFlankingGenes = 20
)

NearbyGenes <- ELMER:::calcDistNearestTSS(  
  links = NearbyGenes,
tssAnnot = getTSS(genome = "hg38"),
  TRange = rowRanges(getMet(data))
)

## End(Not run)
```
## calculateEnrichment

*Calculate motif Enrichment*

**Description**

Calculates fisher exact test

**Usage**

```r
calculateEnrichment(foreground, background)
```

**Arguments**

- `foreground`: A `sparseMatrix` object in each 1 means the motif is found in a region, 0 not.
- `background`: A `sparseMatrix` object in each 1 means the motif is found in a region, 0 not.

**Examples**

```r
ground <- Matrix::Matrix(sample(0:1,size = 100,replace = TRUE),
nrow = 10, ncol = 10,sparse = TRUE)
rownames(foreground) <- paste0("region",1:10)
colnames(foreground) <- paste0("motif",1:10)
background <- Matrix::Matrix(sample(0:1,size = 100,replace = TRUE),
nrow = 10, ncol = 10,sparse = TRUE)
rownames(background) <- paste0("region",1:10)
colnames(background) <- paste0("motif",1:10)
calculateEnrichment(foreground,background)
```

## createBigWigDNAmetArray

*Create a bigwig file for IGV visualization of DNA methylation data (Array)*

**Description**

Create a bigwig for IGV visualization of DNA methylation data (Array)

**Usage**

```r
createBigWigDNAmetArray(
  data = NULL,
  genome = "hg38",
  met.platform = "450K",
  track.names = NULL,
  dir = "IGV_tracks"
)
```
createIGVtrack

Arguments

- **data**: A matrix
- **genome**: Which genome build will be used: hg38 (default) or hg19.
- **met.platform**: DNA methylation platform to retrieve data from: EPIC or 450K (default)
- **track.names**: Provide a list of track names (.bw) otherwise the default is the will be samples.bw
- **dir**: Which directory files will be saved

Author(s)

Tiago Chedraoui Silva (tiagochst at gmail.com)

Examples

```r
## Not run:
data <- assay(getMet(ELMER:::getdata("elmer.data.example")))
createBigWigDNAmetArray(data = data, met.platform = "450K", genome = "hg38")
## End(Not run)
```

createIGVtrack

Create a junction track for IGV visualization of interaction

Description

Create a junction track for IGV visualization of interaction

Usage

```r
createIGVtrack(
pairs,
met.platform = "450K",
genome = "hg38",
filename = "ELMER_interactions.bed",
color.track = "black",
track.name = "junctions",
gene.symbol = NULL,
all.tss = TRUE
)
```

Arguments

- **pairs**: A data frame output from getPairs function
- **met.platform**: DNA methylation platform to retrieve data from: EPIC or 450K (default)
- **genome**: Which genome build will be used: hg38 (default) or hg19.
- **filename**: Filename (".".bed")
createMAE

| color.track | A color for the track (i.e blue, red,#272E6A) |
| track.name | Track name |
| gene.symbol | Filter pairs to a single gene. |
| all.tss | A logical. If TRUE it will link probes to all TSS of a gene (transcript level), if FALSE it will link to the promoter region of a gene (gene level). |

Author(s)

Tiago Chedraoui Silva (tiagochst at gmail.com)

Examples

```r
## Not run:
data <- ELMER:::getdata("elmer.data.example")
nearGenes <- GetNearGenes(TRange=getMet(data)[c("cg00329272","cg10097755"),],
geneAnnot=getExp(data))
Hypo.pair <- get.pair(data=data,
nearGenes=nearGenes,
permu.size=5,
group.col = "definition",
group1 = "Primary solid Tumor",
group2 = "Solid Tissue Normal",
raw.pvalue = 0.2,
Pe = 0.2,
dir.out="./",
label= "hypo")
createIGVtrack(Hypo.pair,met.platform = "450K", genome = "hg38")
```

Description

This function will receive a gene expression and DNA methylation data objects and create a Multi Assay Experiment.

Usage

```r
createMAE(
    exp,
    met,
    colData,
    sampleMap,
    linearize.exp = FALSE,
    filter.probes = NULL,
    met.na.cut = 0.2,
)```
createMAE

```r
filter.genes = NULL,
met.platform = "450K",
genome = NULL,
save = TRUE,
save.filename,
TCGA = FALSE
```

### Arguments

- **exp**: A Summarized Experiment with one assay, or a matrix or path of rda file only containing the data. Rownames should be either Ensembl gene id (ensembl_gene_id) or gene symbol (external_gene_name).
- **met**: A Summarized Experiment with one assay containing beta-values, a matrix or path of rda file only containing the data.
- **colData**: A DataFrame or data.frame of the phenotype data for all participants. Must have column primary (sample ID).
- **sampleMap**: A DataFrame or data.frame of the matching samples and colnames of the gene expression and DNA methylation matrix. This should be used if your matrix have different columns names. This object must have following columns: assay ("DNA methylation" and "Gene expression"), primary (sample ID) and colname (names of the columns of the matrix).
- **linearize.exp**: Take log2(exp + 1) in order to linearize relation between methylation and expression.
- **filter.probes**: A GRanges object contains the coordinate of probes which locate within promoter regions or distal feature regions such as union enhancer from REMC and FANTOM5. See `get.feature.probe` function.
- **met.na.cut**: Define the percentage of NA that the line should have to remove the probes for humanmethylation platforms.
- **filter.genes**: List of genes ensemble ids to filter from object.
- **met.platform**: DNA methylation platform "450K" or "EPIC".
- **genome**: Which is the default genome to make gene information. Options hg19 and hg38.
- **save**: If TRUE, MAE object will be saved into a file named as the argument save.filename if this was set, otherwise as mae_genome_met.platform.rda.
- **save.filename**: Name of the rda file to save the object (must end in .rda).
- **TCGA**: A logical. FALSE indicate data is not from TCGA (FALSE is default). TRUE indicates data is from TCGA and sample section will automatically filled in.

### Value

A MultiAssayExperiment object


Examples

# NON TCGA example: matrices has different column names

gene.exp <- S4Vectors::DataFrame(
  sample1.exp = c("ENSG00000141510"=2.3,"ENSG00000171862"=5.4),
  sample2.exp = c("ENSG00000141510"=1.6,"ENSG00000171862"=2.3)
)

dna.met <- S4Vectors::DataFrame(
  sample1.met = c("cg14324200"=0.5,"cg23867494"=0.1),
  sample2.met = c("cg14324200"=0.3,"cg23867494"=0.9)
)
sample.info <- S4Vectors::DataFrame(
  primary = c("sample1","sample2"),
  sample.type = c("Normal","Tumor")
)
sampleMap <- S4Vectors::DataFrame(
  assay = c("Gene expression","DNA methylation","Gene expression","DNA methylation"),
  primary = c("sample1","sample1","sample2","sample2"),
  colname = c("sample1.exp","sample1.met","sample2.exp","sample2.met")
)

mae <- createMAE(
  exp = gene.exp,
  met = dna.met,
  sampleMap = sampleMap,
  met.platform = "450K",
  colData = sample.info,
  genome = "hg38"
)

# You can also use sample Mapping and Sample information tables from a tsv file
# You can use the createTSVTemplates function to create the tsv files
readr::write_tsv(as.data.frame(sampleMap), path = "sampleMap.tsv")
readr::write_tsv(as.data.frame(sample.info), path = "sample.info.tsv")

mae <- createMAE(
  exp = gene.exp,
  met = dna.met,
  sampleMap = "sampleMap.tsv",
  met.platform = "450K",
  colData = "sample.info.tsv",
  genome = "hg38"
)

# NON TCGA example: matrices has same column names

gene.exp <- S4Vectors::DataFrame(sample1 = c("ENSG00000141510"=2.3,"ENSG00000171862"=5.4),
  sample2 = c("ENSG00000141510"=1.6,"ENSG00000171862"=2.3))
dna.met <- S4Vectors::DataFrame(sample1 = c("cg14324200"=0.5,"cg23867494"=0.1),
  sample2 = c("cg14324200"=0.3,"cg23867494"=0.9))
sample.info <- S4Vectors::DataFrame(primary = c("sample1","sample2"),
  sample.type = c("Normal","Tumor"))
sampleMap <- S4Vectors::DataFrame(
  assay = c("Gene expression","DNA methylation","Gene expression","DNA methylation"),
  primary = c("sample1","sample1","sample2","sample2"),
  colname = c("sample1","sample1","sample2","sample2")
)

mae <- createMAE(
  exp = gene.exp,
  met = dna.met,
  sampleMap = sampleMap,
  met.platform = "450K",
  colData = sample.info,
  genome = "hg38"
)

## Not run:
# TCGA example using TCGAbiolinks
# Testing creating MultyAssayExperiment object
# Load library
library(TCGAbiolinks)
library(SummarizedExperiment)

samples <- c(
  "TCGA-BA-4074", "TCGA-BA-4075", "TCGA-BA-4077", "TCGA-BA-5149",
  "TCGA-UF-A7JK", "TCGA-UF-A7JS", "TCGA-UF-A7JT", "TCGA-UF-A7JV"
)

#1) Get gene expression matrix
query.exp <- GDCquery(
  project = "TCGA-HNSC",
  data.category = "Transcriptome Profiling",
  data.type = "Gene Expression Quantification",
  workflow.type = "STAR - Counts",
  barcode = samples
)

GDCdownload(query.exp)
exp.hg38 <- GDCprepare(query = query.exp)

# DNA Methylation
query.met <- GDCquery(
  project = "TCGA-HNSC",
  data.category = "DNA Methylation",
  data.type = "Methylation Beta Value",
  barcode = samples,
  platform = "Illumina Human Methylation 450"
)

GDCdownload(query.met)
met <- GDCprepare(query = query.met)
distal.enhancer <- get.feature.probe(
  genome = "hg19",
  met.platform = "450k"
mae.hg38 <- createMAE(
  exp = exp.hg38, met = met,
  TCGA = TRUE, genome = "hg38",
  filter.probes = distal.enhancer
)
values(getExp(mae.hg38))

# Considering it is TCGA and not SE
mae.hg19.test <- createMAE(
  exp = assay(exp.hg19), met = assay(met),
  TCGA = TRUE, genome = "hg19",
  filter.probes = distal.enhancer
)
mae.hg38 <- createMAE(
  exp = assay(exp.hg38),
  met = assay(met),
  TCGA = TRUE,
  genome = "hg38",
  filter.probes = distal.enhancer
)
values(getExp(mae.hg38))

# Considering it is not TCGA and SE
# DNA methylation and gene expression Objects should have same sample names in columns
not.tcga.exp <- exp.hg19
colnames(not.tcga.exp) <- substr(colnames(not.tcga.exp),1,15)
not.tcga.met <- met
colnames(not.tcga.met) <- substr(colnames(not.tcga.met),1,15)

phenotype.data <- data.frame(
  row.names = colnames(not.tcga.exp),
  primary = colnames(not.tcga.exp),
  samples = colnames(not.tcga.exp),
  group = c(rep("group1",4),rep("group2",4))
)
distal.enhancer <- get.feature.probe(genome = "hg19",met.platform = "450k")
mae.hg19 <- createMAE(
  exp = not.tcga.exp,
  met = not.tcga.met,
  TCGA = FALSE,
  filter.probes = distal.enhancer,
  genome = "hg19",
  colData = phenotype.data
)

## End(Not run)
createMotifRelevantTfs

Get family of transcription factors

Description

This will output a list each TF motif and TFs that binding the motifs. Multiple TFs may recognize a same motif such as TF family. The association between each motif familial and transcription factor was created using the HOCOMOCO[https://hocomoco11.autosome.org/human/mono?full=true] which TF structural families was created according to TFClass [@wingender2014tfclass] This data is stored as a list whose elements are motifs and contents for each element are TFs which recognize the same motif that is the name of the element. This data is used in function get.TFs in ELMER to identify the real regulator TF whose motif is enriched in a given set of probes and expression associate with average DNA methylation of these motif sites.

