Package 'GeoTcgaData'

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Type Package

Title Processing Various Types of Data on GEO and TCGA

Version 2.12.0

Description Gene Expression Omnibus(GEO) and The Cancer Genome Atlas (TCGA) provide us with a wealth of data, such as RNA-seq, DNA Methylation, SNP and Copy number variation data. It's easy to download data from TCGA using the gdc tool, but processing these data into a format suitable for bioinformatics analysis requires more work. This R package was developed to handle these data.

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Contents

array_preprocess . . . 3
cal_mean_module . . . 3
cluster_array . . . 4
combine_pvalue . . . 5
countToFpkm . . . 5
countToTpm . . . 6
differential_array . . . 7
differential_CNV . . . 8
differential_limma . . . 9
differential_methy . . . 10
differential_RNA . . . 12
differential_SNP . . . 15
differential_SNP_GEO . . . 16
differential_SNP_tcga . . . 17
fpkmToTpm . . . 18
geneExpress . . . 18
gene_ave . . . 19
gene_cov . . . 19
get_geo_array . . . 20
GSE66705_sample2 . . . 20
id_conversion_TCGA . . . 21
kegg_liver . . . 21
Merge_methy_tcga . . . 22
module . . . 22
prepare_chi . . . 23
profile . . . 23
repAssign . . . 24
repRemove . . . 25
SNP_QC . . . 25
ventricle . . . 26

Index **27**

array_preprocess *Preprocess of Microarray data*

Description

Preprocess of Microarray data

Usage

```
array_preprocess(x, missing_value = "knn", string = " /// ")
```

Arguments

x	matrix of Microarray data, each column is a sample, and each row is a gene.
missing_value	Method to impute missing expression data, one of "zero" and "knn".
string	a string, sep of the gene

Value

matrix

Examples

```
arraylist <- get_geo_array("GSE781")
arraylist <- lapply(arraylist, array_preprocess)
```

cal_mean_module *Find the mean value of the gene in each module*

Description

Find the mean value of the gene in each module

Usage

```
cal_mean_module(geneExpress, module)
```

Arguments

geneExpress	a data.frame of gene expression data. Each column is a sample, and each row is a gene.
module	a data.frame of two column. The first column is module name, the second column are genes in this module.

Value

a data.frame, means the mean of gene expression value in the same module

Examples

```
data(geneExpress)
data(module)
result <- cal_mean_module(geneExpress, module)
```

`cluster_array` *cluster probes of Microarray data*

Description

cluster probes of Microarray data

Usage

```
cluster_array(x, clusterCutoff = 0.7)
```

Arguments

`x`	matrix of Microarray data, the first is the name of the gene, and the others are the expression value.
`clusterCutoff`	Pearson correlation threshold to cut off the hierarchical tree.

Value

data.frame

Examples

```
arraylist <- get_geo_array("GSE781")
arraylist <- lapply(arraylist, array_preprocess)
arraylist_cluster <- lapply(arraylist, cluster_array)
```

combine_pvalue *combine pvalues of SNP difference analysis result*

Description

combine pvalues of SNP difference analysis result

Usage

```
combine_pvalue(snpResult, snp2gene, combineMethod = min)
```

Arguments

snpResult	data.frame of SNP difference analysis result.
snp2gene	data frame of two column: snp and gene.
combineMethod	Method of combining the pvalue of multiple snp in a gene.

Value

data.frame

Examples

```
snpResult <- data.frame(pvalue = runif(100), estimate = runif(100))
rownames(snpResult) <- paste0("snp", seq_len(100))
snp2gene <- data.frame(snp = rownames(snpResult),
    gene = rep(paste0("gene", seq_len(20)), 5))
result <- combine_pvalue(snpResult, snp2gene)
```

countToFpkm *Convert count to FPKM*

Description

Convert count to FPKM

Usage

```
countToFpkm(counts_matrix, keyType = "SYMBOL", gene_cov)
```

Arguments

counts_matrix	a matrix, colnames of counts_matrix are sample name, rownames of counts_matrix are gene symbols
keyType	keyType, one of keytypes(org.Hs.eg.db).
gene_cov	data.frame of two column, the first column is gene length, the second column is gene GC content

