Package ‘BLMA’

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Description Suit of tools for bi-level meta-analysis. The package can be used in a wide range of applications, including general hypothesis testings, differential expression analysis, functional analysis, and pathway analysis.
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addCLT

*The additive method for meta-analysis*

**Description**

Combine independent studies using the average of p-values

**Usage**

`addCLT(x)`

**Arguments**

`x` is an array of independent p-values

**Details**

This method is based on the fact that sum of independent uniform variables follow the Irwin-Hall distribution \([1a,1b]\). When the number of p-values is small \((n<20)\), the distribution of the average of p-values can be calculated using a linear transformation of the Irwin-Hall distribution. When \(n\) is large, the distribution is approximated using the Central Limit Theorem to avoid underflow/overflow problems \([2,3,4,5]\).

**Value**

combined p-value

**Author(s)**

Tin Nguyen and Sorin Draghici
References

[1a] P. Hall. The distribution of means for samples of size n drawn from a population in which the variate takes values between 0 and 1, all such values being equally probable. Biometrika, 19(3-4):240-244, 1927.


See Also

fisherMethod, stoufferMethod

Examples

```r
x <- rep(0, 10)
addCLT(x)

x <- runif(10)
addCLT(x)
```

bilevelAnalysisClassic

Bi-level meta-analysis in conjunction with a classical hypothesis testing method

Description

Perform a bi-level meta-analysis in conjunction with any of the classical hypothesis testing methods, such as t-test, Wilcoxon test, etc.

Usage

```r
bilevelAnalysisClassic(x, y = NULL, splitSize = 5, metaMethod = addCLT, func = t.test, p.value = "p.value", ...)
```
Arguments

- **x**: a list of numeric vectors
- **y**: an optional list of numeric vectors
- **splitSize**: the minimum number of size in each split sample. splitSize should be at least 3. By default, splitSize=5
- **metaMethod**: the method used to combine p-values. This should be one of addCLT (additive method [1]), fishersMethod (Fisher’s method [5]), stoufferMethod (Stouffer’s method [6]), max (maxP method [7]), or min (minP method [8])
- **func**: the name of the hypothesis test. By default func=t.test
- **p.value**: the component that returns the p-value after performing the test provided by the `func` parameter. For example, the function t-test returns the class "htest" where the component "p.value" is the p-value of the test. By default, p.value="p.value"
- ... additional parameters for `func`

Details

This function performs a bi-level meta-analysis for the lists of samples [1]. It performs intra-experiment analyses to compare the vectors in x against the corresponding vectors in y using the function `intraAnalysisClassic` in conjunction with the test provided in `func`. For example, it compares the first vector in x with the first vector in y, the second vector in x with the second vector in y, etc. When y is null, then the comparisons are reduced to one-sample tests. After these comparisons, we have a list of p-values, one for each comparision. The function then combines these p-values to obtain a single p-value using `metaMethod`.

Value

the combined p-value

Author(s)

Tin Nguyen and Sorin Draghici

References


See Also

`intraAnalysisClassic`, `intraAnalysisGene`, `bilevelAnalysisGene`

Examples

```r
set.seed(1)
l1 <- lapply(as.list(seq(3)),FUN=function (x) rnorm(n=10, mean=1))
l1
# one-sample t-test
lapply(l1, FUN=function(x) t.test(x, alternative="greater")$p.value)
```
# combining the p-values of one-sample t-tests:
addCLT(unlist(lapply(l1, FUN=function(x) t.test(x, alter="g")$p.value)))

# Bi-level meta-analysis
bilevelAnalysisClassic(x=l1, alternative="greater")

---

**bilevelAnalysisGene**  
*Bi-level meta-analysis of multiple expression datasets at the gene-level*

### Description

Perform a bi-level meta-analysis in conjunction with the moderate t-test (limma package) for the purpose of differential expression analysis of multiple gene expression datasets.

