# Package ‘MHTmult’

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**Type** Package

**Title** Multiple Hypotheses Testing for Multiple Families/Groups Structure

**Version** 0.1.0

**Author** Yalin Zhu, Wenge Guo

**Maintainer** Yalin Zhu <yalin.zhu@outlook.com>

**BugReports** https://github.com/allenzhuaz/MHTmult/issues

**Description** A Comprehensive tool for almost all existing multiple testing methods for multiple families. The package summarizes the existing methods for multiple families multiple testing procedures (MTPs) such as double FDR, group Benjamini-Hochberg (GBH) procedure and average FDR controlling procedure. The package also provides some novel multiple testing procedures using selective inference idea.

**License** GPL (>= 2)

**Encoding** UTF-8

**LazyData** TRUE

**Suggests** structSSI, MHTdiscrete, FixSeqMTP

**NeedsCompilation** yes

**Repository** CRAN

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## Contents

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`avgFDR.p.adjust` *Adjusted P-Values for Benjamini & Bogomolov (2014) BH-q BH-Rq/m Procedure*

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### Description

Given a list/data frame of grouped p-values, selecting thresholds and p-value combining method, retruns adjusted p-values to make decisions

### Usage

```
avgFDR.p.adjust(pval, t, make.decision)
```

### Arguments

| | |
|---|---|
| `pval` | the structural p-values, the type should be "`list`". |
| `t` | the thresholds determining whether the families are selected or not, also affects conditional p-value within families. |
| `make.decision` | logical; if `TRUE`, then the output include the decision rules compared adjusted p-values with significant level $\alpha$. |

### Value

A list of the adjusted conditional p-values, a list of `NULL` means the family is not selected to do the test in the second stage.

### Author(s)

Yalin Zhu

### References

Benjamini, Y., & Bogomolov, M. (2014). Selective inference on multiple families of hypotheses. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, **76**: 297-318.

### Examples

```
# data is from Example 4.1 in Mehrotra and Adewale (2012)
pval <- list(c(0.031,0.023,0.029,0.005,0.031,0.000,0.874,0.399,0.293,0.077),
             c(0.216,0.843,0.864),
             c(1,0.878,0.766,0.598,0.011,0.864),
             c(0.889,0.557,0.767,0.009,0.644),
             c(1,0.583,0.147,0.789,0.217,1,0.02,0.784,0.579,0.439),
             c(0.898,0.619,0.193,0.806,0.611,0.526,0.702,0.196))
avgFDR.p.adjust(pval = pval, t=0.1)
sum(unlist(avgFDR.p.adjust(pval = pval,t=0.1)) <= 0.1)
```

`cFDR.cp.adjust` *Adjusted Conditional P-values for Two-stage cFDR Controlling Procedures*

## Description

Given a list/data frame of grouped p-values, selecting thresholds and p-value combining method, retruns adjusted conditional p-values to make decisions

## Usage

```
cFDR.cp.adjust(pval, t, comb.method = c("Fisher", "Stouffer", "minP"),
make.decision, sig.level)
```

## Arguments

| | |
|---|---|
| `pval` | the structural p-values, the type should be `"list"`. |
| `t` | the thresholds determining whether the families are selected or not, also affects conditional p-value within families. |
| `comb.method` | p-value combining methods including `"Fisher"`, `"Stouffer"`, and `"minP"` combining methods. |
| `make.decision` | logical; if `TRUE`, then the output include the decision rules compared adjusted p-values with significant level $\alpha$. |
| `sig.level` | significant level used to compare with adjusted p-values to make decisions, the default value is 0.05. |

## Value

A list of the adjusted conditional p-values, a list of `NULL` means the family is not selected to do the test in the second stage.

## Author(s)

Yalin Zhu

## References

Heller, R., Chatterjee, N., Krieger, A., & Shi, J. (2016). Post-selection Inference Following Aggregate Level Hypothesis Testing in Large Scale Genomic Data. *bioRxiv*, 058404.

## Examples

```
# data is from Example 4.1 in Mehrotra and Adewale (2012)
pval <- list(c(0.031,0.023,0.029,0.005,0.031,0.000,0.874,0.399,0.293,0.077),
             c(0.216,0.843,0.864),
             c(1,0.878,0.766,0.598,0.011,0.864),
             c(0.889,0.557,0.767,0.009,0.644),
```

```
             c(1,0.583,0.147,0.789,0.217,1,0.02,0.784,0.579,0.439),
             c(0.898,0.619,0.193,0.806,0.611,0.526,0.702,0.196))
sum(p.adjust(unlist(pval), method = "BH")<=0.1)
DFDR.p.adjust(pval = pval,t=0.1)
DFDR2.p.adjust(pval = pval,t=0.1)
sum(unlist(DFDR.p.adjust(pval = pval,t=0.1))<=0.1)
sum(unlist(DFDR2.p.adjust(pval = pval,t=0.1))<=0.1)

t=select.thres(pval,select.method = "BH", comb.method = "minP", alpha = 0.1)
cFDR.cp.adjust(pval, t=t, comb.method="minP")

t1=select.thres(pval, select.method = "bonferroni", comb.method = "minP", alpha = 0.1, k=3)
cFDR.cp.adjust(pval, t=t1, comb.method="minP")

t2=select.thres(pval, select.method = "sidak", comb.method = "minP", alpha = 0.1, k=3)
cFDR.cp.adjust(pval, t=t2, comb.method="minP")
```