Value

a matrix

Examples

```
data(gene_cov)
lung_squ_count2 <- matrix(c(1, 2, 3, 4, 5, 6, 7, 8, 9), ncol = 3)
rownames(lung_squ_count2) <- c("DISC1", "TCOF1", "SPPL3")
colnames(lung_squ_count2) <- c("sample1", "sample2", "sample3")
result <- countToFpkm(lung_squ_count2,
    keyType = "SYMBOL",
    gene_cov = gene_cov
)
```

---

countToTpm *Convert count to Tpm*

Description

Convert count to Tpm

Usage

```
countToTpm(counts_matrix, keyType = "SYMBOL", gene_cov)
```

Arguments

counts_matrix	a matrix, colnames of counts_matrix are sample name, rownames of counts_matrix are gene symbols
keyType	keyType, one of keytypes(org.Hs.eg.db).
gene_cov	data.frame of two column, the first column is gene length, the second column is gene GC content

Value

a matrix

Examples

```
data(gene_cov)
lung_squ_count2 <- matrix(c(1, 2, 3, 4, 5, 6, 7, 8, 9), ncol = 3)
rownames(lung_squ_count2) <- c("DISC1", "TCOF1", "SPPL3")
colnames(lung_squ_count2) <- c("sample1", "sample2", "sample3")
result <- countToTpm(lung_squ_count2,
    keyType = "SYMBOL",
    gene_cov = gene_cov
)
```

differential_array *Differential analysis of Microarray data*

Description

Differential analysis of Microarray data

Usage

```
differential_array(df, group, method = "limma", adjust.method = "BH")
```

Arguments

df	data.frame of the omic data, each column is a sample, and each row is a gene.
group	a vector, group of samples.
method	method to do differential analysis, one of "limma", "ttest", "wilcox".
adjust.method	adjust.method, one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", and "none".

Value

data.frame

Examples

```
library(GeoTcgaData)
library(data.table)
# Use real GEO data as example
arrayData <- read.table("GSE54807_series_matrix.txt.gz",
    sep = "\t", header = TRUE,
        fill=TRUE, comment.char = "!", check.names=FALSE)
gpl <- fread("GPL6244-17930.txt", sep = "\t", header = TRUE)
gpl <- gpl[, c("ID", "gene_assignment")]
class(gpl) <- "data.frame"

for (i in seq_len(nrow(gpl))) {
        aa <- strsplit(gpl[i, 2], " // ")[[1]][5]
        gpl[i, 2] <- as.character(strsplit(aa, " /// ")[[1]][1])
}
gpl[,1] <- as.character(gpl[,1])
arrayData[, 1] <- as.character(arrayData[, 1])
rownames(gpl) <- gpl[, 1]
arrayData[, 1] <- gpl[arrayData[, 1], 2]


arrayData <- repRemove(arrayData," /// ")

# Remove rows that do not correspond to genes
```

```
arrayData <- arrayData[!is.na(arrayData[, 1]), ]
arrayData <- arrayData[!arrayData[, 1] == "", ]
arrayData <- arrayData[!arrayData[, 1] == "---", ]


arrayData <- arrayData[order(arrayData[, 1]), ]
arrayData <- gene_ave(arrayData, 1)

keep <- apply(arrayData, 1, function(x) sum(x < 1) < (length(x)/2))
arrayData <- arrayData[keep, ]

group <- c(rep("group1", 12), rep("group2", 12))
result <- differential_array(df = arrayData, group = group)

# Use random data as example
arrayData <- matrix(runif(200), 25, 8)
rownames(arrayData) <- paste0("gene", 1:25)
colnames(arrayData) <- paste0("sample", 1:8)
group <- c(rep("group1", 4), rep("group2", 4))
names(group) <- colnames(arrayData)
result <- differential_array(df = arrayData, group = group)
```

`differential_CNV` *Do difference analysis of gene level copy number variation data*

Description

Do difference analysis of gene level copy number variation data

Usage

```
differential_CNV(
  cnvData,
  sampleGroup,
  method = "Chisquare",
  adjust.method = "BH",
  ...
)
```

