

Package ‘AWFisher’

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Type Package

Title An R package for fast computing for adaptively weighted fisher's method

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biocViews StatisticalMethod, Software

VignetteBuilder knitr

Description Implementation of the adaptively weighted fisher's method, including fast p-value computing, variability index, and meta-pattern.

License GPL-3

Depends R (>= 3.6)

Imports edgeR, limma, stats

BugReports <https://github.com/Caleb-Huo/AWFisher/issues>

Suggests knitr, tightClust

RoxygenNote 6.1.1

NeedsCompilation no

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| | |
|-----------------|-----------------|
| AWFisher_pvalue | <i>AWFisher</i> |
|-----------------|-----------------|

Description

R package for fast computing for adaptively weighted fisher's method

Usage

```
AWFisher_pvalue(p.values)
```

Arguments

`p.values` Input G by K p-value matrix. Each row represent a gene and each column represent a study. Note that K has to be ≥ 2 and ≤ 100 .

Details

fast computing for adaptively weighted fisher's method

Value

A list consisting of AWFisher pvalues and AWweight.

`pvalues` AWFisher pvalues.

`weights` G by K binary weight matrix W. $W_{gk} = 1$ represents for gene g , study k contributes to the meta-analysis result. $W_{gk} = 0$ otherwise.

Author(s)

Zhiguang Huo

Examples

```
K <- 40
G <- 10000
p.values = matrix(rbeta(K*G, 1,1), ncol=K)
res = AWFisher_pvalue(p.values)
hist(res$pvalues, breaks=40)
table(rowSums(res$weights))
pvalues=res$pvalues[order(res$pvalues)]
plot(-log10((1:NROW(pvalues))/(1+NROW(pvalues))),
     -log10(pvalues),xlab='theoretical quantile', ylab='observed quantile')
lines(c(0,100), c(0,100), col=2)
```

biomarkerCategorization
biomarker categorization

Description

biomarker categorization

Usage

```
biomarkerCategorization(studies, afunction, B = 10, DEindex = NULL,
  fdr = NULL, silence = FALSE)
```

Arguments

| | |
|-----------|---|
| studies | a list of K studies. Each element (kth study) of the list is another list consisting gene expression matrix and label information. |
| afunction | A function for DE analysis. Options can be function_limma or function_edgeR. Default option is function_limma. However, use could define their own function. The input of afunction should be list(data, label) which is consistent with one element of the studies list/argument. The return of afunction should be list(pvalue=apvalue, effectSize=aeffectsize) |
| B | number of permutation should be used. B=1000 is suggested. |
| DEindex | If NULL, BH method will be applied to p-values and FDR 0.05 will be used. User could specify a logical vector as DEindex. |
| fdr | Default is 0.05. The co-membership matrix calculation will base on genes with this specified fdr. |
| silence | If TRUE, will print out the bootstrapping procedure. |

Details

biomarker categorization via bootstrap AW weight.

Value

A list consisting of biomarker categorization result.

| | |
|---------------|--|
| variability | Variability index for all genes |
| dissimilarity | Dissimilarity matrix of genes of DEindex==TRUE |
| DEindex | DEindex for Dissimilarity |

Author(s)

Zhiguang Huo

Examples

```

N0 = 10
G <- 1000
GDEp <- 50
GDEn <- 50
K = 4

studies <- NULL
set.seed(15213)
for(k in seq_len(K)){
  astudy <- matrix(rnorm(N0*2*G),nrow=G,ncol=N0*2)
  ControlLabel <- seq_len(N0)
  caseLabel <- (N0 + 1):(2*N0)

  astudy[1:GDEp,caseLabel] <- astudy[1:GDEp,caseLabel] + 2
  astudy[1:GDEp + GDEn,caseLabel] <- astudy[1:GDEp + GDEn,caseLabel] - 2

  alabel = c(rep(0,length(ControlLabel)),rep(1,length(caseLabel)))

  studies[[k]] <- list(data=astudy, label=alabel)
}

result <- biomarkerCategorization(studies,function_limma,B=100,DEindex=NULL)
sum(result$DEindex)
head(result$variability)
print(result$dissimilarity[1:4,1:4])

```

data_mouseMetabolism *Mouse metabolism microarray data*

Description

The purpose of the multi-tissue mouse metabolism transcriptomic data is to study how the gene expression changes with respect to the energy deficiency using mouse models. Very long-chain acyl-CoA dehydrogenase (VLCAD) deficiency was found to be associated with energy metabolism disorder in children. Two genotypes of the mouse model - wild type (VLCAD +/+) and VLCAD-deficient (VLCAD -/-) - were studied for three types of tissues (brown fat, liver, heart) with 3 to 4 mice in each genotype group. The sample size information is available in the table below. A total of 6,883 genes are available in this example dataset.