Usage

createMotifRelevantTfs(classification = "family")

Arguments

classification Select if we will use Family classification or sub-family

Value

A list of TFs and its family members

createSummaryDocument Create summary document for TCGA.pipe function

Description

This function will create a text file with the date of the last run, which analysis were performed, the values of the arguments so the user can keep track

Usage

createSummaryDocument(
    analysis = "all",
    argument.values = "defaults",
    genome = NULL,
    mae.path = NULL,
    mode = NULL,
    direction = NULL,
    group.col = NULL,
createTSVTemplates

Arguments

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<th>Description</th>
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</thead>
<tbody>
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<td>Which analysis were performed</td>
</tr>
<tr>
<td>argument.values</td>
<td>Other argument values changed</td>
</tr>
<tr>
<td>genome</td>
<td>Genome of reference hg38 and hg19</td>
</tr>
<tr>
<td>mae.path</td>
<td>Where mae is stored</td>
</tr>
<tr>
<td>mode</td>
<td>Mode &quot;supervised&quot; or &quot;unsupervised&quot; used in the analysis</td>
</tr>
<tr>
<td>direction</td>
<td>Hypo or hyper direction</td>
</tr>
<tr>
<td>group.col</td>
<td>Group col</td>
</tr>
<tr>
<td>group1</td>
<td>Group 1</td>
</tr>
<tr>
<td>group2</td>
<td>Group 2</td>
</tr>
<tr>
<td>results.path</td>
<td>Path where the results were saved</td>
</tr>
</tbody>
</table>

createTSVTemplates Create examples files for Sample mapping and information used in createMAE function

Description

This function will receive the DNA methylation and gene expression matrix and will create some examples of table for the argument colData and sampleMap used in createMae function.

Usage

createTSVTemplates(met, exp)

Arguments

<table>
<thead>
<tr>
<th></th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>met</td>
<td>DNA methylation matrix or Summarized Experiment</td>
</tr>
<tr>
<td>exp</td>
<td>Gene expression matrix or Summarized Experiment</td>
</tr>
</tbody>
</table>

Examples

gene.exp <- S4Vectors::DataFrame(sample1.exp = c("ENSG00000141510"=2.3,"ENSG00000171862"=5.4),
  sample2.exp = c("ENSG00000141510"=1.6,"ENSG00000171862"=2.3))
dna.met <- S4Vectors::DataFrame(sample1.met = c("cg14324200"=0.5,"cg23867494"=0.1),
  sample2.met = c("cg14324200"=0.3,"cg23867494"=0.9))
createTSVTemplates(met = dna.met, exp = gene.exp)
ELMER

**ELMER (Enhancer Linking by Methylation/Expression Relationships)**

**Description**

ELMER is designed to use DNA methylation and gene expression from a large number of samples to infer regulatory element landscape and transcription factor network in primary tissue.

**findMotifRegion**

*Use Hocomoco motif and homer to identify motifs in a given region*

**Description**

To find for each probe the known motif we will use HOMER software (http://homer.salk.edu/homer/). Homer and genome should be installed before this function is executed. Step: 1 - get DNA methylation probes annotation with the regions 2 - Make a bed file from it 3 - Execute section: Finding Instance of Specific Motifs from http://homer.salk.edu/homer/ngs/peakMotifs.html to the HOCOMOCO TF motifs Also, as HOMER is using more RAM than the available we will split the files in to 100k probes. Obs: for each probe we create a window of 500 bp (size 500) around it. This might lead to false positives, but will not have false negatives. The false positives will be removed latter with some statistical tests.

**Usage**

```r
findMotifRegion(
  regions,
  output.filename = "mapped_motifs_regions.txt",
  region.size = NULL,
  genome = "hg38",
  nstep = 10000,
  cores = 1
)
```

**Arguments**

- **regions**
  A GRanges object. Names will be used as the identifier.
- **output.filename**
  Final file name
- **region.size**
  If NULL the motif will be mapped to the region. If set a window around its center will be considered. For example if region.size is 500, then +-250bp round it will be searched.
- **genome**
  Homer genome (hg38, hg19)
- **nstep**
  Number of regions to evaluate in homer, the bigger, more memory it will use at each step.
- **cores**
  A integer which defines the number of cores to be used in parallel process. Default is 1: no parallel process.
get.diff.meth

Examples

## Not run:
# use the center of the region and +-250bp around it
gr0 <- GRanges(Rle(c("chr2", "chr2", "chr1", "chr3"), c(1, 3, 2, 4)),
               IRanges(1:10, width=10:1))
names(gr0) <- paste0("ID",c(1:10))
findMotifRegion(regions = gr0, region.size = 500, genome = "hg38", cores = 1)

# use the region size itself
gr1 <- GRanges(Rle(c("chr2", "chr2", "chr1", "chr3"), c(1, 3, 2, 4)),
               IRanges(1:10, width=sample(200:1000,10)))
names(gr1) <- paste0("ID",c(1:10))
findMotifRegion(regions = gr1, genome = "hg38", cores = 1)

## End(Not run)

get.diff.meth

Identify hypo/hyper-methylated CpG sites between two groups (i.e.
normal vs tumor samples, treated vs untreated).

Description

get.diff.meth applys one-way t-test to identify the CpG sites that are significantly hypo/hyper-
methyalated using proportional samples (defined by minSubgroupFrac option) from group 1 and
group 2. The P values will be adjusted by Benjamini-Hochberg method. Option pvalue and sig.dif
will be the criteria (cutoff) for selecting significant differentially methylated CpG sites. If save is
TURE, two getMethdiff.XX.csv files will be generated (see detail).

Usage

get.diff.meth(
data,
diff.dir = "hypo",
cores = 1,
mode = "unsupervised",
minSubgroupFrac = 0.2,
pvalue = 0.01,
group.col,
min.samples = 5,
group1,
group2,
test = t.test,
sig.dif = 0.3,
dir.out = "/",
save = TRUE
)
Arguments

data A multiAssayExperiment with DNA methylation and Gene Expression data. See createMAE function.

diff.dir A character can be "hypo", "hyper" or "both", showing differential methylation direction. It can be "hypo" which is only selecting hypomethylated probes (one tailed test); "hyper" which is only selecting hypermethylated probes (one tailed test); or "both" which are probes differenly methylated (two tailed test).

cores A integer which defines the number of cores to be used in parallel process. Default is 1: no parallel process.

mode A character. Can be "unsupervised" or "supervised". If "supervised", the minSubgroupFrac argument will be set to 1 to use all samples from both groups to find the differently methylated regions. The supervised mode should be used when all samples from both groups are considered homogenous (i.e. treated vs untreated, molecular subtype A vs molecular subtype B), while unsupervised mode should be used when there is at least one group with heterogenous samples (i.e tumor samples).

minSubgroupFrac A number ranging from 0 to 1, specifying the fraction of extreme samples from group 1 and group 2 that are used to identify the differential DNA methylation. The default is 0.2 because we typically want to be able to detect a specific (possibly unknown) molecular subtype among tumor; these subtypes often make up only a minority of samples, and 20% was chosen as a lower bound for the purposes of statistical power. If you are using pre-defined group labels, such as treated replicates vs. untreated replicated, use a value of 1.0 (Supervised mode)

pvalue A number specifies the significant P value (adjusted P value by BH) threshold Limit for selecting significant hypo/hyper-methylated probes. Default is 0.01 If pvalue is smaller than pvalue than it is considered significant.

group.col A column defining the groups of the sample. You can view the available columns using: colnames(MultiAssayExperiment::colData(data)).

min.samples Minimum number of samples to use in the analysis. Default 5. If you have 10 samples in one group, minSubgroupFrac is 0.2 this will give 2 samples in the lower quintile, but then 5 will be used.

group1 A group from group.col. ELMER will run group1 vs group2. That means, if direction is hyper, get probes hypermethylated in group 1 compared to group 2.

group2 A group from group.col. ELMER will run group1 vs group2. That means, if direction is hyper, get probes hypermethylated in group 1 compared to group 2.

test Statistical test to be used. Options: t.test (DEFAULT), wilcox.test

sig.dif A number specifies the smallest DNA methylation difference as a cutoff for selecting significant hypo/hyper-methylated probes. Default is 0.3.

dir.out A path specify the directory for outputs. Default is is current directory.

save A logic. When TRUE, two getMethdiff.XX.csv files will be generated (see detail)
get.enriched.motif

Details

save: When save is TRUE, function will generate two XX.csv files. The first one is named getMethdiff.hypo.probes.csv (or getMethdiff.hyper.probes.csv depends on diff.dir). The first file contains all statistic results for each probe. Based on this file, user can change different P value or sig.dir cutoff to select the significant results without redo the analysis. The second file is named getMethdiff.hypo.probes.significant.csv (or getMethdiff.hyper.probes.significant.csv depends on diff.dir). This file contains statistic results for the probes that pass the significant criteria (P value and sig.dir). When save is FALSE, a data frame R object will be generate which contains the same information with the second file.

Value

Statistics for all probes and significant hypo or hyper-methylated probes.

References


Examples

data <- ELMER:::getdata("elmer.data.example")
Hypo.probe <- get.diff.meth(data,
  diff.dir="hypo",
  group.col = "definition",
  group1 = "Primary solid Tumor",
  group2 = "Solid Tissue Normal",
  sig.dif = 0.1)  # get hypomethylated probes

Hyper.probe <- get.diff.meth(data,
  diff.dir="hyper",
  group.col = "definition",
  sig.dif = 0.1)  # get hypomethylated probes

get.enriched.motif

get.enriched.motif is a function make use of Probes.motif data from ELMER.data package to calculate the motif enrichment Odds Ratio and 95% confidence interval for a given set of probes using fisher test function, after performing the Fisher's exact test, the results for all transcription factors are corrected for multiple testing with the Benjamini-Hochberg procedure. If save is TURE, two output files will be saved: getMotif.XX.enriched.motifs.rda and getMotif.XX.motif.enrichment.csv (see detail).
Usage

get.enriched.motif(data, probes.motif, probes, min.motif.quality = "DS",
background.probes, pvalue = 0.05, lower.OR = 1.1, min.incidence = 10,
dir.out = "/", label = NULL, save = TRUE, plot.title="")

Arguments

data A multi Assay Experiment from createMAE function. If set and probes.motif/background
probes are missing this will be used to get this other two arguments correctly.
This argument is not require, you can set probes.motif and the background.probes
manually.

probes.motif A matrix contains motifs occurrence within probes regions. Probes.motif in
ELMER.data will be used if probes.motif is missing (detail see Probes.motif.hg19.450K
in ELMER.data).

probes A vector lists the name of probes to define the set of probes in which motif
enrichment OR and confidence interval will be calculated.

min.motif.quality
Minimum motif quality score to consider. Possible values: A, B, C, D, AS (A
and S), BS (A, B and S), CS (A, B, C and S), DS (all - default) Description: Each
PWM has a quality rating from A to D where A represents motifs with the high-
est confidence, and D motifs only weakly describe the pattern with a limited ap-
lications for quantitative analyses. Special S quality marks the single-box mo-
tifs (secondary motif). Source: http://hocomoco.autosome.ru/help#description_quality_score
full#sec-8

background.probes
A vector lists name of probes which are considered as background for mo-
tif.enrichment calculation (see detail).

pvalue FDR P-value cut off (default 0.05)

lower.OR A number specifies the smallest lower boundary of 95% confidence interval for
Odds Ratio. The motif with higher lower boudnary of 95% confidence interval
for Odds Ratio than the number are the significantly enriched motifs (detail see
reference).

min.incidence A non-negative integer specifies the minimum incidence of motif in the given
probes set. 10 is default.

dir.out A path. Specifies the directory for outputs. Default is current directory

label A character. Labels the outputs such as "hypo", "hyper"

save If save is TURE, two files will be saved: getMotif.XX.enriched.motifs.rda and
getMotif.XX.motif.enrichment.csv (see detail).