Arguments

`cnvData`	data.frame of CNV data, each column is a sample, and each row is a CNV.
`sampleGroup`	vector of sample group
`method`	method to do diffenenital analysis, one of "Chisquare", "fisher", and "CATT"(Cochran-Armitage trend test)
`adjust.method`	adjust.method, one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", and "none".
`...`	parameters for "Chisquare", "fisher", and "CATT"(Cochran-Armitage trend test)

Value

data.frame with pvalue and estimate

Examples

```
# use TCGAbiolinks data as example
library(TCGAbiolinks)
query <- GDCquery(
        project = "TCGA-ACC",
        data.category = "Copy Number Variation",
        data.type = "Gene Level Copy Number",
        access = "open"
)
GDCdownload(query)
cnvData <- GDCprepare(query)
aa <- assays(cnvData)$copy_number
bb <- aa
aa[bb == 2] <- 0
aa[bb < 2] <- -1
aa[bb > 2] <- 1
sampleGroup <- sample(c("A", "B"), ncol(cnvData), replace = TRUE)
diffCnv <- differential_CNV(aa, sampleGroup)

# Use sangerbox CNV data as example
cnvData <- fread("Merge_GeneLevelCopyNumber.txt")
class(cnvData) <- "data.frame"
rownames(cnvData) <- cnvData[, 1]
cnvData <- cnvData[, -c(1, 2, 3)]
sampleGroup <- sample(c("A", "B"), ncol(cnvData), replace = TRUE)
diffCnv <- differential_CNV(cnvData, sampleGroup)

# use random data as example
aa <- matrix(sample(c(0, 1, -1), 200, replace = TRUE), 25, 8)
rownames(aa) <- paste0("gene", 1:25)
colnames(aa) <- paste0("sample", 1:8)
sampleGroup <- sample(c("A", "B"), ncol(aa), replace = TRUE)
diffCnv <- differential_CNV(aa, sampleGroup)
```

`differential_limma` *differential_limma*

Description

differential_limma

Usage

```
differential_limma(df, group, adjust.method = "BH")
```

Arguments

df	data.frame of the omic data
group	a vector, group of samples.
adjust.method	adjust.method.

Value

data.frame

Examples

```
df <- matrix(runif(200), 25, 8)
df <- as.data.frame(df)
rownames(df) <- paste0("gene", 1:25)
colnames(df) <- paste0("sample", 1:8)
group <- sample(c("group1", "group2"), 8, replace = TRUE)
result <- differential_limma(df = df, group = group)
```

---

differential_methy *differential_methy*

Description

Get methylation difference gene

Usage

```
differential_methy(
  cpgData,
  sampleGroup,
  groupCol,
  combineMethod = "stouffer",
  missing_value = "knn",
  cpg2gene = NULL,
  normMethod = "PBC",
  region = "TSS1500",
  model = "gene",
  adjust.method = "BH",
  adjPvalCutoff = 0.05,
  ucscData = FALSE
)
```

Arguments

cpgData	data.frame of cpg beta value, , or SummarizedExperiment object
sampleGroup	vector of sample group
groupCol	group column
combineMethod	method to combine the cpg pvalues, a function or one of "stouffer", "fisher" and "rhoScores".
missing_value	Method to impute missing expression data, one of "zero" and "knn".
cpg2gene	data.frame to annotate cpg locus to gene
normMethod	Method to do normalization: "PBC" or "BMIQ".
region	region of genes, one of "Body", "TSS1500", "TSS200", "3'UTR", "1stExon", "5'UTR", and "IGR". Only used when cpg2gene is NULL.
model	if "cpg", step1: calculate difference cpgs; step2: calculate difference genes. if "gene", step1: calculate the methylation level of genes; step2: calculate difference genes.
adjust.method	character string specifying the method used to adjust p-values for multiple testing. See p.adjust for possible values.
adjPvalCutoff	adjusted pvalue cutoff
ucscData	Logical, whether the data comes from UCSC Xena.