### Usage

```r
bilevelAnalysisGene(dataList, groupList, splitSize = 5, metaMethod = addCLT)
```

### Arguments

- **dataList**: a list of datasets. Each dataset is a data frame where the rows are the gene IDs and the columns are the samples.
- **groupList**: a list of vectors. Each vector represents the phenotypes of the corresponding dataset in dataList, which are either 'c' (control) or 'd' (disease).
- **splitSize**: the minimum number of disease samples in each split dataset. splitSize should be at least 3. By default, splitSize=5.
- **metaMethod**: the method used to combine p-values. This should be one of addCLT (additive method [1]), fishersMethod (Fisher’s method [5]), stoufferMethod (Stouffer’s method [6]), max (maxP method [7]), or min (minP method [8]).

### Details

The bi-level framework combines the datasets at two levels: an intra-experiment analysis, and an inter-experiment analysis [1]. At the intra-experiment analysis, the framework splits a dataset into smaller datasets, performs a moderated t-test (limma package) on split datasets, and then combines the p-values of individual genes using metaMethod. At the inter-experiment analysis, the p-values obtained for each individual datasets are combined using metaMethod.

### Value

A data frame containing the following components:

- **rownames**: gene IDs that are common in all datasets
- **pLimma**: the p-values obtained by combining pLimma values of individual datasets
- **pLimma.fdr**: FDR-corrected p-values of pLimma
- **pBilevel**: the p-values obtained from combining pIntra values of individual datasets
- **pBilevel.fdr**: FDR-corrected p-values of pBilevel
Author(s)
Tin Nguyen and Sorin Draghici

References

See Also
bilevelAnalysisGene, intraAnalysisClassic

Examples
```r
dataSets <- c("GSE17054", "GSE57194", "GSE33223", "GSE42140")
data(list=dataSets, package="BLMA")
names(dataSets) <- dataSets
dataList <- lapply(dataSets, function(dataset) get(paste0("data_", dataset)))
groupList <- lapply(dataSets, function(dataset) get(paste0("group_", dataset)))
Z <- bilevelAnalysisGene(dataList = dataList, groupList = groupList)
head(Z)
```

---

bilevelAnalysisGeneset

**Bi-level meta-analysis – applied to geneset enrichment analysis**

Description
Perform a bi-level meta-analysis in conjunction with geneset enrichment methods (ORA/GSA/PADOG) to integrate multiple gene expression datasets.

Usage
```r
bilevelAnalysisGeneset(gslist, gs.names, dataList, groupList, splitSize = 5,
metaMethod = addCLT, enrichment = "ORA", pCutoff = 0.05,
percent = 0.05, mc.cores = 1, ...)
```

Arguments
- `gslist`: a list of gene sets.
- `gs.names`: names of the gene sets.
- `dataList`: a list of datasets to be combined. Each dataset is a data frame where the rows are the gene IDs and the columns are the samples.
- `groupList`: a list of vectors. Each vector represents the phenotypes of the corresponding dataset in dataList. The elements of each vector are either 'c' (control) or 'd' (disease).
splitSize: the minimum number of disease samples in each split dataset. splitSize should be at least 3. By default, splitSize=5

metaMethod: the method used to combine p-values. This should be one of addCLT (additive method [1]), fisherMethod (Fisher’s method [5]), stoufferMethod (Stouffer’s method [6]), max (maxP method [7]), or min (minP method [8])

enrichment: the method used for enrichment analysis. This should be one of "ORA", "GSA", or "PADOG". By default, enrichment is set to "ORA".

pCutoff: cutoff p-value used to identify differentially expressed (DE) genes. This parameter is used only when the enrichment method is "ORA". By default, pCutoff=0.05 (five percent)

percent: percentage of genes with highest foldchange to be considered as differentially expressed (DE). This parameter is used when the enrichment method is "ORA". By default percent=0.05 (five percent). Please note that only genes with p-value less than pCutoff will be considered

mc.cores: the number of cores to be used in parallel computing. By default, mc.cores=1

... additional parameters of the GSA/PADOG functions

Details

The bi-level framework combines the datasets at two levels: an intra-experiment analysis, and an inter-experiment analysis [1]. At the intra-level analysis, the framework splits a dataset into smaller datasets, performs enrichment analysis for each split dataset (using ORA [2], GSA [3], or PADOG [4]), and then combines the results of these split datasets using metaMethod. At the inter-level analysis, the results obtained for individual datasets are combined using metaMethod.