Details

background.probes: For enhancer study, it is better to use probes within distal enhancer probes as
background.probes. For promoter study, it is better to use probes within promoter regions as back-
ground.probes. Because enhancer and promoter have different CG content and harbors different
clusters of TFs motif.
save: if save is TRUE, two files will be save on the disk. The first file is getMotif.XX.motif.enrichment.csv (XX depends on option label). This file reports the Odds Ratio and 95% confidence interval for these Odds Ratios which pass the significant cutoff (lower.OR and min.incidence). The second file is getMotif.XX.enriched.motifs.rda (XX depends on option label). This file contains a list R object with enriched motifs as name and probes containing the enriched motif as contents. This object will be used in get.TFs function. if save is FALSE, the function will return a R object which is the same with second file.

Value

A list contains enriched motifs with the probes regions harboring the motif.
A list (R object) with enriched motifs as name and probes containing the enriched motif as contents. And hypo.motif.enrichment.pdf plot will be generated.

Author(s)

Lijing Yao (creator: lijingya@usc.edu)

References


Examples

```r
probes <- c("cg00329272","cg10097755","cg08928189","cg17153775","cg21156590", "cg19749688","cg12590404","cg24517858","cg0329272","cg0010107", "cg15386853","cg10097755","cg09247779","cg09181854","cg19371916")
data <- tryCatch(ELMER:::getdata("elmer.data.example"), error = function(e) {
  message(e)
data(elmer.data.example, envir = environment())
})
bg <- rownames(getMet(data))
data(Probes.motif.hg38.450K,package = "ELMER.data")
enriched.motif <- get.enriched.motif(
  probes.motif = Probes.motif.hg38.450K,
  probes = probes,
  background.probes = bg,
  pvalue = 1,
  min.incidence = 2,
  label = "hypo"
)
# If the MAE is set, the background and the probes.motif will
# be automatically set
enriched.motif <- get.enriched.motif(
  data = data,
  min.motif.quality = "DS",
  probes=probes,
  pvalue = 1,
  min.incidence=2,
  label="hypo"
```
get.feature.probe

Description

get.feature.probe is a function to select the probes falling into distal feature regions or promoter regions.

This function selects the probes on HM450K that either overlap distal biofeatures or TSS promoter.

Usage

get.feature.probe(
  feature = NULL,
  TSS,  
  genome = "hg38",  
  met.platform = "450K",  
  TSS.range = list(upstream = 2000, downstream = 2000),  
  promoter = FALSE,  
  rm.chr = NULL
)

Arguments

feature A GRange object containing biofeature coordinate such as enhancer coordinates. If NULL, only distal probes (2Kbp away from TSS) will be selected. feature option is only usable when promoter option is FALSE.

TSS A GRange object contains the transcription start sites. When promoter is FALSE, Union.TSS in ELMER.data will be used by default. When promoter is TRUE, UCSC gene TSS will be used as default (see detail). User can specify their own preference TSS annotation.

genome Which genome build will be used: hg38 (default) or hg19.

met.platform DNA methylation platform to retrieve data from: EPIC or 450K (default)

TSS.range A list specify how to define promoter regions. Default is upstream=2000bp and downstream=2000bp.

promoter A logical. If TRUE, function will output the promoter probes. If FALSE, function will output the distal probes overlapping with features. The default is FALSE.

rm.chr A vector of chromosome need to be remove from probes such as chrX chrY or chrM
Details

In order to get real distal probes, we use more comprehensive annotated TSS by both GENCODE and UCSC. However, to get probes within promoter regions need more accurate annotated TSS such as UCSC. Therefore, there are different settings for promoter and distal probe selection. But user can specify their own favorable TSS annotation. Then there won’t be any difference between promoter and distal probe selection. @return A GRanges object contains the coordinate of probes which locate within promoter regions or distal feature regions such as union enhancer from REMC and FANTOM5. @usage get.feature.probe( feature, TSS, TSS.range = list(upstream = 2000, downstream = 2000), promoter = FALSE, rm.chr = NULL )

Value

A GRange object containing probes that satisfy selecting critiria.

Examples

# get distal enhancer probe
## Not run:
Probe <- get.feature.probe()

## End(Not run)
# get promoter probes
## Not run:
Probe <- get.feature.probe(promoter=FALSE)

## End(Not run)
# get distal enhancer probe remove chrX chrY
Probe2 <- get.feature.probe(rm.chr=c("chrX", "chrY"))

Description

get.pair is a function to predict enhancer-gene linkages using associations between DNA methylation at enhancer CpG sites and expression of 20 nearby genes of the CpG sites (see reference). Two files will be saved if save is true: getPair.XX.all.pairs.statistic.csv and getPair.XX.pairs.significant.csv (see detail).

Usage

get.pair(data,
    nearGenes,
    minSubgroupFrac = 0.4,
    permu.size = 10000,
    permu.dir = NULL,
    raw.pvalue = 0.001,
    Pe = 0.001,
get.pair

mode = "unsupervised",
diff.dir = NULL,
dir.out = "./",
diffExp = FALSE,
group.col,
group1 = NULL,
group2 = NULL,
cores = 1,
correlation = "negative",
filter.probes = TRUE,
filter.portion = 0.3,
filter.percentage = 0.05,
label = NULL,
addDistNearestTSS = FALSE,
save = TRUE)

Arguments

data A multiAssayExperiment with DNA methylation and Gene Expression data. See createMAE function.
nearGenes Can be either a list containing output of GetNearGenes function or path of rda file containing output of GetNearGenes function.

minSubgroupFrac A number ranging from 0 to 1, specifying the fraction of extreme samples that define group U (unmethylated) and group M (methylated), which are used to link probes to genes. The default is 0.4 (the lowest quintile of samples is the U group and the highest quintile samples is the M group) because we typically want to be able to detect a specific (possibly unknown) molecular subtype among tumor; these subtypes often make up only a minority of samples, and 20% was chosen as a lower bound for the purposes of statistical power. If you are using pre-defined group labels, such as treated replicates vs. untreated replicated, use a value of 1.0 (Supervised mode).

permu.size A number specify the times of permutation used in the unsupervised mode. Default is 10000.

permu.dir A path where the output of permutation will be.

raw.pvalue A number specify the raw p-value cutoff for defining significant pairs. Default is 0.001. It will select the significant P value cutoff before calculating the empirical p-values.

Pe A number specify the empirical p-value cutoff for defining significant pairs. Default is 0.001

mode A character. Can be "unsupervised" or "supervised". If unsupervised is set the U (unmethylated) and M (methylated) groups will be selected among all samples based on methylation of each probe. Otherwise U group and M group will set as the samples of group1 or group2 as described below: If diff.dir is "hypo, U will be the group 1 and M the group2. If diff.dir is "hyper" M group will be the group1 and U the group2.
get.pair

diff.dir A character can be "hypo" or "hyper", showing differential methylation direction in group 1. It can be "hypo" which means the probes are hypomethylated in group1; "hyper" which means the probes are hypermethylated in group1; This argument is used only when mode is supervised and it should be the same value from get.diff.meth function.

dir.out A path specify the directory for outputs. Default is current directory.

diffExp A logic. Default is FALSE. If TRUE, t test will be applied to test whether putative target gene are differentially expressed between two groups.

group.col A column defining the groups of the sample. You can view the available columns using: colnames(MultiAssayExperiment::colData(data)).

group1 A group from group.col. ELMER will run group1 vs group2. That means, if direction is hyper, get probes hypermethylated in group 1 compared to group 2.

group2 A group from group.col. ELMER will run group1 vs group2. That means, if direction is hyper, get probes hypermethylated in group 1 compared to group 2.

cores A interger which defines number of core to be used in parallel process. Default is 1: don’t use parallel process.

correlation Type of correlation to evaluate (negative or positive). Negative (default) checks if hypomethylated region has a upregulated target gene. Positive checks if region hypermethylated has a upregulated target gene.

filter.probes Should filter probes by selecting only probes that have at least a certain number of samples below and above a certain cut-off. See preAssociationProbeFiltering function.

filter.portion A number specify the cut point to define binary methylation level for probe loci. Default is 0.3. When beta value is above 0.3, the probe is methylated and vice versa. For one probe, the percentage of methylated and unmethylated samples should be above filter.percentage value. Only used if filter.probes is TRUE. See preAssociationProbeFiltering function.

filter.percentage Minimum percentage of samples to be considered in methylated and unmethylated for the filter.portion option. Default 5%. Only used if filter.probes is TRUE. See preAssociationProbeFiltering function.

label A character labels the outputs.

addDistNearestTSS Calculated distance to the nearest TSS instead of gene distance. Having to calculate the distance to nearest TSS will take some time.

save Two files will be saved if save is true: getPair.XX.all.pairs.statistic.csv and getPair.XX.pairs.significant.csv (see detail).

Value

Statistics for all pairs and significant pairs

Author(s)

Lijing Yao (creator: lijingya@usc.edu) Tiago C Silva (maintainer: tiagochst@usp.br)
get.permu

**References**


**Examples**

```r
data <- ELMER::getdata("elmer.data.example")
nearGenes <- GetNearGenes(TRange=getMet(data)[c("cg00329272","cg10097755"),],
                         geneAnnot=getExp(data))
Hypo.pair <- get.pair(data=data,
                      nearGenes=nearGenes,
                      permu.size=5,
                      group.col = "definition",
                      group1 = "Primary solid Tumor",
                      group2 = "Solid Tissue Normal",
                      raw.pvalue = 0.2,
                      Pe = 0.2,
                      dir.out="./",
                      label= "hypo")
```

```r
Hypo.pair <- get.pair(data = data,
                      nearGenes = nearGenes,
                      permu.size = 5,
                      raw.pvalue = 0.2,
                      Pe = 0.2,
                      dir.out = "./",
                      label = "hypo")
```

---

**get.permu**

`get.permu` to generate permutation results for calculation of empirical P values for each enhancer-gene linkage.

**Description**

`get.permu` is a function to use the same statistic model to calculate random enhancer-gene pairs. Based on the permutation value, empirical P value can be calculated for the real enhancer-gene pair (see reference).

**Usage**

`get.permu(data,
          geneID,
          methy = NULL,
          unmethy = NULL,
          percentage = 0.2,`
get.permu

```r
glm.probes = NULL,
correlation = "negative",
permu.size = 10000,
permu.dir = NULL,
cores = 1)
```

**Arguments**

- `data`: A multiAssayExperiment with DNA methylation and Gene Expression data. See `createMAE` function.
- `geneID`: A vector lists the genes' ID.
- `methy`: Index of M (methylated) group.
- `unmethy`: Index of U (unmethylated) group.
- `percentage`: A number ranges from 0 to 1 specifying the percentage of samples of group 1 and group 2 groups used to link probes to genes. Default is 0.2.
- `rm.probes`: A vector lists the probes name.
- `correlation`: Type of correlation to identify. Default is negative: look for hypomethylation and increase target expression.
- `permu.size`: A number specify the times of permuation. Default is 10000.
- `permu.dir`: A path where the output of permuation will be.
- `cores`: A interger which defines number of core to be used in parallel process. Default is 1: don’t use parallel process.

**Value**

Permutations

**Note**

Permutation is the most time consuming step. It is recommended to use multiple cores for this step. Default permutation time is 1000 which may need 12 hrs by 4 cores. However 10,000 permutations is recommended to get high confidence results. But it may cost 2 days.

**Author(s)**

Lijing Yao (creator: lijingya@usc.edu) Tiago C Silva (maintainer: tiagochst@usp.br)

**References**

Examples

```r
data <- ELMER:::getdata("elmer.data.example")
permu <- get.permu(data = data,
    geneID = rownames(getExp(data)),
    rm.probes = c("cg00329272","cg10097755"),
    permu.size = 5)
```

---

**Get.Pvalue.p**

*Calculate empirical Pvalue*

---

**Description**

Calculate empirical Pvalue

**Usage**

```r
Get.Pvalue.p(U.matrix, permu)
```

**Arguments**

- **permu**: data frame of permutation. Output from .Stat.nonpara.permu

**Value**

A data frame with empirical Pvalue.