Value

data.frame

Examples

```
# use TCGAbiolinks data
library(TCGAbiolinks)
query <- GDCquery(project = "TCGA-ACC",
    data.category = "DNA Methylation",
    data.type = "Methylation Beta Value",
    platform = "Illumina Human Methylation 450")
GDCdownload(query, method = "api", files.per.chunk = 5,
    directory = Your_Path)
merge_result <- Merge_methy_tcga(Your_Path_to_DNA_Methylation_data)
library(ChAMP) # To avoid reporting errors
differential_gene <- differential_methy(cpgData = merge_result,
    sampleGroup = sample(c("C","T"),
    ncol(merge_result[[1]]), replace = TRUE))

# use user defined data
library(ChAMP)
cpgData <- matrix(runif(2000), nrow = 200, ncol = 10)
rownames(cpgData) <- paste0("cpg", seq_len(200))
colnames(cpgData) <- paste0("sample", seq_len(10))
sampleGroup <- c(rep("group1", 5), rep("group2", 5))
names(sampleGroup) <- colnames(cpgData)
cpg2gene <- data.frame(cpg = rownames(cpgData),
```

```
    gene = rep(paste0("gene", seq_len(20)), 10))
result <- differential_methy(cpgData, sampleGroup,
    cpg2gene = cpg2gene, normMethod = NULL)
# use SummarizedExperiment object input
library(ChAMP)
cpgData <- matrix(runif(2000), nrow = 200, ncol = 10)
rownames(cpgData) <- paste0("cpg", seq_len(200))
colnames(cpgData) <- paste0("sample", seq_len(10))
sampleGroup <- c(rep("group1", 5), rep("group2", 5))
names(sampleGroup) <- colnames(cpgData)
cpg2gene <- data.frame(cpg = rownames(cpgData),
    gene = rep(paste0("gene", seq_len(20)), 10))
colData <- S4Vectors::DataFrame(
    row.names = colnames(cpgData),
    group = sampleGroup
)
data <- SummarizedExperiment::SummarizedExperiment(
         assays=S4Vectors::SimpleList(counts=cpgData),
         colData = colData)
result <- differential_methy(cpgData = data,
    groupCol = "group", normMethod = NULL,
    cpg2gene = cpg2gene)
```

`differential_RNA` *differential_RNA*

Description

Do difference analysis of RNA-seq data

Usage

```
differential_RNA(
  counts,
  group,
  groupCol,
  method = "limma",
  geneLength = NULL,
  gccontent = NULL,
  filter = TRUE,
  edgeRNorm = TRUE,
  adjust.method = "BH",
  useTopconfects = TRUE,
  ucscData = FALSE
)
```

Arguments

counts	a dataframe or numeric matrix of raw counts data, or SummarizedExperiment object
group	sample groups
groupCol	group column
method	one of "DESeq2", "edgeR" , "limma", "dearseq", "NOISeq", "Wilcoxon", and "auto".
geneLength	a vector of gene length.
gccontent	a vector of gene GC content.
filter	if TRUE, use filterByExpr to filter genes.
edgeRNorm	if TRUE, use edgeR to do normalization for dearseq method.
adjust.method	character string specifying the method used to adjust p-values for multiple testing. See p.adjust for possible values.
useTopconfects	if TRUE, use topconfects to provide a more biologically useful ranked gene list.
ucscData	Logical, whether the data comes from UCSC Xena.