Value

A data frame (rownames are geneset/pathway IDs) that consists of the following information:

- **Name**: name/description of the corresponding pathway/geneset
- Columns that include the pvalues obtained from the intra-experiment analysis of individual datasets
- **pBLMA**: p-value obtained from the inter-experiment analysis using addCLT
- **rBLMA**: ranking of the geneset/pathway using addCLT
- **pBLMA.fdr**: FDR-corrected p-values

Author(s)

Tin Nguyen and Sorin Draghici

References


See Also

bilevelAnalysisPathway, phyper, GSA, padog

Examples

# load KEGG pathways and create gene sets
x <- loadKEGGPathways()
gslist <- lapply(x$kpg,FUN=function(y){return (nodes(y));})
gs.names <- x$kpn[names(gslist)]

# load example data
dataSets <- c("GSE17054", "GSE57194", "GSE33223", "GSE42140")
data(list=dataSets, package="BLMA")
names(dataSets) <- dataSets
dataList <- lapply(dataSets, function(dataset) get(paste0("data_", dataset)))
groupList <- lapply(dataSets, function(dataset) get(paste0("group_", dataset)))

# perform bi-level meta-analysis in conjunction with ORA
ORAComb <- bilevelAnalysisGeneset(gslist, gs.names, dataList, groupList, enrichment = "ORA")
head(ORAComb[, c("Name", "pBLMA", "pBLMA.fdr", "rBLMA")])

# perform bi-level meta-analysis in conjunction with GSA
GSAComb <- bilevelAnalysisGeneset(gslist, gs.names, dataList, groupList, enrichment = "GSA", nperms = 200, random.seed = 1)
head(GSAComb[, c("Name", "pBLMA", "pBLMA.fdr", "rBLMA")])

# perform bi-level meta-analysis in conjunction with PADOG
set.seed(1)
PADOGComb <- bilevelAnalysisGeneset(gslist, gs.names, dataList, groupList, enrichment = "PADOG", NI=200)
head(PADOGComb[, c("Name", "pBLMA", "pBLMA.fdr", "rBLMA")])
Description

Perform a bi-level meta-analysis conjunction with Impact Analysis to integrate multiple gene expression datasets

Usage

```r
bilevelAnalysisPathway(kpg, kpn, dataList, groupList, splitSize = 5,
metaMethod = addCLT, pCutoff = 0.05, percent = 0.05, mc.cores = 1,
nboot = 200, seed = 1)
```

Arguments

- `kpg`: list of pathway graphs as objects of type graph (e.g., graphNEL)
- `kpn`: names of the pathways.
- `dataList`: a list of datasets to be combined. Each dataset is a data frame where the rows are the gene IDs and the columns are the samples.
- `groupList`: a list of vectors. Each vector represents the phenotypes of the corresponding dataset in dataList, which are either 'c' (control) or 'd' (disease).
- `splitSize`: the minimum number of disease samples in each split dataset. splitSize should be at least 3. By default, splitSize=5
- `metaMethod`: the method used to combine p-values. This should be one of addCLT (additive method [1]), fisherMethod (Fisher’s method [5]), stoufferMethod (Stouffer’s method [6]), max (maxP method [7]), or min (minP method [8])
- `pCutoff`: cutoff p-value used to identify differentially expressed (DE) genes. This parameter is used only when the enrichment method is "ORA". By default, pCutoff=0.05 (five percent)
- `percent`: percentage of genes with highest foldchange to be considered as differentially expressed (DE). This parameter is used when the enrichment method is "ORA". By default percent=0.05 (five percent). Please note that only genes with p-value less than pCutoff will be considered
- `mc.cores`: the number of cores to be used in parallel computing. By default, mc.cores=1
- `nboot`: number of bootstrap iterations. By default, nboot=200
- `seed`: seed. By default, seed=1.