---

**get.tab**

*summarize MR TF as a binary table with 1 if TF was found in the analysis, 0 if not*

---

**Description**

summarize MR TF as a binary table with 1 if TF was found in the analysis, 0 if not

**Usage**

```r
get.tab(dir, classification, top = TRUE)
```

**Arguments**

- **dir**: Directory with ELMER results
- **classification**: Which columns to retrieve family or subfamily
- **top**: Consider only top 1 within each (sub)family
Examples

```r
# Not run:
dir.create("out")
dir.create("out2")
data <- tryCatch(
  ELMER:::getdata("elmer.data.example"),
  error = function(e) {
    message(e)
    data(elmer.data.example, envir = environment())
  })
enriched.motif <- list("P53_HUMAN.H11MO.1.A" = c("cg00329272", "cg10097755", "cg08928189",
             "cg17153775", "cg21156590", "cg19749688", "cg12590404",
             "cg24517858", "cg00329272", "cg09010107", "cg15386853",
             "cg10097755", "cg09247779", "cg09181054"))
TF <- get.TFs(data,
enriched.motif,
group.col = "definition",
group1 = "Primary solid Tumor",
group2 = "Solid Tissue Normal",
TFs = data.frame(
  external_gene_name=c("TP53","TP63","TP73"),
  ensembl_gene_id= c("ENSG00000141510",
                  "ENSG00000073282",
                  "ENSG00000078900"),
  stringsAsFactors = FALSE),
dir.out = "out",
label="hypo")
TF <- get.TFs(data,
enriched.motif,
group.col = "definition",
group1 = "Primary solid Tumor",
group2 = "Solid Tissue Normal",
TFs = data.frame(
  external_gene_name=c("TP53","TP63","TP73"),
  ensembl_gene_id= c("ENSG00000141510",
                  "ENSG00000073282",
                  "ENSG00000078900"),
  stringsAsFactors = FALSE),
dir.out = "out2",
label="hypo")
ta.family <- get.tab(dir = c("out","out2"), classification = "family")
ta.subfamily <- get.tab(dir = c("out","out2"), classification = "subfamily")
unlink("out")
unlink("out2")
```

## End(Not run)
**Description**

Code used to create matrix for MR TF heatmap

**Usage**

```r
get.tabs(dir, classification = "family", top = TRUE)
```

**Arguments**

- `dir`: Vector of directory with results
- `classification`: Consider family or subfamily
- `top`: Consider only top 1 within each (sub)family

**Examples**

```r
## Not run:
elmer.results <- dirname(
dir(path = "analysis",
    pattern = ".*\.hypo.pairs.significant\.csv",
    recursive = T,
    full.names = T,
    all.files = T))
tabs <- get.tabs(dir = elmer.results, classification = "subfamily")
## End(Not run)
```

---

**get.TFs**

*get.TFs to identify regulatory TFs.*

**Description**

get.TFs is a function to identify regulatory TFs based on motif analysis and association analysis between the probes containing a particular motif and expression of all known TFs. If save is true, two files will be saved: getTF.XX.significant.TFs.with.motif.summary.csv and getTF.hypo.TFs.with.motif.pvalue.rda (see detail).

**Usage**

```r
get.TFs(data,
enriched.motif,
TFs,
group.col,
group1,
group2,
mode = "unsupervised",
correlation = "negative",
diff.dir = NULL,
```
motif.relevant.TFs, minSubgroupFrac = 0.4, dir.out = "/",
label = NULL, save.plots = FALSE, cores = 1, topTFper = 0.05, save = TRUE)

Arguments

data A multiAssayExperiment with DNA methylation and Gene Expression data. See createMAE function.
enriched.motif A list containing output of get.enriched.motif function or a path of XX.rda file containing output of get.enriched.motif function.
TFs A data.frame containing TF GeneID and Symbol or a path of XX.csv file containing TF GeneID and Symbol. If missing, human.TF list will be used (human.TF data in ELMER.data). For detail information, refer the reference paper.
group.col A column defining the groups of the sample. You can view the available columns using: colnames(MultiAssayExperiment::colData(data)).
group1 A group from group.col. ELMER will run group1 vs group2. That means, if direction is hyper, get probes hypermethylated in group 1 compared to group 2.
group2 A group from group.col. ELMER will run group1 vs group2. That means, if direction is hyper, get probes hypermethylated in group 1 compared to group 2.
mode A character. Can be "unsupervised" or "supervised". If unsupervised is set the U (unmethylated) and M (methylated) groups will be selected among all samples based on methylation of each probe. Otherwise U group and M group will set as the samples of group1 or group2 as described below: If diff.dir is "hypo, U will be the group 1 and M the group2. If diff.dir is "hyper" M group will be the group1 and U the group2.
correlation Type of correlation to evaluate (negative or positive). Negative checks if hypomethylated is upregulated. Positive if hypermethylated is upregulated.
diff.dir A character can be "hypo" or "hyper", showing differential methylation direction in group 1. It can be "hypo" which means the probes are hypomethylated in group1; "hyper" which means the probes are hypermethylated in group1; This argument is used only when mode is supervised nad it should be the same value from get.diff.meth function.
motif.relevant.TFs A list containing motif as names and relevant TFs as contents for each list element or a path of XX.rda file containing a list as above. If missing, motif.relevant.TFs will be used (motif.relevant.TFs data in ELMER.data). For detail information, refer the reference paper.
minSubgroupFrac A number ranging from 0 to 1 specifying the percentage of samples used to create the groups U (unmethylated) and M (methylated) used to link probes to TF expression. Default is 0.4 (lowest quintile of all samples will be in the U group and the highest quintile of all samples in the M group).
**get.TFs**

**dir.out**  A path specifies the directory for outputs of get.pair function. Default is current directory

**label**  A character labels the outputs.

**save.plots**  Create TF ranking plots?

**cores**  A integer which defines the number of cores to be used in parallel process. Default is 1: no parallel process.

**topTFper**  Top ranked TF to be retrieved (default "0.05" - 5 percent)

**save**  A logic. If save is true, two files will be saved: getTF.XX.significant.TFs.with.motif.summary.csv and getTF.hypo.TFs.with.motif.pvalue.rda (see detail). If save is false, a data frame contains the same content with the first file.

**Details**

save: If save is true, two files will be saved. The first file is getTF.XX.significant.TFs.with.motif.summary.csv (XX depends on option label). This file contain the regulatory TF significantly associate with average DNA methylation at particular motif sites. The second file is getTF.hypo.TFs.with.motif.pvalue.rda (XX depends on option label). This file contains a matrix storing the statistic results for significant associations between TFs (row) and average DNA methylation at motifs (column). If save is false, a data frame which contains the same content with the first file will be reported.

**Value**

Potential responsible TFs will be reported in a dataframe with 4 columns:

- **motif**: the names of motif.
- **top.potential.TF.family**: the highest ranking upstream TFs which are known recognized the motif. First item in potential.TFs.family
- **top.potential.TF.subfamily**: the highest ranking upstream TFs which are known recognized the motif. First item in potential.TFs.subfamily
- **potential.TFs.family**: TFs which are within top $5\%$ list and are known recognized the motif (considering family classification).
- **potential.TFs.subfamily**: TFs which are within top $5\%$ list and are known recognized the motif (considering subfamily classification).
- **top_5percent**: all TFs which are within top $5\%$ list.

**Author(s)**

Lijing Yao (creator: lijingya@usc.edu) Tiago C Silva (maintainer: tiagochst@usp.br)

**References**

get450K

get450K to download HM40K DNA methylation data for certain cancer types from TCGA website. @description get450K is a function to download latest version of HM450K DNA methylation for all samples of certain cancer types from GDC website.

Examples

data <- tryCatch(
  ELMER:::getdata("elmer.data.example"),
  error = function(e) {
    message(e)
    data(elmer.data.example, envir = environment())
  })

enriched.motif <- list(
  "P53_HUMAN.H11MO.1.A" = c(
    "cg00329272", "cg10097755", "cg08928189",
    "cg17153775", "cg21156590", "cg19749688", "cg12590404",
    "cg24517858", "cg00329272", "cg09010107", "cg15386853",
    "cg10097755", "cg09247779", "cg09181054"
  )
)

TF <- get.TFs(
  data,
  enriched.motif,
  group.col = "definition",
  group1 = "Primary solid Tumor",
  group2 = "Solid Tissue Normal",
  TFs = data.frame(
    external_gene_name=c("TP53","TP63","TP73"),
    ensembl_gene_id = c(
      "ENSG00000141510",
      "ENSG00000073282",
      "ENSG00000078900"
    ),
    stringsAsFactors = FALSE
  ),
  label = "hypo"
)

# This case will use Uniprot database to get list of transcription factors
TF <- get.TFs(
  data,
  group.col = "definition",
  group1 = "Primary solid Tumor",
  group2 = "Solid Tissue Normal",
  enriched.motif,
  label = "hypo"
)
Description

get450K to download HM40K DNA methylation data for certain cancer types from TCGA website.

Usage

get450k(disease, basedir="./Data", filter=0.2, genome = "hg38")

Arguments

disease A character specifies the disease to download from TCGA such as BLCA

basedir A path. Shows where the data will be stored.

filter For each probe, the percentage of NA among the all the samples should smaller than filter.

genome Data aligned against which genome of reference. Options: "hg38" (default)

Value

Download all DNA methylation from HM450K level 3 data for the specified disease.

Description

getClinic is a function to download latest version of clinic data for all samples of certain cancer types from TCGA website.

Usage

getcClinic(disease, basedir = "./Data")

Arguments

disease A character specifies the disease to download from TCGA such as BLCA

basedir A path shows where the data will be stored.

Value

Download all clinic information for the specified disease.
getExp

Get Gene expression object from MAE

Description
Get Gene expression object from MAE

Usage
getExp(data)

Arguments
- data A multiAssayExperiment with DNA methylation and Gene Expression data. See createMAE function.

getExpSamples

Get Gene expression object samples from MAE

Description
Get Gene expression object samples from MAE

Usage
gerExpSamples(data)

Arguments
- data A multiAssayExperiment with DNA methylation and Gene Expression data. See createMAE function.

getGeneID

geneID to report gene id from symbol

Description
geneID to report gene id from symbol

Usage
geneID(data, symbol)
getMet

Arguments

data A multiAssayExperiment with DNA methylation and Gene Expression data. See createMAE function.
symbol A vector of characters which are gene symbols

Value

The gene ID for these gene symbols

Examples

data <- ELMER:::getdata("elmer.data.example")
getGeneID(data, symbol="ZNF697")

getMet

Get DNA methylation object from MAE

Description

Get DNA methylation object from MAE

Usage

gemet(data)

Arguments

data A multiAssayExperiment with DNA methylation and Gene Expression data. See createMAE function.

getMetSamples

Get DNA methylation object samples from MAE

Description

Get DNA methylation object samples from MAE

Usage

gemetSamples(data)

Arguments

data A multiAssayExperiment with DNA methylation and Gene Expression data. See createMAE function.
Description

GetNearGenes is a function to collect equal number of gene on each side of one locus. It can receive either multi Assay Experiment with both DNA methylation and gene Expression matrix and the names of probes to select nearby genes, or it can receive two granges objects TRange and geneAnnot.

Usage

GetNearGenes(
  data = NULL,
  probes = NULL,
  geneAnnot = NULL,
  TRange = NULL,
  numFlankingGenes = 20
)

Arguments

data  A multi Assay Experiment with both DNA methylation and gene Expression objects
probes Name of probes to get nearby genes (it should be rownames of the DNA methylation object in the data argument object)
geneAnnot A GRange object or Summarized Experiment object that contains coordinates of promoters for human genome.
TRange A GRange object or Summarized Experiment object that contains coordinates of a list of targets loci.
numFlankingGenes A number determines how many gene will be collected totally. Then the number divided by 2 is the number of genes collected from each side of targets (number should be even) Default to 20.