Value

data.frame

Examples

```
library(TCGAbiolinks)

query <- GDCquery(
    project = "TCGA-ACC",
    data.category = "Transcriptome Profiling",
    data.type = "Gene Expression Quantification",
    workflow.type = "STAR - Counts"
)

GDCdownload(query,
    method = "api", files.per.chunk = 3,
    directory = Your_Path
)

dataRNA <- GDCprepare(
    query = query, directory = Your_Path,
    save = TRUE, save.filename = "dataRNA.RData"
)
## get raw count matrix
dataPrep <- TCGAanalyze_Preprocessing(
    object = dataRNA,
    cor.cut = 0.6,
    datatype = "STAR - Counts"
)
```

```
# Use `differential_RNA` to do difference analysis.
# We provide the data of human gene length and GC content in `gene_cov`.
group <- sample(c("grp1", "grp2"), ncol(dataPrep), replace = TRUE)
library(cqn) # To avoid reporting errors: there is no function "rq"
## get gene length and GC content
library(org.Hs.eg.db)
genes_bitr <- bitr(rownames(gene_cov),
    fromType = "ENTREZID", toType = "ENSEMBL",
    OrgDb = org.Hs.eg.db, drop = TRUE
)
genes_bitr <- genes_bitr[!duplicated(genes_bitr[, 2]), ]
gene_cov2 <- gene_cov[genes_bitr$ENTREZID, ]
rownames(gene_cov2) <- genes_bitr$ENSEMBL
genes <- intersect(rownames(dataPrep), rownames(gene_cov2))
dataPrep <- dataPrep[genes, ]
geneLength <- gene_cov2(genes, "length")
gccontent <- gene_cov2(genes, "GC")
names(geneLength) <- names(gccontent) <- genes
##    Difference analysis
DEGAll <- differential_RNA(
    counts = dataPrep, group = group,
    geneLength = geneLength, gccontent = gccontent
)
# Use `clusterProfiler` to do enrichment analytics:
diffGenes <- DEGAll$logFC
names(diffGenes) <- rownames(DEGAll)
diffGenes <- sort(diffGenes, decreasing = TRUE)
library(clusterProfiler)
library(enrichplot)
library(org.Hs.eg.db)
gsego <- gseGO(gene = diffGenes, OrgDb = org.Hs.eg.db, keyType = "ENSEMBL")
dotplot(gsego)

# use user-defined data
df <- matrix(rnbinom(400, mu = 4, size = 10), 25, 16)
df <- as.data.frame(df)
rownames(df) <- paste0("gene", 1:25)
colnames(df) <- paste0("sample", 1:16)
group <- sample(c("group1", "group2"), 16, replace = TRUE)
result <- differential_RNA(counts = df, group = group,
    filte = FALSE, method = "Wilcoxon")
# use SummarizedExperiment object input
df <- matrix(rnbinom(400, mu = 4, size = 10), 25, 16)
rownames(df) <- paste0("gene", 1:25)
colnames(df) <- paste0("sample", 1:16)
group <- sample(c("group1", "group2"), 16, replace = TRUE)

nrows <- 200; ncols <- 20
 counts <- matrix(
   runif(nrows * ncols, 1, 1e4), nrows,
   dimnames = list(paste0("cg",1:200),paste0("S",1:20))
)
```

```
colData <- S4Vectors::DataFrame(
  row.names = paste0("sample", 1:16),
  group = group
)
data <- SummarizedExperiment::SummarizedExperiment(
         assays=S4Vectors::SimpleList(counts=df),
         colData = colData)

result <- differential_RNA(counts = data, groupCol = "group",
    filte = FALSE, method = "Wilcoxon")
```

`differential_SNP` *Do difference analysis of SNP data*

Description

Do difference analysis of SNP data

Usage

```
differential_SNP(snpDf, sampleGroup, combineMethod = min)
```

Arguments

`snpDf`	data.frame of SNP data, each column is a sample, and each row is a SNP.
`sampleGroup`	vector of sample group.
`combineMethod`	Method of combining the pvalue of multiple snp in a gene.

Value

data.frame

Examples

```
library(TCGAbiolinks)
query <- GDCquery(
    project = "TCGA-CHOL",
    data.category = "Simple Nucleotide Variation",
    access = "open",
    legacy = FALSE,
    data.type = "Masked Somatic Mutation",
    workflow.type = "Aliquot Ensemble Somatic Variant Merging and Masking"
)
GDCdownload(query)
data_snp <- GDCprepare(query)
samples <- unique(data_snp$Tumor_Sample_Barcode)
sampleGroup <- sample(c("A", "B"), length(samples), replace = TRUE)
names(sampleGroup) <- samples
pvalue <- differential_SNP_tcga(snpData = data_snp,
```

```
    sampleGroup = sampleGroup)

# use demo data
snpDf <- matrix(sample(c("mutation", NA), 100, replace = TRUE), 10, 10)
snpDf <- as.data.frame(snpDf)
sampleGroup <- sample(c("A", "B"), 10, replace = TRUE)
result <- differential_SNP(snpDf, sampleGroup)
```

`differential_SNP_GEO` *Do difference analysis of SNP data downloaded from GEO*

Description

Do difference analysis of SNP data downloaded from GEO

Usage

```
differential_SNP_GEO(snpData, sampleGroup, method = "Chisquare")
```

Arguments

`snpData`	data.frame of SNP data downloaded from GEO
`sampleGroup`	vector of sample group
`method`	one of "Chisquare", "fisher", and "CATT"(Cochran-Armitage trend test)