Details

The bi-level framework combines the datasets at two levels: an intra-experiment analysis, and an inter-experiment analysis [1]. At the intra-level analysis, the framework splits a dataset into smaller datasets, performs pathway analysis for each split dataset using Impact Analysis [2,3], and then combines the results of these split datasets using `metaMethod`. At the inter-level analysis, the results obtained for individual datasets are combined using `metaMethod`
Value

A data frame (rownames are geneset/pathway IDs) that consists of the following information:

- **Name**: name-description of the corresponding pathway/geneset
- **Columns** that include the p-values obtained from the intra-experiment analysis of individual datasets
  - **pBLMA**: p-value obtained from the inter-experiment analysis using addCLT
  - **rBLMA**: ranking of the geneset/pathway using addCLT
  - **pBLMA.fdr**: FDR-corrected p-values

Author(s)

Tin Nguyen and Sorin Draghici

References


See Also

`bilevelAnalysisGeneset`, `pe`, `phyper`

Examples

```r
# load KEGG pathways
x <- loadKEGGPathways()

# load example data
dataSets <- c("GSE17054", "GSE57194", "GSE33223", "GSE42140")
data(list=dataSets, package="BLMA")
names(dataSets) <- dataSets
dataList <- lapply(dataSets, function(dataset) get(paste0("data_", dataset)))
groupList <- lapply(dataSets, function(dataset) get(paste0("group_", dataset)))

IAComb <- bilevelAnalysisPathway(x$kpg, x$kpn, dataList, groupList)
```
fisherMethod

head(IAComb[, c("Name", "pBLMA", "pBLMA.fdr", "rBLMA")])

fisherMethod

Fisher's method for meta-analysis

Description

Combine independent p-values using the minus log product

Usage

fisherMethod(x)

Arguments

x is an array of independent p-values

Details

Considering a set of \( m \) independent significance tests, the resulted p-values are independent and uniformly distributed between 0 and 1 under the null hypothesis. Fisher's method uses the minus log product of the p-values as the summary statistic, which follows a chi-square distribution with \( 2m \) degrees of freedom. This chi-square distribution is used to calculate the combined p-value.

Value

combined p-value

Author(s)

Tin Nguyen and Sorin Draghici

References


See Also

stoufferMethod, addCLT

Examples

x <- rep(0,10)
fisherMethod(x)

x <- runif(10)
fisherMethod(x)
getStatistics

Intergrative genes statistic

Description

Calculate genes summary statistic across multiple datasets

Usage

getStatistics(allGenes, dataList, groupList, ncores = 1, method = addCLT)

Arguments

allGenes Vector of all genes names for the analysis.
dataList A list of expression matrices, in which rows are genes and columns are samples.
groupList A list of vectors indicating sample group corresponding with expression matrices in dataList.
ncores Number of core to use in parallel processing.
method Function for combining p-values. It must accept one input which is a vector of p-values and return a combined p-value. Three methods are embeded in this package are addCLT, fisherMethod, and stoufferMethod.

Details

To estimate the effect sizes of genes across all studies, first standardized mean difference for each gene in individual studies is compute. Next, the overall effect size and standard error are estimated using the random-eects model. This overall effect size represents the gene’s expression change under the effect of the condition. The, z-scores and p-values of observing such effect sizes are computed. The p-values is obtained from classical hypothesis testing. By default, linear model and empirical Bayesian testing (`limma`) are used to compute the p-values for differential expression. The two-tailed p-values are converted to one-tailed p-values (left- and right-tailed). For each gene, the one-tailed p-values across all datasets are then combined using the addCLT, stouffer or fisher method. These p-values represent how likely the differential expression is observed by chance.

