

# Package ‘AWFisher’

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**Type** Package

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

**Version** 1.19.0

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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

**git\_url** <https://git.bioconductor.org/packages/AWFisher>

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AWFisher\_pvalue

*AWFisher*

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**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  $\geq 2$  and  $\leq 100$ .

**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)
```

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biomarkerCategorization  
*biomarker categorization*

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## 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])

```

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data\_mouseMetabolism *Mouse metabolism microarray data*

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**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](https://projecteuclid.org/download/pdfview_1/euclid.aoas/1310562214)

**Examples**

```
data(data_mouseMetabolism)
```

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function_edgeR	<i>use edgeR function to get pvalue</i>
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**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)
```

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function\_limma            *use limma function to get pvalue*

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### 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)
```

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variabilityIndex	<i>Variability Index</i>
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**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
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**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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