Value

data.frame

Examples

```
file1 <- read.table("GSE66903_series_matrix.txt.gz",
    fill=TRUE, comment.char="!", header = TRUE)
rownames(file1) <- file1[, 1]
snpData <- file1[, -1]
sampleGroup <- sample(c("A", "B"), ncol(snpData ), replace = TRUE)
names(sampleGroup) <- colnames(snpData)
snpData <- SNP_QC(snpData)
sampleGroup <- sample(c("A", "B"), ncol(snpData ), replace = TRUE)
result1 <- differential_SNP_GEO(snpData = snpData,
    sampleGroup = sampleGroup, method = "Chisquare")

# use demo data
snpDf <- matrix(sample(c("AA", "Aa", "aa"), 100, replace = TRUE), 10, 10)
snpDf <- as.data.frame(snpDf)
sampleGroup <- sample(c("A", "B"), 10, replace = TRUE)
result <- differential_SNP_GEO(snpDf, sampleGroup, method = "fisher")
```

differential_SNP_tcga *Do difference analysis of SNP data downloaded from TCGAbiolinks*

Description

Do difference analysis of SNP data downloaded from TCGAbiolinks

Usage

```
differential_SNP_tcga(snpData, sampleGroup, combineMethod = NULL)
```

Arguments

snpData	data.frame of SNP data downloaded from TCGAbiolinks
sampleGroup	vector of sample group
combineMethod	Method of combining the pvalue of multiple snp in a gene.

Value

data.frame

Examples

```
library(TCGAbiolinks)
query <- GDCquery(
    project = "TCGA-CHOL",
    data.category = "Simple Nucleotide Variation",
    access = "open",
    legacy = FALSE,
    data.type = "Masked Somatic Mutation",
    workflow.type = "Aliquot Ensemble Somatic Variant Merging and Masking"
)
GDCdownload(query)
data_snp <- GDCprepare(query)
samples <- unique(data_snp$Tumor_Sample_Barcode)
sampleGroup <- sample(c("A", "B"), length(samples), replace = TRUE)
names(sampleGroup) <- samples
pvalue <- differential_SNP_tcga(snpData = data_snp,
    sampleGroup = sampleGroup)

# use demo data
snpDf <- matrix(sample(c("mutation", NA), 100, replace = TRUE), 10, 10)
snpDf <- as.data.frame(snpDf)
sampleGroup <- sample(c("A", "B"), 10, replace = TRUE)
result <- differential_SNP(snpDf, sampleGroup)
```

fpkmToTpm *Convert fpkm to Tpm*

Description

Convert fpkm to Tpm

Usage

```
fpkmToTpm(fpkm_matrix)
```

Arguments

fpkm_matrix	a matrix, colnames of fpkm_matrix are sample name, rownames of fpkm_matrix are genes

Value

a matrix

Examples

```
lung_squ_count2 <- matrix(c(0.11, 0.22, 0.43, 0.14, 0.875,
    0.66, 0.77, 0.18, 0.29), ncol = 3)
rownames(lung_squ_count2) <- c("DISC1", "TCOF1", "SPPL3")
colnames(lung_squ_count2) <- c("sample1", "sample2", "sample3")
result <- fpkmToTpm(lung_squ_count2)
```

geneExpress *a data.frame of gene expression data*

Description

It is a randomly generated expression data used as an example of functions in this package. the rowname is gene symbols the columns are gene expression values

Usage

```
geneExpress
```

Format

A data.frame with 10779 rows and 2 column

gene_ave *Average the values of same genes in gene expression profile*

Description

Average the values of same genes in gene expression profile

Usage

```
gene_ave(file_gene_ave, k = 1)
```

Arguments

file_gene_ave	a data.frame of gene expression data, each column is a sample, and each row is a gene.
k	a number, indicates which is the gene column.