Value

A data.frame of gene statistics with following columns:

- `pTwoTails` Two-tailed p-values
- `pTwoTails.fdr` Two-tailed p-values with false discovery rate correction
- `pLeft` left-tailed p-values
- `pLeft.fdr` left-tailed p-values with false discovery rate correction
- `pRight.fdr` right-tailed p-values with false discovery rate correction
- `pRight` right-tailed p-values
getStatistics

ES  Effect size
ES.pTwoTails  Two-tailed p-values for effect size
ES.pTwoTails.fdr  Two-tailed p-values for effect size with false discovery rate correction
ES.pLeft  Left-tailed p-values for effect size
ES.pLeft.fdr  Left-tailed p-values for effect size with false discovery rate correction
ES.pRight  Right-tailed p-values for effect size
ES.pRight.fdr  Right-tailed p-values for effect size with false discovery rate correction

Author(s)
Tin Nguyen, Hung Nguyen, and Sorin Draghici

References

See Also
addCLT

Examples

datasets <- c("GSE17054", "GSE57194", "GSE33223", "GSE42140")
data(list = datasets, package = "BLMA")
dataList <- lapply(datasets, function(dataset) {
  get(paste0("data_", dataset))
})
groupList <- lapply(datasets, function(dataset) {
  get(paste0("group_", dataset))
})
names(dataList) <- datasets
names(groupList) <- datasets
allGenes <- Reduce(intersect, lapply(dataList, rownames))
geneStat <- getStatistics(allGenes, dataList, groupList)
head(geneStat)

# perform pathway analysis
library(ROntoTools)
# get gene network
kpg <- loadKEGGPathways()$kpg
# get gene network name
kpn <- loadKEGGPathways()$kpn
# get geneset
gslist <- lapply(kpg, function(y) nodes(y))

# get differential expressed genes
DEGenes.Left <- rownames(geneStat)[geneStat$pLeft < 0.05 & geneStat$ES.pLeft < 0.05]
DEGenes.Right <- rownames(geneStat)[geneStat$pRight < 0.05 & geneStat$ES.pRight < 0.05]

DEGenes <- union(DEGenes.Left, DEGenes.Right)

# perform pathway analysis with ORA
oraRes <- lapply(gslist, function(gs){
  pORACalc(geneSet = gs, DEGenes = DEGenes, measuredGenes = rownames(geneStat))
})
oraRes <- data.frame(p.value = unlist(oraRes), pathway = names(oraRes))
rownames(oraRes) <- kpn[rownames(oraRes)]

# print results
print(head(oraRes))

# perfrom pathway analysis with Pathway-Express from ROntoTools
ES <- geneStat[DEGenes, "ES"]
names(ES) <- DEGenes
peRes = pe(x = ES, graphs = kpg, ref = allGenes, nboot = 1000, seed=1)

peRes.Summary <- Summary(peRes, comb.pv.func = fisherMethod)
peRes.Summary[, ncol(peRes.Summary) + 1] <- rownames(peRes.Summary)
rownames(peRes.Summary) <- kpn[rownames(peRes.Summary)]
colnames(peRes.Summary)[ncol(peRes.Summary)] = "pathway"

# print results
print(head(peRes.Summary))

GSE17054

Gene expression dataset GSE17054 from Majeti et al.

Description
This dataset consists of 5 acute myeloid leukemia and 4 control samples. The data frame data_GSE17054 includes the expression data while the vector group_GSE17054 includes the grouping information.

Usage
data(GSE17054)

Format
data_GSE17054 is a data frame with 4738 rows and 9 columns. The rows represent the genes and the columns represent the samples.
group_GSE17054 is a vector that represents the sample grouping for data_GSE17054. The elements of group_GSE17054 are either 'c' (control) or 'd' (disease).