Value

A data frame of nearby genes and information: genes’ IDs, genes’ symbols, distance with target and side to which the gene locate to the target.

References

getRandomPairs

**Examples**

```r
geneAnnot <- getTSS(genome = "hg38")
probe <- GenomicRanges::GRanges(seqnames = c("chr1","chr2"),
range=IRanges::IRanges(start = c(16058489,236417627), end= c(16058489,236417627)),
name= c("cg18108049","cg17125141"))
names(probe) <- c("cg18108049","cg17125141")
NearbyGenes <- GetNearGenes(numFlankingGenes = 20,geneAnnot=geneAnnot,TRange=probe)
```

---

**Description**

This function will receive a pair gene probes and will return a random object with the following pattern, if a probe is linked to R1 and L3 genes the random pairs will be a random probes (a distal probe not in the input pairs) also linked to its R1 and L3 gene.

**Usage**

```r
getRandomPairs(pairs, genome = "hg38", met.platform = "450K", cores = 1)
```

**Arguments**

- **pairs**: A data frame with probe, gene and side information. See example below.
- **genome**: Which genome build will be used: hg38 (default) or hg19.
- **met.platform**: DNA methylation platform to retrieve data from: EPIC or 450K (default)
- **cores**: An integer which defines the number of cores to be used in parallel process. Default is 1: no parallel process.

**Value**

A data frame with the random linkages

**Examples**

```r
## Not run:
data <- ELMER:::getdata("elmer.data.example")
nearGenes <- GetNearGenes(TRange=getMet(data)[c("cg00329272","cg10097755"),],
geneAnnot=getExp(data))

pair <- get.pair(data = data,
group.col = "definition",
group1 = "Primary solid Tumor",
group2 = "Solid Tissue Normal",
mode = "supervised",
diff.dir = "hypo",
nearGenes = nearGenes,
permu.size = 5,
```
getRegionNearGenes

Identifies nearest genes to a region

Description

Auxiliary function for GetNearGenes. This will get the closest genes (n=numFlankingGenes) for a target region (TRange) based on a genome reference gene annotation (geneAnnot). If the transcript level annotation (tssAnnot) is provided, the distance will be updated to the distance to the nearest TSS.

Usage

getRegionNearGenes(
  TRange = NULL,
  numFlankingGenes = 20,
  geneAnnot = NULL,
  tssAnnot = NULL
)

Arguments

- **TRange**: A GRang3 object contains coordinate of targets.
- **numFlankingGenes**: A number determine how many genes will be collected from each
- **geneAnnot**: A GRang3 object contains gene coordinates of for human genome.
- **tssAnnot**: A GRang3 object contains tss coordinates of for human genome.

Value

A data frame of nearby genes and information: genes’ IDs, genes’ symbols,

Author(s)

Tiago C Silva (maintainer: tiagochst@usp.br)
getRNAseq

Examples

geneAnnot <- ELMER:::get.GRCh("hg38", as.granges = TRUE)
tssAnnot <- getTSS(genome = "hg38")
probe <- GenomicRanges::GRanges(seqnames = c("chr1", "chr2"),
range = IRanges::IRanges(start = c(16058489, 236417627), end = c(16058489, 236417627)),
name = c("cg18108049", "cg17125141"))
names(probe) <- c("cg18108049", "cg17125141")
NearbyGenes <- getRegionNearGenes(numFlankingGenes = 20,
  geneAnnot = geneAnnot,
  TRange = probe,
  tssAnnot = tssAnnot)

getRNAseq

getRNAseq to download all RNAseq data for a certain cancer type from TCGA.

Description

getRNAseq is a function to download RNAseq data for all samples of a certain cancer type from TCGA.

Usage

getRNAseq(disease, basedir = "./Data", genome = "hg38")

Arguments

disease A character specifies disease in TCGA such as BLCA
basedir Download all RNA seq level 3 data for the specified disease.
genome Data aligned against which genome of reference. Options: "hg38" (default)

Value

Download all RNA seq level 3 data for the specified disease.

getSymbol

getSymbol to report gene symbol from id

Description

getSymbol to report gene symbol from id

Usage

getSymbol(data, geneID)
getTCGA

Arguments

- **data**
  A multiAssayExperiment with DNA methylation and Gene Expression data. See `createMAE` function.

- **geneID**
  A character which is the ensembl_gene_id

Value

The gene symbol for input genes.

Examples

```r
data <- ELMER:::getdata("elmer.data.example")
getSymbol(data, geneID="ENSG00000143067")
```

Description

getTCGA is a function to download DNA methylation, RNA expression and clinic data for all samples of certain cancer type from TCGA website. And downloaded data will be transform to matrixes or data frame for further analysis.

Usage

```r
getTCGA(disease, Meth=TRUE, RNA=TRUE, Clinic=TRUE, basedir="./Data", genome = "hg38")
```

Arguments

- **disease**
  A character specifies the disease to download in TCGA such as BLCA

- **Meth**
  A logic if TRUE HM450K DNA methylation data will download.

- **RNA**
  A logic if TRUE RNA-seq Hiseq-V2 from TCGA level 3 will be download.

- **Clinic**
  A logic if TRUE clinic data will be download for that disease.

- **basedir**
  A path shows where the data will be stored.

- **genome**
  Data aligned against which genome of reference. Options: "hg38" (default)

Value

Download DNA methylation (HM450K)/RNAseq(HiseqV2)/Clinic data for the specified disease from TCGA.
getTF

Examples

    getTCGA(
        disease = "BRCA",
        Meth = FALSE,
        RNA = FALSE,
        Clinic = TRUE,
        basedir = tempdir(),
        genome = "hg38"
    )

getTF  Get human TF list from the UNiprot database

Description

This function gets the last version of human TF list from the UNiprot database

Usage

    getTF()

Value

A data frame with the ensemble gene id.

getTFBindingSites  Get MR TF binding regions inferred by ELMER

Description

Saves a bed file with the unmethylated probes (+-250bp) regions that was inferred to be bound by a
given TF

Usage

    getTFBindingSites(
        tf = NULL,
        results.dir = NULL,
        genome = "hg38",
        met.platform = "450K"
    )
**getTFtargets**

**Arguments**

- **tf**: TF name
- **results.dir**: path to the directory with the results (i.e. analysis/unsupervised/definition-Primary.solid.Tumor_vs_Solid.Tissue.Normal/hypo/)
- **genome**: Human genome (hg38, hg19)
- **met.platform**: DNA Methylation Array platform (EPIC, 450K)

**Examples**

```r
## Not run:
getTFBindingSites("HNF1A",
    results.dir = "analysis/unsupervised/group-Tumor_vs_Normal/hypo/"
)
## End(Not run)
```

**Description**

This function uses ELMER analysis results and summarizes the possible genes targets for each TF

**Usage**

```r
getTFtargets(
    pairs,
    enriched.motif,
    TF.result,
    dmc.analysis,
    mae,
    save = TRUE,
    dir.out = "./",
    classification = "family",
    cores = 1,
    label = NULL
)
```

**Arguments**

- **pairs**: Output of get.pairs function: dataframe or file path
- **enriched.motif**: List of probes for each enriched motif: list of file path. The file created by ELMER is getMotif..enriched.motifs.rda
- **TF.result**: Output get.TF function: dataframe or file path
- **dmc.analysis**: DMC results file or data frame
- **mae**: A multiAssayExperiment outputed from createMAE function
getTSS

save A logic. If save is true, a files will be saved: getTFTarget.XX.csv If save is false, only a data frame contains the same content with the first file.
dir.out A path specifies the directory for outputs of get.pair function. Default is current directory
classification use family or subfamily classification to consider potential TF
cores Number of cores to be used in parallel
label A character labels the outputs.

Examples

pairs <- data.frame(Probe = c("cg26992600","cg26992800","cg26992900"),
    Symbol = c("KEAP1","DSP","ATP86"))
enriched.motif <- list("FOXD3_HUMAN.H11MO.0.D"= c("cg26992800","cg26992900"))
TF.result <- data.frame(motif = c("FOXD3_HUMAN.H11MO.0.D"),
    potential.TF.family = c("TP63;TP73"))
getTFtargets(pairs,enriched.motif,TF.result)

## Not run:
getTFtargets("../LUAD_LUSC_analysis_hg38/hyper/getPair.hyper.pairs.significant.csv",
enriched.motif = "../LUAD_analysis_hg38/hyper/getMotif.hyper.enriched.motifs.rda",
TF.result = "../LUAD_analysis_hg38/hyper/getTF.hyper.significant.TFs.with.motif.summary.csv")

## End(Not run)

getTSS

getTSS to fetch GENCODE gene annotation (transcripts level) from Bioconductor package biomaRt If upstream and downstream are specified in TSS list, promoter regions of GENCODE gene will be generated.

Description

getTSS to fetch GENCODE gene annotation (transcripts level) from Bioconductor package biomaRt If upstream and downstream are specified in TSS list, promoter regions of GENCODE gene will be generated.

Usage

getTSS(genome = "hg38", TSS = list(upstream = NULL, downstream = NULL))

Arguments

genome Which genome build will be used: hg38 (default) or hg19.
TSS A list. Contains upstream and downstream like TSS=list(upstream, downstream). When upstream and downstream is specified, coordinates of promoter regions with gene annotation will be generated.
**Value**

GENCODE gene annotation if TSS is not specified. Coordinates of GENCODE gene promoter regions if TSS is specified.

**Author(s)**

Lijing Yao (maintainer: lijingya@usc.edu)

**Examples**

```r
# get GENCODE gene annotation (transcripts level)
## Not run:
getTSS <- getTSS()
getTSS <- getTSS(genome.build = "hg38", TSS=list(upstream=1000, downstream=1000))
## End(Not run)
```

**Description**

This heatmap will sort samples by their gene expression and show the DNA methylation levels of the paired probes to that gene. If no pairs are given, nearest probes will be selected. To use this function you MAE object (input data) will need all probes and not only the distal ones. This plot can be used to evaluate promoter, and intro, exons regions and closer distal probes of a gene to verify if their DNA methylation level is affecting the gene expression.