Value

a data.frame, the values of same genes in gene expression profile

Examples

```
aa <- c("MARCH1", "MARC1", "MARCH1", "MARCH1", "MARCH1")
bb <- c(2.969058399, 4.722410064, 8.165514853, 8.24243893, 8.60815086)
cc <- c(3.969058399, 5.722410064, 7.165514853, 6.24243893, 7.60815086)
file_gene_ave <- data.frame(aa = aa, bb = bb, cc = cc)
colnames(file_gene_ave) <- c("Gene", "GSM1629982", "GSM1629983")

result <- gene_ave(file_gene_ave, 1)
```

gene_cov *a data.frame of gene length and GC content*

Description

the gene length and GC content data comes from TxDb.Hsapiens.UCSC.hg38.knownGene and BSgenome.Hsapiens.UCSC.hg38

Usage

```
gene_cov
```

Format

A data.frame with 27341 rows and 2 column

get_geo_array *Get Microarray matrix data from GEO*

Description

Get Microarray matrix data from GEO

Usage

```
get_geo_array(gse)
```

Arguments

gse	GSE number, such as GSE781.

Value

a list of matrix

Examples

```
arraylist <- get_geo_array("GSE781")
```

GSE66705_sample2 *a matrix of gene expression data in GEO*

Description

the first column represents the gene symbol

Usage

```
GSE66705_sample2
```

Format

A matrix with 999 rows and 3 column

Details

the other columns represent the expression of genes

id_conversion_TCGA *Convert ENSEMBL gene id to gene Symbol in TCGA*

Description

Convert ENSEMBL gene id to gene Symbol in TCGA

Usage

```
id_conversion_TCGA(profiles, toType = "SYMBOL")
```

Arguments

profiles	a data.frame of gene expression data, each column is a sample, and each row is a gene.
toType	one of 'keytypes(org.Hs.eg.db)'

Value

a data.frame, gene symbols and their expression value

Examples

```
library(org.Hs.eg.db)
data(profile)
result <- id_conversion_TCGA(profile)
```

kegg_liver *a matrix of gene expression data in TCGA*

Description

It is a randomly generated expression data used as an example of functions in this package. the first column represents the gene symbol

Usage

```
kegg_liver
```

Format

A matrix with 100 rows and 150 column

Details

the other columns represent the expression(count) of genes

Merge_methy_tcga *Merge methylation data downloaded from TCGA*

Description

When the methylation data is downloaded from TCGA, each sample is saved in a folder, which contains the methylation value file and the descriptive file. This function can directly extract and consolidate all folders.

Usage

```
Merge_methy_tcga(dirr = NULL)
```

Arguments

dirr	a string for the directory of methylation data download from tcga useing the tools gdc

Value

a matrix, a combined methylation expression spectrum matrix

Examples

```
merge_result <- Merge_methy_tcga(system.file(file.path("extdata", "methy"),
    package = "GeoTcgaData"))
```

module *a matrix of module name, gene symbols, and the number of gene symbols*

Description

It is a randomly generated expression data used as an example of functions in this package.

Usage

```
module
```

Format

A matrix with 176 rows and 3 column

prepare_chi *Preparer file for chi-square test*

Description

Preparer file for chi-square test

Usage

```
prepare_chi(cnv)
```

Arguments

cnv	result of ann_merge()

Value

a matrix

Examples

```
cnv <- matrix(c(
    -1.09150, -1.47120, -0.87050, -0.50880,
    -0.50880, 2.0, 2.0, 2.0, 2.0, 2.0, 2.601962, 2.621332, 2.621332,
    2.621332, 2.621332, 2.0, 2.0, 2.0, 2.0, 2.0, 2.0, 2.0, 2.0,
    2.0, 2.0, 2.0, 2.0, 2.0, 2.0, 2.0
), nrow = 5)
cnv <- as.data.frame(cnv)
rownames(cnv) <- c("AJAP1", "FHAD1", "CLCNKB", "CROCCP2", "AL137798.3")
colnames(cnv) <- c(
    "TCGA-DD-A4NS-10A-01D-A30U-01", "TCGA-ED-A82E-01A-11D-A34Y-01",
    "TCGA-WQ-A9G7-01A-11D-A36W-01", "TCGA-DD-AADN-01A-11D-A40Q-01",
    "TCGA-ZS-A9CD-10A-01D-A36Z-01", "TCGA-DD-A1EB-11A-11D-A12Y-01"
)
cnv_chi_file <- prepare_chi(cnv)
```

profile *a matrix of gene expression data in TCGA*

Description

It is a randomly generated expression data used as an example of functions in this package. the first column represents the gene symbol