Source

References

GSE33223
Gene expression dataset GSE33223 from Bacher et al.

Description
This dataset consists of 20 acute myeloid leukemia and 10 control samples. The data frame data_GSE33223 includes the expression data while the vector group_GSE33223 includes the grouping information.

Usage
data(GSE33223)

Format
data_GSE33223 is a data frame with 4114 rows and 30 columns. The rows represent the genes and the columns represent the samples.

group_GSE33223 is a vector that represents the sample grouping for data_GSE33223. The elements of group_GSE33223 are either 'c' (control) or 'd' (disease).

Source

References
Description

This dataset consists of 26 acute myeloid leukemia and 5 control samples. The data frame data_GSE42140 includes the expression data while the vector group_GSE42140 includes the grouping information.

Usage

data(GSE42140)

Format

data_GSE42140 is a data frame with 4114 rows and 31 columns. The rows represent the genes and the columns represent the samples.

group_GSE42140 is a vector that represents the sample grouping for data_GSE42140. The elements of group_GSE42140 are either 'c' (control) or 'd' (disease).

References


Description

This dataset consists of 6 acute myeloid leukemia and 6 control samples. The data frame data_GSE57194 includes the expression data while the vector group_GSE57194 includes the grouping information.

Usage

data(GSE57194)

Format

data_GSE57194 is a data frame with 4114 rows and 12 columns. The rows represent the genes and the columns represent the samples.

group_GSE57194 is a vector that represents the sample grouping for data_GSE57194. The elements of group_GSE57194 are either 'c' (control) or 'd' (disease).

Source

References


---

**intraAnalysisClassic**

Intra-experiment analysis in conjunction with classical hypothesis tests

**Description**

Perform an intra-experiment analysis in conjunction with any of the classical hypothesis testing methods, such as t-test, Wilcoxon test, etc.

**Usage**

```r
intraAnalysisClassic(x, y = NULL, splitSize = 5, metaMethod = addCLT, func = t.test, p.value = "p.value", ...)
```

**Arguments**

- `x`: a numeric vector of data values
- `y`: an optional numeric vector of values
- `splitSize`: the minimum number of size in each split sample. `splitSize` should be at least 3. By default, `splitSize=5`
- `metaMethod`: the method used to combine p-values. This should be one of addCLT (additive method [1]), fishersMethod (Fisher’s method [5]), stoufferMethod (Stouffer’s method [6]), max (maxP method [7]), or min (minP method [8])
- `func`: the name of the hypothesis test. By default `func=t.test`
- `p.value`: the component that returns the p-value after performing the test provided by the `func` parameter. For example, the function t-test returns the class "htest" where the component "p.value" is the p-value of the test. By default, `p.value="p.value"
- `...`: additional parameters for `func`

**Details**

This function performs an intra-experiment analysis for the given sample(s) [1]. Given `x` as the numeric vector, this function first splits `x` into smaller samples with size `splitSize`, performs hypothesis testing using `func`, and then combines the p-values using `metaMethod`

**Value**

intra-experiment p-value
Author(s)
Tin Nguyen and Sorin Draghici

References

See Also
bilevelAnalysisClassic, intraAnalysisGene, bilevelAnalysisGene

Examples
```r
set.seed(1)
x <- rnorm(10, mean = 0)
# p-value obtained from a one-sample t-test
t.test(x, mu=1, alternative = "less")$p.value
# p-value obtained from an intra-experiment analysis
intraAnalysisClassic(x, func=t.test, mu=1, alternative = "less")

# p-value obtained from a one-sample wilcoxon test
wilcox.test(x, mu=1, alternative = "less")$p.value
# p-value obtained from an intra-experiment analysis
intraAnalysisClassic(x, func= wilcox.test, mu=1, alternative = "less")

set.seed(1)
x <- rnorm(20, mean=0); y <- rnorm(20, mean=1)
# p-value obtained from a two-sample t-test
t.test(x,y,alternative="less")$p.value
# p-value obtained from an intra-experiment analysis
intraAnalysisClassic(x, y, func=t.test, alternative = "less")
# p-value obtained from a two-sample wilcoxon test
wilcox.test(x,y,alternative="less")$p.value
# p-value obtained from an intra-experiment analysis
intraAnalysisClassic(x, y, func= wilcox.test, alternative = "less")
```