**Usage**

```r
heatmapGene(
  data,
  group.col,
  group1,
  group2,
  pairs,
  GeneSymbol,
  scatter.plot = FALSE,
  correlation.method = "pearson",
  correlation.table = FALSE,
  annotation.col = NULL,
  met.metadata = NULL,
  exp.metadata = NULL,
  dir.out = ".",
  filter.by.probe.annotation = TRUE,
  numFlankingGenes = 10,
)```
heatmapGene

width = 10,
height = 10,
scatter.plot.width = 10,
scatter.plot.height = 10,
filename = NULL
)

Arguments

data A MultiAssayExperiment with a DNA methylation SummarizedExperiment (all
probes) and a gene Expression SummarizedExperiment.
group.col A column from the sample matrix from the MultiAssayExperiment object. Ac-
cessed with colData(mae)
group1 A group from group.col. ELMER will run group1 vs group2. That means, if
direction is hyper, get probes hypermethylated in group 1 compared to group 2.
group2 A group from group.col. ELMER will run group1 vs group2. That means, if
direction is hyper, get probes hypermethylated in group 1 compared to group 2.
pairs List of probe and pair genes
GeneSymbol Gene Symbol
scatter.plot Plot scatter plots
correlation.method Correlation method: Pearson or spearman
correlation.table save table with spearman correlation analysis ?
annotation.col A vector of columns from the sample matrix from the MultiAssayExperiment
object. Accessed with colData(mae) to be added as annotation to the heatmap
met.metadata A vector of metdatada columns available in the DNA methylation GRanges to
should be added to the heatmap.
exp.metadata A vector of metdatada columns available in the Gene expression GRanges to
should be added to the heatmap.
dir.out Where to save the plots
filter.by.probe.annotation Filter probes to plot based on probes annotation
numFlankingGenes numFlankingGenes to plot.
width Figure width
height Figure height
scatter.plot.width Scatter plot width
scatter.plot.height Scatter plot height
filename File names (.pdf) to save the file (i.e. "plot.pdf"). If NULL return plot.
Value

A heatmap

Author(s)

Tiago Chedraoui Silva (tiagochst at gmail.com)

Examples

```r
## Not run:
data <- ELMER:::getdata("elmer.data.example")
group.col <- "subtype_Expression.Subtype"
group1 <- "classical"
group2 <- "secretory"
pairs <- data.frame(ID = c("cg15924102" ,"cg19403323" , "cg22396950" ),
                      GeneID = c("ENSG00000196878", "ENSG00000009790", "ENSG00000009790" ),
                      Symbol = c("TRAF3IP3","LAMB3","LAMB3"),
                      Side = c("R1","L1","R3"),
                      Distance = c(6017,168499,0),
                      stringsAsFactors = FALSE)
heatmapGene(data = data,
group.col = group.col,
group1 = group1,
group2 = group2,
pairs = pairs,
GeneSymbol = "LAMB3",
height = 5,
annotation.col = c("ethnicity","vital_status"),
filename = "heatmap.pdf")
\dontrun{
  heatmapGene(data = data,
group.col = group.col,
group1 = group1,
group2 = group2,
GeneSymbol = "ACP6",
annotation.col = c("ethnicity","vital_status"),
filename = "heatmap_closer_probes.pdf")
}
## End(Not run)
```

Description

Heatmap plot of pairs gene and probes anti-correlated
**Usage**

```r
heatmapPairs(
  data,        
group.col,    
group1,       
group2,       
pairs,        
subset = FALSE,
cluster.within.groups = TRUE,
plot.distNearestTSS = FALSE,
annotation.col = NULL,
met.metadata = NULL,
exp.metadata = NULL,
width = 10,    
height = 7,    
filename = NULL
)
```

**Arguments**

- **data**: A MultiAssayExperiment with a DNA methylation SummarizedExperiment (all probes) and a gene Expression SummarizedExperiment.
- **group.col**: A column from the sample matrix from the MultiAssayExperiment object. Accessed with `colData(mae)`
- **group1**: A group from `group.col`. ELMER will run group1 vs group2. That means, if direction is hyper, get probes hypermethylated in group 1 compared to group 2.
- **group2**: A group from `group.col`. ELMER will run group1 vs group2. That means, if direction is hyper, get probes hypermethylated in group 1 compared to group 2.
- **pairs**: List of probe and pair genes
- **subset**: Subset MAE object to keep only groups compared ?
- **cluster.within.groups**: Cluster columns based on the groups
- **plot.distNearestTSS**: Plot track with distNearestTSS ?
- **annotation.col**: A vector of columns from the sample matrix from the MultiAssayExperiment object. Accessed with `colData(mae)` to be added as annotation to the heatmap.
- **met.metadata**: A vector of metadata columns available in the DNA methylation GRanges to should be added to the heatmap.
- **exp.metadata**: A vector of metadata columns available in the Gene expression GRanges to should be added to the heatmap.
- **width**: Figure width
- **height**: Figure height
- **filename**: File names (.pdf) to save the file (i.e. "plot.pdf"). If NULL return plot.
Value
A heatmap

Author(s)
Tiago Chedraoui Silva (tiagochst at gmail.com)

Examples
```r
## Not run:
data <- ELMER:::getdata("elmer.data.example")
group.col <- "subtype_Expression.Subtype"
group1 <- "classical"
group2 <- "secretory"
pairs <- data.frame(Probe = c("cg15924102", "cg19403323", "cg22356959"),
                    GeneID = c("ENSG00000196878", "ENSG00000009790", "ENSG00000009790" ),
                    Symbol = c("TRAF3IP3", "LAMB3", "LAMB3"),
                    Distance = c(6017, 168499, 0),
                    Raw.p = c(0.001, 0.00001, 0.001),
                    Pe = c(0.001, 0.00001, 0.001))
heatmapPairs(
data = data, group.col = group.col,
group1 = group1, group2 = group2,
annotation.col = c("ethnicity", "vital_status", "age_at_diagnosis"),
pairs, filename = "heatmap.pdf",
height = 4, width = 11
)
## End(Not run)
```

Description
lable linear regression formula

Usage
```r
lm_eqn(df, Dep, Exp)
```

Arguments
- **df**
  A data.frame object contains two variables: dependent variable (Dep) and explanation variable (Exp).
- **Dep**
  A character specify dependent variable. The first column will be dependent variable as default.
- **Exp**
  A character specify explanation variable. The second column will be explanation variable as default.
**Value**

A linear regression formula

---

**Description**

`scatter.plot` is a function to plot various scatter plots between gene expression and DNA methylation. When `byPair` is specified, scatter plot for individual probe-gene pairs will be generated. When `byProbe` is specified, scatter plots for one probes with nearby 20 gene pairs will be generated. When `byTF` is specified, scatter plot for TF expression and average DNA methylation at certain motif sites will be generated.

**Usage**

```r
metBoxPlot(
  data,
  group.col,
  group1,
  group2,
  probe,
  min.samples = 5,
  minSubgroupFrac = 0.2,
  diff.dir = "hypo",
  legend.col = NULL,
  title = NULL,
  filename = NULL,
  save = TRUE
)
```

**Arguments**

- `data`: A multiAssayExperiment with DNA methylation and Gene Expression data. See `createMAE` function.
- `group.col`: A column defining the groups of the sample. You can view the available columns using: `colnames(MultiAssayExperiment::colData(data))`.
- `group1`: A group from `group.col`. ELMER will run group1 vs group2. That means, if direction is hyper, get probes hypermethylated in group 1 compared to group 2.
- `group2`: A group from `group.col`. ELMER will run group1 vs group2. That means, if direction is hyper, get probes hypermethylated in group 1 compared to group 2.
- `probe`: Character with probe name (i.e. "cg24517858")
- `min.samples`: Minimum number of samples to use in the analysis. Default 5. If you have 10 samples in one group, percentage is 0.2 this will give 2 samples in the lower quintile, but then 5 will be used.
motif.enrichment.plot

minSubgroupFrac

A number ranges from 0 to 1 specifying the percentage of samples from group1 and group2 that are used to identify the differential methylation. Default is 0.2 because we did not expect all cases to be from a single molecular subtype. But, if you are working with molecular subtypes please set it to 1.

diff.dir

A character can be "hypo" or "hyper", showing differential methylation direction. It can be "hypo" which is only selecting hypomethylated probes; "hyper" which is only selecting hypermethylated probes;

legend.col

legend title

title

plot title

filename

File names (.png) to save the file (i.e. "plot.png")

save

Save plot as PNG

Value

Box plot

Author(s)

Tiago Chedraoui Silva (tiagochst at gmail.com)

Examples

## Not run:

```r
data <- ELMER:::getdata("elmer.data.example")
group.col <- "subtype_Expression.Subtype"
group1 <- "classical"
group2 <- "secretory"
metBoxPlot(data,
    group.col = group.col,
    group1 = group1,
    group2 = group2,
    probe = "cg17898069",
    minSubgroupFrac = 0.2,
    diff.dir = "hypo")

## End(Not run)
```

motif.enrichment.plot

motif.enrichment.plot to plot bar plots showing motif enrichment ORs and 95% confidence interval for ORs

Description

motif.enrichment.plot to plot bar plots showing motif enrichment ORs and 95% confidence interval for ORs. Option motif.enrichment can be a data frame generated by `get.enriched.motif` or a path of XX.csv saved by the same function.
Usage

```
motif.enrichment.plot(motif.enrichment, 
  significant = NULL, 
  dir.out ="./", 
  save = TRUE, 
  label = NULL, 
  title = NULL, 
  width = 10, 
  height = NULL, 
  summary = FALSE)
```

Arguments

motif.enrichment

A data frame or a file path of get.enriched.motif output motif.enrichment.csv file.

significant

A list to select subset of motif. Default is NULL.

dir.out

A path specify the directory to which the figures will be saved. Current directory is default.

save

A logic. If true (default), figure will be saved to dir.out.

label

A character. Labels the outputs figure.

title

Plot title. Default: no title

width

Plot width

height

Plot height. If NULL a default value will be calculated

summary

Create a summary table along with the plot, it is necessary to add two new columns to object (NumOfProbes and PercentageOfProbes)

Details

motif.enrichment If input data.frame object, it should contain "motif", "OR", "lowerOR", "upperOR" columns. motif specifies name of motif; OR specifies Odds Ratio, lowerOR specifies lower boundary of OR (95 upperOR specifies upper boundary of OR(95

significant A list used to select subset of motif.enrichment by the cutoff of OR, lowerOR, upperOR. significant=list(OR=1). More than one cutoff can be specified such as significant = list(OR=1, lowerOR=1,upperOR=4)

Value

A figure shows the enrichment level for selected motifs.

Author(s)

Lijing Yao (creator: lijingya@usc.edu)
References


Examples

```r
motif.enrichment <- data.frame(motif = c("TP53", "NR3C1", "E2F1", "EBF1", "RFX5", "ZNF143", "CTCF"),
                              OR = c(19.33, 4.83, 1, 4.18, 3.67, 3.03, 2.49),
                              lowerOR = c(10, 3.1, 1.09, 1.91, 1.5, 0.82),
                              upperOR = c(23, 5, 6, 5, 5),
                              stringsAsFactors = FALSE)

motif.enrichment.plot(motif.enrichment = motif.enrichment,
                       significant = list(OR = 3),
                       label = "hypo", save = FALSE)

motif.enrichment.plot(motif.enrichment = motif.enrichment,
                       significant = list(OR = 3),
                       label = "hypo",
                       title = "OR for paired probes hypomethylated in Mutant vs WT",
                       save = FALSE)

motif.enrichment <- data.frame(motif = c("TP53", "NR3C1", "E2F1", "EBF1", "RFX5", "ZNF143", "CTCF"),
                               OR = c(19.33, 4.83, 1, 4.18, 3.67, 3.03, 2.49),
                               lowerOR = c(10, 3.1, 1.09, 1.91, 1.5, 0.82),
                               upperOR = c(23, 5, 6, 5, 5),
                               NumOfProbes = c(23, 5, 6, 5, 5),
                               PercentageOfProbes = c(0.23, 0.05, 0.03, 0.07, 0.06, 0.05, 0.05),
                               stringsAsFactors=FALSE)

motif.enrichment.plot(motif.enrichment = motif.enrichment,
                       significant = list(OR = 3),
                       label = "hypo", save = FALSE)

motif.enrichment.plot(motif.enrichment = motif.enrichment,
                       significant = list(OR = 3),
                       label = "hypo",
                       summary = TRUE,
                       title = "OR for paired probes hypomethylated in Mutant vs WT",
                       save = TRUE)
```

Description

This function has some filters to the DNA methylation data in each it selects probes to avoid correlations due to non-cancer contamination and for additional stringency.

- Filter 1: We usually call locus unmethylated when the methylation value < 0.3 and methylated when the methylation value > 0.3. Therefore Meth_B is the percentage of methylation value > K. Basically, this step will make sure we have at least a percentage of beta values lesser than K and n percentage of beta values greater K. For example, if percentage is 5%, the number of
samples 100 and $K = 0.3$, this filter will select probes that we have at least 5 (5% of 100%) samples have beta values $> 0.3$ and at least 5 samples have beta values $< 0.3$. This filter is importante as true promoters and enhancers usually have a pretty low value (of course purity can screw that up). we often see lots of PMD probes across the genome with intermediate values like 0.4. Choosing a value of 0.3 will certainly give some false negatives, but not compared to the number of false positives we thought we might get without this filter.

Usage

```r
preAssociationProbeFiltering(data, K = 0.3, percentage = 0.05)
```

Arguments

- `data`: A MultiAssayExperiment with a DNA methylation matrix or a DNA methylation matrix
- `K`: Cut off to consider probes as methylated or unmethylated. Default: 0.3
- `percentage`: The percentage of samples we should have at least considered as methylated and unmethylated

Value

An object with the same class, but with the probes removed.

References


Examples