Usage

```
profile
```

Format

A matrix with 10 rows and 10 column

Details

the other columns represent the expression(FPKM) of genes

`repAssign` *Handle the case where one id corresponds to multiple genes*

Description

Handle the case where one id corresponds to multiple genes

Usage

```
repAssign(input_file, string)
```

Arguments

`input_file`	input file, a data.frame or a matrix, the first column should be genes.
`string`	a string, sep of the gene

Value

a data.frame, when an id corresponds to multiple genes, the expression value is assigned to each gene

Examples

```
aa <- c("MARCH1 /// MMA", "MARC1", "MARCH2 /// MARCH3",
    "MARCH3 /// MARCH4", "MARCH1")
bb <- c("2.969058399", "4.722410064", "8.165514853",
    "8.24243893", "8.60815086")
cc <- c("3.969058399", "5.722410064", "7.165514853",
    "6.24243893", "7.60815086")
input_file <- data.frame(aa = aa, bb = bb, cc = cc)

repAssign_result <- repAssign(input_file, " /// ")
```

repRemove *Handle the case where one id corresponds to multiple genes*

Description

Handle the case where one id corresponds to multiple genes

Usage

```
repRemove(input_file, string)
```

Arguments

input_file	input file, a data.frame or a matrix, the first column should be genes.
string	a string,sep of the gene

Value

a data.frame, when an id corresponds to multiple genes, the expression value is deleted

Examples

```
aa <- c("MARCH1 /// MMA", "MARC1", "MARCH2 /// MARCH3",
    "MARCH3 /// MARCH4", "MARCH1")
bb <- c("2.969058399", "4.722410064", "8.165514853",
    "8.24243893", "8.60815086")
cc <- c("3.969058399", "5.722410064", "7.165514853",
    "6.24243893", "7.60815086")
input_file <- data.frame(aa = aa, bb = bb, cc = cc)
repRemove_result <- repRemove(input_file, " /// ")
```

SNP_QC *Do quality control of SNP data downloaded from TCGAbiolinks*

Description

Do quality control of SNP data downloaded from TCGAbiolinks

Usage

```
SNP_QC(
  snpData,
  geon = 0.02,
  mind = 0.02,
  maf = 0.05,
  hwe = 1e-06,
  miss = "NoCall"
)
```

Arguments

snpData	data.frame of SNP data downloaded from TCGAbiolinks
geon	filters out all variants with missing call rates exceeding the provided value (default 0.02) to be removed
mind	filters out all samples with missing call rates exceeding the provided value (default 0.02) to be removed
maf	filters out all variants with minor allele frequency below the provided threshold
hwe	filters out all variants which have Hardy-Weinberg equilibrium exact test p-value below the provided threshold
miss	character of miss value

Value

data.frame

Examples

```
# use demo data
snpDf <- matrix(sample(c("AA", "Aa", "aa"), 100, replace = TRUE), 10, 10)
snpDf <- as.data.frame(snpDf)
sampleGroup <- sample(c("A", "B"), 10, replace = TRUE)
result <- SNP_QC(snpDf)
```

---

ventricle *a matrix of gene expression data in GEO*

Description

It is a randomly generated expression data used as an example of functions in this package. the first column represents the gene symbol

Usage

```
ventricle
```

Format

A matrix with 32 rows and 20 column

Details

the other columns represent the expression of genes

Index

∗ **datasets**
  gene_cov, 19
  geneExpress, 18
  GSE66705_sample2, 20
  kegg_liver, 21
  module, 22
  profile, 23
  ventricle, 26

array_preprocess, 3

cal_mean_module, 3
cluster_array, 4
combine_pvalue, 5
countToFpkm, 5
countToTpm, 6

differential_array, 7
differential_CNV, 8
differential_limma, 9
differential_methy, 10
differential_RNA, 12
differential_SNP, 15
differential_SNP_GEO, 16
differential_SNP_tcga, 17

fpkmToTpm, 18

gene_ave, 19
gene_cov, 19
geneExpress, 18
get_geo_array, 20
GSE66705_sample2, 20

id_conversion_TCGA, 21

kegg_liver, 21

Merge_methy_tcga, 22
module, 22

p.adjust, *11*, *13*

prepare_chi, 23
profile, 23

repAssign, 24
repRemove, 25

SNP_QC, 25

ventricle, 26