intraAnalysisGene

Intra-experiment analysis of an expression dataset at the gene-level

Description
perform an intra-experiment analysis in conjunction with the moderated t-test (limma package) for the purpose of differential expression analysis of a gene expression dataset

Usage
```
intraAnalysisGene(data, group, splitSize = 5, metaMethod = addCLT)
```
Arguments

data a data frame where the rows are the gene IDs and the columns are the samples

group sample grouping. The elements of group are either 'c' (control) or 'd' (disease).

names(group) should be identical to colnames(data)

splitSize the minimum number of disease samples in each split dataset. splitSize should be at least 3. By default, splitSize=5

metaMethod the method used to combine p-values. This should be one of addCLT (additive method [1]), fishersMethod (Fisher’s method [5]), stoufferMethod (Stouffer’s method [6]), max (maxP method [7]), or min (minP method [8])

Details

This function performs an intra-experiment analysis [1] for individual genes of the given dataset. The function first splits the dataset into smaller datasets, performs a moderated t-test (limma package) for the genes of the split datasets, and then combines the p-values for individual genes using metaMethod

Value

A data frame (rownames are gene IDs) that consists of the following information:

- logFC: log foldchange (diseases versus controls)
- pLimma: p-value obtained from limma without splitting
- pLimma.fdr: FDR-corrected p-values of pLimma
- pIntra: p-value obtained from intra-experiment analysis
- pIntra.fdr: FDR-corrected p-values of pIntra

Author(s)

Tin Nguyen and Sorin Draghici

References


See Also

bilevelAnalysisGene, intraAnalysisClassic, link{bilevelAnalysisClassic}

Examples

data(GSE33223)
X <- intraAnalysisGene(data_GSE33223, group_GSE33223)
head(X)
Description

Load KEGG pathways and names

Usage

loadKEGGPathways(organism = "hsa", updateCache = FALSE)

Arguments

organism organism code. Default value is "hsa" (human)
updateCache re-download KEGG pathways. Default value is FALSE

Value

A list of the following components

- *kpg* a list of *graphNEL* objects encoding the pathway information.
- *kpn* a named vector of pathway tiles. The names of the vector are the pathway KEGG IDs.

Author(s)

Tin Nguyen and Sorin Draghici

See Also

keggPathwayGraphs, keggPathwayNames

Examples

x <- loadKEGGPathways()
pORACalc

Description
Calculate p-value for over-representation Analysis

Usage
pORACalc(geneSet, DEGenes, measuredGenes, minSize = 0)

Arguments
- geneSet: a vector of gene names belong to the geneset
- DEGenes: a vector of differential expressed genes
- measuredGenes: a vector of all genes in the analysis
- minSize: the minimum number of DE genes in the geneSet

Value
p-value

stoufferMethod

Stouffer's method for meta-analysis

Description
Combine independent studies using the sum of p-values transformed into standard normal variables

Usage
stoufferMethod(x)

Arguments
- x: is an array of independent p-values

Details
Considering a set of \( m \) independent significance tests, the resulted p-values are independent and uniformly distributed between 0 and 1 under the null hypothesis. Stouffer's method is similar to Fisher's method (fisherMethod), with the difference is that it uses the sum of p-values transformed into standard normal variables instead of the log product.
stoufferMethod

Value
combined p-value

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References

See Also
fisherMethod, addCLT

Examples
x <- rep(0, 10)
stoufferMethod(x)

x <- runif(10)
stoufferMethod(x)
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