Usage

```
data_mouseMetabolism
```

Format

A list of data.frame with 6,883 genes (rows) and 3 - 4 mouse samples in each genotype group (columns).

brown data for the brown fat tissue

heart data for the heart tissue

liver data for the liver tissue

Source

https://projecteuclid.org/download/pdfview_1/euclid.aoas/1310562214

Examples

```
data(data_mouseMetabolism)
```

| | |
|----------------|---|
| function_edgeR | <i>use edgeR function to get pvalue</i> |
|----------------|---|

Description

use edgeR function to get pvalue

Usage

```
function_edgeR(astudy)
```

Arguments

astudy A list contains a data matrix and a vector of group label

Details

use edgeR function to get pvalue

Value

A list of pvalue and effect size

Author(s)

Zhiguang Huo

Examples

```
N0 = 10
G <- 1000
GDEp <- 50
GDEn <- 50

set.seed(15213)

astudy <- matrix(rpois(N0*2*G,10),nrow=G,ncol=N0*2)
ControlLabel <- 1:N0
caseLabel <- (N0 + 1):(2*N0)

astudy[1:GDEp,caseLabel] <- astudy[1:GDEp,caseLabel] + 2
astudy[1:GDEp + GDEn,caseLabel] <- astudy[1:GDEp,caseLabel] - 2

alabel <- c(rep(0,length(ControlLabel)),rep(1,length(caseLabel)))
Study <- list(data=astudy, label=alabel)
```

```
result <- function_edgeR(Study)
fdr <- p.adjust(result$pvalue)
sum(fdr<=0.05)
```

function_limma *use limma function to get pvalue*

Description

use limma function to get pvalue

Usage

```
function_limma(astudy)
```

Arguments

astudy A list contains a data matrix and a vector of group label

Details

use limma function to get pvalue

Value

A list of pvalue and effect size

Author(s)

Zhiguang Huo

Examples

```
N0 = 10
G <- 1000
GDEp <- 50
GDEn <- 50

set.seed(15213)

astudy <- matrix(rnorm(N0*2*G),nrow=G,ncol=N0*2)
ControlLabel <- 1:N0
caseLabel <- (N0 + 1):(2*N0)

astudy[1:GDEp,caseLabel] <- astudy[1:GDEp,caseLabel] + 2
astudy[1:GDEp + GDEn,caseLabel] <- astudy[1:GDEp,caseLabel] - 2

alabel <- c(rep(0,length(ControlLabel)),rep(1,length(caseLabel)))
Study <- list(data=astudy, label=alabel)

result <- function_limma(Study)
fdr <- p.adjust(result$pvalue)
sum(fdr<=0.05)
```

| | |
|------------------|--------------------------|
| variabilityIndex | <i>Variability Index</i> |
|------------------|--------------------------|

Description

Variability Index

Usage

```
variabilityIndex(studies, afunction, B = 10, silence = FALSE)
```

Arguments

| | |
|-----------|---|
| studies | a list of K studies. Each element (kth study) of the list is another list consisting gene expression matrix and label information. |
| afunction | A function for DE analysis. Options can be function_limma or function_edgeR. Default option is function_limma. However, use could define their own function. The input of afunction should be list(data, label) which is consistent with one element of the studies list/argument. The return of afunction should be list(pvalue=apvalue, effectSize=aeffectsize) |
| B | number of permutation should be used. B=1000 is suggested. |
| silence | If TRUE, will print out the bootstrapping procedure. |

Details

Variability Index via bootstrap AW weight.

Value

A list consisting of biomarker categorization result.

| | |
|-------------|--------------------------------|
| variability | Varibility index for all genes |
|-------------|--------------------------------|

Author(s)

Zhiguang Huo

Examples

```
N0 = 10
G <- 1000
GDEp <- 50
GDEn <- 50
K = 4

studies <- NULL
set.seed(15213)
for(k in 1:K){
  astudy <- matrix(rnorm(N0*2*G), nrow=G, ncol=N0*2)
  ControlLabel <- 1:N0
  caseLabel <- (N0 + 1):(2*N0)
```

```
astudy[1:GDEp,caseLabel] <- astudy[1:GDEp,caseLabel] + 2
astudy[1:GDEp + GDEn,caseLabel] <- astudy[1:GDEp + GDEn,caseLabel] - 2

alabel = c(rep(0,length(ControlLabel)),rep(1,length(caseLabel)))

studies[[k]] <- list(data=astudy, label=alabel)
}

result <- variabilityIndex(studies,function_limma,B=100)
head(result)
```

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