```r
c random.probe <- runif(100, 0, 1)
c bias_l.probe <- runif(100, 0, 0.3)
c bias.g.probe <- runif(100, 0.3, 1)
c met <- rbind(random.probe, bias_l.probe, bias.g.probe)
c met <- preAssociationProbeFiltering(data = met, K = 0.3, percentage = 0.05)
c met <- rbind(random.probe, random.probe, random.probe)
c met <- preAssociationProbeFiltering(met, K = 0.3, percentage = 0.05)
c data <- ELMER::getdata("elmer.data.example") # Get data from ELMER.data
c data <- preAssociationProbeFiltering(data, K = 0.3, percentage = 0.05)

c cg24741609 <- runif(100, 0, 1)
c cg17468663 <- runif(100, 0, 0.3)
c cg14036402 <- runif(100, 0.3, 1)
c met <- rbind(cg24741609, cg14036402, cg17468663)
c colnames(met) <- paste("sample", 1:100)
c exp <- met

c rownames(exp) <- c("ENSG00000141510", "ENSG00000171862", "ENSG00000171863")
c sample.info <- S4Vectors::DataFrame(primary = paste("sample", 1:100),
                   sample.type = rep(c("Normal", "Tumor"), 50))
c rownames(sample.info) <- colnames(exp)
```
mae <- createMAE(exp = exp, met = met, colData = sample.info, genome = "hg38")
mae <- preAssociationProbeFiltering(mae, K = 0.3, percentage = 0.05)

---

promoterMeth

*promoterMeth to calculate associations of gene expression with DNA methylation at promoter regions*

---

**Description**

promoterMeth is a function to calculate associations of gene expression with DNA methylation at promoter regions.

**Usage**

```r
promoterMeth(data, sig.pvalue = 0.01, minSubgroupFrac = 0.4,
             upstream = 200, downstream = 2000, save = TRUE, cores = 1)
```

**Arguments**

- `data`: A Multi Assay Experiment object with DNA methylation and gene expression Summarized Experiment objects
- `sig.pvalue`: A number specifies significant cutoff for gene silenced by promoter methylation. Default is 0.01. P value is raw P value without adjustment.
- `minSubgroupFrac`: A number ranging from 0 to 1 specifying the percentage of samples used to create the groups U (unmethylated) and M (methylated) used to link probes to genes. Default is 0.4 (lowest quintile of all samples will be in the U group and the highest quintile of all samples in the M group).
- `upstream`: Number of bp upstream of TSS to consider as promoter region
- `downstream`: Number of bp downstream of TSS to consider as promoter region
- `save`: A logic. If it is true, the result will be saved.
- `cores`: Number of cores to be used in paralellization. Default 1 (no paralellization)

**Details**

- promoterMeth

**Value**

A data frame contains genes whose expression significantly anti-correlated with promoter methylation.
## Not run:
```r
data(elmer.data.example.promoter)
Gene.promoter <- promoterMeth(mae.promoter)
```
## End(Not run)

---

**render_report**

*Build report for TCGA.pipe function*

### Description

Build HTML report

### Usage

```r
render_report(
  title = "Report",
  mae.file, 
  group.col, 
  group1, 
  group2, 
  direction, 
  dir.out, 
  genome = "hg38", 
  mode = "supervised", 
  minSubgroupFrac = 0.2, 
  minMetdiff = 0.3, 
  metfdr = 0.01, 
  permu = 10000, 
  rawpval = 0.01, 
  pe = 0.01, 
  nprobes = 10, 
  lower.OR = 1.1, 
  out_file = file.path(getwd(), "report.html"), 
  funcivar = FALSE 
)
```

### Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>title</td>
<td>HTML report title</td>
</tr>
<tr>
<td>mae.file</td>
<td>Absolute path to the mae used in the analysis (.rda or .rds)</td>
</tr>
<tr>
<td>group.col</td>
<td>Group col</td>
</tr>
<tr>
<td>group1</td>
<td>Group 1</td>
</tr>
<tr>
<td>group2</td>
<td>Group 2</td>
</tr>
<tr>
<td>direction</td>
<td>direction used in the analysis</td>
</tr>
</tbody>
</table>
Examples

## Not run:
render_report(
  group.col = "TN",
  group1 = "Tumor",
  group2 = "Normal",
  dir.out = "~/paper_elmer/Result/BRCA/TN_Tumor_vs_Normal/hypo/",
  direction = "hypo",
  mae.file = "~/paper_elmer/Result/BRCA/BRCA_mae_hg38.rda"
)

## End(Not run)

scatter

Description

scatter

Usage

scatter(
  meth,
  exp,
  legend.title = "Legend",
  category = NULL,
  xlab = NULL,
  ylab = NULL,
scatter.plot

```r
ylim = NULL,
dots.size = 0.9,
title = NULL,
correlation = FALSE,
correlation.text.size = 3,
color.value = NULL,
lm_line = FALSE
```

**Arguments**

- `meth`: A vector of number.
- `exp`: A vector of number or matrix with sample in column and gene in rows.
- `legend.title`: Plot legend title
- `category`: A vector of sample labels.
- `xlab`: A character specify the title of x axis.
- `ylab`: A character specify the title of y axis.
- `ylim`: y-axis limit i.e. c(0,25)
- `dots.size`: Control dots size
- `title`: A character specify the figure title.
- `correlation`: Show spearman correlation values
- `correlation.text.size`: Correlation values
- `color.value`: A vector specify the color of each category, such as
- `lm_line`: A logic. If it is TRUE, regression line will be added to the graph.

**Value**

A ggplot figure object

---

**scatter.plot**

`scatter.plot` to plot scatter plots between gene expression and DNA methylation.

**Description**

`scatter.plot` is a function to plot various scatter plots between gene expression and DNA methylation. When byPair is specified, scatter plot for individual probe-gene pairs will be generated. When byProbe is specified, scatter plots for one probes with nearby 20 gene pairs will be generated. When byTF is specified, scatter plot for TF expression and average DNA methylation at certain motif sites will be generated.
Usage

scatter.plot(data,
             byPair = list(probe = c(), gene = c()),
             byProbe = list(probe = c(), numFlankingGenes = 20),
             byTF = list(TF = c(), probe = c()),
             category = NULL,
             ylim = NULL,
             dots.size = 0.9,
             correlation = FALSE,
             width = 7,
             height = 6,
             dir.out = "./",
             save = TRUE, ...)

Arguments

data A multiAssayExperiment with DNA methylation and Gene Expression data. See createMAE function.
byPair A list: byPair = list(probe = c(), gene = c()); probe contains a vector of probes’ name and gene contains a vector of gene ID. The length of probe should be the same with length of gene. Output see numFlankingGenes.
byProbe A list byProbe = list(probe = c(), geneNum = 20); probe contains a vector of probes’ name and geneNum specify the number of gene near the probes will ploted. 20 is default for numFlankingGenes. Output see detail.
byTF A list byTF = list(TF = c(), probe = c()); TF contains a vector of TF’s symbol and probe contains the a vector of probes’ name. Output see detail.
category A vector labels subtype of samples or a character which is the column name in the colData(data) in the multiAssayExperiment object. Once specified, samples will label different color. The color can be customized by using color.value.
ylim y-axis limit i.e. c(0,25)
dots.size Control dots size
correlation Add pearson correlation values to the plot
width PDF width
height PDF height
dir.out A path specify the directory to which the figures will be saved. Current directory is default.
save A logic. If true, figure will be saved to dir.out.
... color.value, lm_line in scatter function

Details

byPair The output will be scatter plot for individual pairs.
byProbe The output will be scatter plot for the probe and nearby genes.
byTF The output will be scatter plot for the TFs and the average DNA methylation at the probes set specified in byTF list.
**schematic.plot**

### Value

Scatter plots.

### Author(s)

Lijing Yao (maintainer: lijingya@usc.edu)

### Examples

```r
data <- ELMER:::getdata("elmer.data.example")
schematic.plot(data,
   byProbe=list(probe=c("cg19403323"),numFlankingGenes=20),
   category="definition", save=FALSE)
schematic.plot(data,byProbe=list(probe=c("cg19403323"),numFlankingGenes=20),
   category="definition", save=TRUE) ## save to pdf
# b. generate one probe-gene pair
schematic.plot(data,byPair=list(probe=c("cg19403323"),gene=c("ENSG00000143322")),
   category="definition", save=FALSE, lm_line=TRUE)
```

---

**schematic.plot**  
schematic.plot to plot schematic plots showing the locations of genes and probes.

---

### Description

schematic.plot is a function to plot schematic plots showing the locations of genes and probes.

### Usage

```r
schematic.plot(data,
   group.col = NULL,
   group1 = NULL,
   group2 = NULL,
   pair,
   byProbe,
   byGeneID,
   byCoordinate=list(chr=c(), start=c(), end=c(),
   statehub.tracks,
   dir.out="/",
   save=TRUE,...)
```

### Arguments

- **data**  
  A Multi Assay Experiment object with DNA methylation and gene expression Summarized Experiment objects

- **group.col**  
  A column defining the groups of the sample. You can view the available columns using: colnames(MultiAssayExperiment::colData(data)).
group1 A group from group.col. ELMER will run group1 vs group2. That means, if direction is hyper, get probes hypermethylated in group 1 compared to group 2.

group2 A group from group.col. ELMER will run group1 vs group2. That means, if direction is hyper, get probes hypermethylated in group 1 compared to group 2.

pair A data frame with three columns: Probe, Gene ID (Ensemble gene ID) and Pe (empirical p-value). This is the output of get.pair function.

byProbe A vector of probe names
byGeneID A vector of gene ID
byCoordinate A list contains chr, start and end. byCoordinate=list(chr=c(), start=c(), end=c()).

Details

byProbes: When a vector of probes’ name are provided, function will produce schematic plots for each individual probes. The schematic plot contains probe, nearby 20 (or the number of gene user specified.) genes and the significantly linked gene to the probe.

byGene: When a vector of gene ID are provided, function will produce schematic plots for each individual genes. The schematic plot contains the gene and all the significantly linked probes.

byCoordinate: When a genomic coordinate is provided, function will produce a schematic plot for this coordinate. The schematic plot contains all genes and significantly linked probes in the range and the significant links.

Examples

data <- ELMER:::getdata("elmer.data.example")
pair <- data.frame(Probe = c("cg19403323", "cg19403323", "cg26403223"),
                   GeneID = c("ENSG00000196878", "ENSG00000009790", "ENSG00000009790" ),
                   Symbol = c("TRAF3IP3", "LAMB3", "LAMB3"),
                   Raw.p =c(0.001,0.00001,0.001),
                   Pe = c(0.001,0.00001,0.001))
schematic.plot(data,
               group.col = "definition",
               group1 = "Primary solid Tumor",
               group2 = "Solid Tissue Normal",
               pair = pair,
               byProbe = "cg19403323")
schematic.plot(data,
               group.col = "definition",
               group1 = "Primary solid Tumor",
               group2 = "Solid Tissue Normal",
               pair = pair,
               byGeneID = "ENSG00000009790")
schematic.plot(data,
    group.col = "definition",
    group1 = "Primary solid Tumor",
    group2 = "Solid Tissue Normal",
    pair = pair,
    byCoordinate = list(chr="chr1", start = 209000000, end = 209960000))
## Not run:
schematic.plot(data,
    group.col = "definition",
    group1 = "Primary solid Tumor",
    group2 = "Solid Tissue Normal",
    pair = pair,
    byProbe = "cg19403323",
    statehub.tracks = "hg38/ENCODE/mcf-7.16mark.segmentation.bed")
## End(Not run)

---

Stat.diff.meth  

Stat.diff.meth

Description

Stat.diff.meth

Usage

Stat.diff.meth(
    meth, 
    groups, 
    group1, 
    group2, 
    test = t.test, 
    min.samples = 5, 
    percentage = 0.2, 
    Top.m = NULL
)

Arguments

meth  A matrix contain DNA methylation data.
groups  A vector of category of samples.
group1  Group 1 label in groups vector
group2  Group 2 label in groups vector
test  A function specify which statistic test will be used.
min.samples  Minimum number of samples to use in the analysis. Default 5. If you have 10 samples in one group, percentage is 0.2 this will give 2 samples in the lower quintile, but then 5 will be used.
percentage  A number specify the percentage of normal and tumor samples used in the test.

Top.m  A logic. If to identify hypomethylated probe Top.m should be FALSE. hyper-methylated probe is TRUE.

Value

Statistic test results to identify differentially methylated probes.

Stat.nonpara  \textit{U test (non parameter test) for permutation. This is one probe vs nearby gene which is good for computing each probes for nearby genes.}

Description

\textit{U test (non parameter test) for permutation. This is one probe vs nearby gene which is good for computing each probes for nearby genes.}

Usage

\begin{verbatim}
Stat.nonpara(
    Probe,
    NearGenes,
    Top = NULL,
    correlation = "negative",
    unmethy = NULL,
    methy = NULL,
    Meths = Meths,
    Exps = Exps
)
\end{verbatim}

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Probe</td>
<td>A character of name of Probe in array.</td>
</tr>
<tr>
<td>NearGenes</td>
<td>A list of nearby gene for each probe which is output of GetNearGenes function.</td>
</tr>
<tr>
<td>Top</td>
<td>A number determines the percentage of top methylated/unmethylated samples. Only used if unmethy and methy are not set.</td>
</tr>
<tr>
<td>correlation</td>
<td>Type of correlation to evaluate (negative or positive). Negative (default) checks if hypomethylated region has a upregulated target gene. Positive checks if region hypermethylated has a upregulated target gene.</td>
</tr>
<tr>
<td>unmethy</td>
<td>Index of U (unmethylated) group.</td>
</tr>
<tr>
<td>methy</td>
<td>Index of M (methylated) group.</td>
</tr>
<tr>
<td>Meths</td>
<td>A matrix contains methylation for each probe (row) and each sample (column).</td>
</tr>
<tr>
<td>Exps</td>
<td>A matrix contains Expression for each gene (row) and each sample (column).</td>
</tr>
</tbody>
</table>
**Value**

U test results

---

**Description**

Stat.nonpara.permu

**Usage**

Stat.nonpara.permu(
   Probe,
   Gene,
   Top = 0.2,
   correlation = "negative",
   unmethy = NULL,
   methy = NULL,
   Meths = Meths,
   Exps = Exps
)

**Arguments**

- **Probe**: A character of name of Probe in array.
- **Gene**: A vector of gene ID.
- **Top**: A number determines the percentage of top methylated/unmethylated samples. Only used if unmethy and methy are not set.
- **correlation**: Type of correlation to evaluate (negative or positive). Negative (default) checks if hypomethylated region has a upregulated target gene. Positive checks if region hypermethylated has a upregulated target gene.
- **unmethy**: Index of U (unmethylated) group.
- **methy**: Index of M (methylated) group.
- **Meths**: A matrix contains methylation for each probe (row) and each sample (column).
- **Exps**: A matrix contains Expression for each gene (row) and each sample (column).

**Value**

U test results
summarizeTF  

**Make MR TF binary table**

**Description**

This function uses ELMER analysis results and summarizes the MR TF identified in each analysis.

**Usage**

```r
summarizeTF(files = NULL, path = NULL, classification = "family", top = FALSE)
```

**Arguments**

- `files`: Output of get.pairs function: dataframe or file path.
- `path`: Directory path with the ELMER results. Files with the following pattern will be selected: TF.*with.motif.summary.csv.
- `classification`: Consider subfamily or family classifications.
- `top`: Get only the top potential (default) or all potentials.

**TCGA.pipe**  

**ELMER analysis pipeline for TCGA data.**

**Description**

ELMER analysis pipeline for TCGA data. This pipeline combines every step of ELMER analyses: get.feature.probe, get.diff.meth, get.pair, get.permu, get.enriched.motif and get.TFs. Every steps’ results are saved.

**Usage**

```r
TCGA.pipe(
    disease,
    genome = "hg38",
    analysis = "all",
    wd = getwd(),
    cores = 1,
    mode = "unsupervised",
    Data = NULL,
    diff.dir = "hypo",
    genes = NULL,
    mutant_variant_classification = c("Frame_Shift_Del", "Frame_Shift_Ins", "Missense_Mutation", "Nonsense_Mutation", "Splice_Site", "In_Frame_Del", "In_Frame_Ins", "Translation_Start_Site", "Nonstop_Mutation"),
    group.col = "TN",
```

```r
```
group1 = "Tumor",
group2 = "Normal",
...
)

Arguments

disease TCGA short form disease name such as COAD
genome Data aligned against which genome of reference. Options: "hg19", "hg38" (default)
analysis A vector of characters listing the analysis need to be done. Analysis can be "download", "distal.probes", "diffMeth", "pair", "motif", "TF.search". Default is "all" meaning all the analysis will be processed.
wd A path shows working directory. Default is "/"
cores A integer which defines number of core to be used in parallel process. Default is 1: don’t use parallel process.
mode This option will automatically set the percentage of samples to be used in the analysis. Options: "supervised" (use 100% of samples) or "unsupervised" (use 20% of samples).

Data

diff.dir A character can be "hypo" or "hyper", showing direction DNA methylation changes. If it is "hypo", get.diff.meth function will identify all significantly hypomethylated CpG sites; If "hyper", get.diff.meth function will identify all significantly hypermethylated CpG sites
genesis List of genes for which mutations will be verified. A column in the MAE with the name of the gene will be created with two groups WT (tumor samples without mutation), MUT (tumor samples with mutation), NA (not tumor samples)
mutant.variant.classification List of TCGA variant classification from MAF files to consider a samples mutant. Only used when argument gene is set.
group.col A column defining the groups of the sample. You can view the available columns using: colnames(MultiAssayExperiment::colData(data)).
group1 A group from group.col. ELMER will run group1 vs group2. That means, if direction is hyper, get probes hypermethylated in group 1 compared to group 2.
group2 A group from group.col. ELMER will run group1 vs group2. That means, if direction is hyper, get probes hypermethylated in group 1 compared to group 2.
...

Value

Different analysis results.
Examples

```r
data <- ELMER:::getdata("elmer.data.example")
TCGA.pipe(
    disease = "LUSC",
    data = data,
    analysis = c("diffMeth","pair", "motif","TF.search"),
    mode = "supervised",
    group.col = "definition",
    group1 = "Primary solid Tumor",
    group2 = "Solid Tissue Normal",
    diff.dir = c("hypo"),
    dir.out = "pipe",
    sig.dif = 0.0001,
    pvalue = 1.0,
    min.incidence = 0,
    lower.OR = 0.0
)
```

## Not run:
```
distal.probe <- TCGA.pipe(disease = "LUSC", analysis="distal.enhancer", wd="~/")
TCGA.pipe(disease = "LUSC",analysis = "all", genome = "hg19", cores = 1, permu.size=300, Pe=0.01)
projects <- TCGAbiolinks:::getGDCprojects()$project_id
projects <- gsub("TCGA-",",projects[grepl("^TCGA",projects/perl=TRUE)])
for(proj in projects) TCGA.pipe(disease = proj,analysis = "download")
plyr::alply(sort(projects),1,function(proj) {
    tryCatch({
        print(proj);
        TCGA.pipe(disease = proj,analysis = c("createMAE"))
    },.progress = "text")
}
plyr::alply(sort(projects),1,function(proj) {
    tryCatch({
        print(proj);
        TCGA.pipe(disease = proj,
            analysis = c("diffMeth","pair", "motif","TF.search"))
    },.progress = "text")
}
```

## Evaluation mutation
```
TCGA.pipe(disease = "LUSC",analysis = "createMAE",gene = "NFE2L2")
TCGA.pipe(
    disease = "LUSC",analysis = c("diffMeth","pair", "motif","TF.search"),
    mode = "supervised",
    group.col = "NFE2L2", group1 = "Mutant", group2 = "WT",
    diff.dir = c("hypo"),
    dir.out = "LUSC_NFE2L2_MutvsWT"
)
```

## End(Not run)

---

**TF.rank.plot**

*TF.rank.plot* to plot the scores (-log10(P value)) which assess the correlation between TF expression and average DNA methylation at motif sites.
**TF.rank.plot**

**Description**

TF.rank.plot is a function to plot the scores (-log10(P value)) which assess the correlation between TF expression and average DNA methylation at motif sites. The motif relevant TF and top3 TFs will be labeled in a different color.

**Usage**

```r
TF.rank.plot(
  motif.pvalue,
  motif,
  title = NULL,
  TF.label = NULL,
  dir.out = "./",
  save = TRUE,
  cores = 1
)
```

**Arguments**

- **motif.pvalue**: A matrix or a path specifying location of "XXX.with.motif.pvalue.rda" which is output of getTF.
- **motif**: A vector of characters specify the motif to plot.
- **title**: Title title (the motif will still be added to the title).
- **TF.label**: A list shows the label for each motif. If TF.label is not specified, the motif relevant TF and top3 TF will be labeled.
- **dir.out**: A path specify the directory to which the figures will be saved. Current directory is default.
- **save**: A logic. If true (default), figure will be saved to dir.out.
- **cores**: An integer which defines the number of cores to be used in parallel process. Default is 1: no parallel process.

**Value**

A plot shows the score (-log(P value)) of association between TF expression and DNA methylation at sites of a certain motif.

**Author(s)**

Lijing Yao (maintainer: lijingya@usc.edu)

**Examples**

```r
library(ELMER)
data <- tryCatch(ELMER:::getdata("elmer.data.example"), error = function(e) {
  message(e)
  data(elmer.data.example, envir = environment())
})
enriched.motif <- list("P53_HUMAN.H11MO.0.A" = c("cg00329272", "cg1097755", "cg08928189",
```
TF <- get.TFs(data,
enriched.motif,
group.col = "definition",
group1 = "Primary solid Tumor",
group2 = "Solid Tissue Normal",
TFs = data.frame(
  external_gene_name=c("TP53","TP63","TP73"),
  ensembl_gene_id = c("ENSG00000141510",
                     "ENSG00000073282",
                     "ENSG00000078900"),
  stringsAsFactors = FALSE),
label="hypo")
TF.meth.cor <- get(load("getTF.hypo.TFs.with.motif.pvalue.rda"))
TF.rank.plot(motif.pvalue=TF.meth.cor,
motif="P53_HUMAN.H11MO.0.A",
TF.label=createMotifRelevantTfs("subfamily")["P53_HUMAN.H11MO.0.A"],
save=TRUE)
TF.rank.plot(motif.pvalue=TF.meth.cor,
motif="P53_HUMAN.H11MO.0.A",
save=TRUE)
# Same as above
TF.rank.plot(motif.pvalue=TF.meth.cor,
motif="P53_HUMAN.H11MO.0.A",
dir.out = "TFplots",
TF.label=createMotifRelevantTfs("family")["P53_HUMAN.H11MO.0.A"],
save=TRUE)

TFsurvival.plot

Creates survival plot of based on the expression of a TF

Description

This function will create a survival plot for the samples with higher, medium, low expression of a given transcription factor. By default, samples with higher expression are the top 30.

Usage

TFsurvival.plot(data, TF, xlim = NULL, percentage = 0.3, save = TRUE)

Arguments

data A multi assay Experiment with clinical data in the phenotypic data matrix containing the following columns: vital_status, days_to_last_follow_up and days_to_death. Default from GDC and TCGAbiolinks

TF A gene symbol

xlim Limit x axis showed in plot
percentage  A number ranges from 0 to 1 specifying the percentage of samples in the higher and lower expression groups. Default is 0.3

save  Save plot as PDF
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