---

`DFDR.p.adjust` *Adjusted P-Values for the Double FDR Procedure*

---

## Description

Given a list/data frame of grouped p-values, retruns adjusted p-values to make decisions

## Usage

```
DFDR.p.adjust(pval, t, make.decision, alpha)
```

## Arguments

| | |
|---|---|
| `pval` | the structural p-values, the type should be `"list"`. |
| `t` | the threshold selecting significant families. |
| `make.decision` | logical; if `TRUE`, then the output include the decision rules compared adjusted p-values with significant level $\alpha$. |
| `alpha` | significant level used to compare with adjusted p-values to make decisions, the default value is 0.05. |

## Value

A list of the adjusted p-values, a list of `NULL` means the family is not selected to do the test in the second stage.

## Author(s)

Yalin Zhu

### References

Mehrotra, D. V., & Heyse, J. F. (2004). Use of the false discovery rate for evaluating clinical safety data. *Statistical methods in medical research*, **13**: 227-238.

### See Also

DFDR2.p.adjust, p.adjust.

### Examples

```
# data is from Example 4.1 in Mehrotra and Adewale (2012)
pval <- list(c(0.031,0.023,0.029,0.005,0.031,0.000,0.874,0.399,0.293,0.077),
             c(0.216,0.843,0.864),
             c(1,0.878,0.766,0.598,0.011,0.864),
             c(0.889,0.557,0.767,0.009,0.644),
             c(1,0.583,0.147,0.789,0.217,1,0.02,0.784,0.579,0.439),
             c(0.898,0.619,0.193,0.806,0.611,0.526,0.702,0.196))
DFDR.p.adjust(pval = pval,t=0.1)
sum(unlist(DFDR.p.adjust(pval = pval,t=0.1))<=0.1)
```

---

## DFDR2.p.adjust — *Adjusted P-Values for the Modified Double FDR Procedure*

---

### Description

Given a list/data frame of grouped p-values, retruns adjusted p-values to make decisions

### Usage

```
DFDR2.p.adjust(pval, t, make.decision)
```

### Arguments

| | |
|---|---|
| pval | the structural p-values, the type should be "list". |
| t | the threshold selecting significant families and testing hypotheses. |
| make.decision | logical; if TRUE, then the output include the decision rules compared adjusted p-values with significant level $\alpha$. |

### Value

A list of the adjusted p-values, a list of NULL means the family is not selected to do the test in the second stage.

### Author(s)

Yalin Zhu

### References

Mehrotra, D. V., & Adewale, A. J. (2012). Flagging clinical adverse experiences: reducing false discoveries without materially compromising power for detecting true signals. *Statistics in medicine*, **31**: 1918-1930.

### See Also

DFDR.p.adjust, p.adjust.

### Examples

```
# data is from Example 4.1 in Mehrotra and Adewale (2012)
pval <- list(c(0.031,0.023,0.029,0.005,0.031,0.000,0.874,0.399,0.293,0.077),
             c(0.216,0.843,0.864),
             c(1,0.878,0.766,0.598,0.011,0.864),
             c(0.889,0.557,0.767,0.009,0.644),
             c(1,0.583,0.147,0.789,0.217,1,0.02,0.784,0.579,0.439),
             c(0.898,0.619,0.193,0.806,0.611,0.526,0.702,0.196))
DFDR2.p.adjust(pval = pval,t=0.1)
sum(unlist(DFDR2.p.adjust(pval = pval,t=0.1))<=0.1)
```

---

## GBH.p.adjust — *Adjusted P-values for the Group BH Procedure*

---

### Description

Given a list/data frame of grouped p-values, selecting thresholds and p-value combining method, retruns adjusted conditional p-values to make decisions

### Usage

```
GBH.p.adjust(pval, t, make.decision)
```

### Arguments

| | |
|---|---|
| pval | the structural p-values, the type should be "list". |
| t | the thresholds determining whether the families are selected or not, also affects conditional p-value within families. |
| make.decision | logical; if TRUE, then the output include the decision rules compared adjusted p-values with significant level $\alpha$ |

### Value

A list of the adjusted conditional p-values, a list of NULL means the family is not selected to do the test in the second stage.

## Author(s)

Yalin Zhu

## References

Hu, J. X., Zhao, H., & Zhou, H. H. (2010). False discovery rate control with groups. *Journal of the American Statistical Association*, **105**: 1215-1227.

## Examples

```
# data is from Example 4.1 in Mehrotra and Adewale (2012)
pval <- list(c(0.031,0.023,0.029,0.005,0.031,0.000,0.874,0.399,0.293,0.077),
             c(0.216,0.843,0.864),
             c(1,0.878,0.766,0.598,0.011,0.864),
             c(0.889,0.557,0.767,0.009,0.644),
             c(1,0.583,0.147,0.789,0.217,1,0.02,0.784,0.579,0.439),
             c(0.898,0.619,0.193,0.806,0.611,0.526,0.702,0.196))
sum(p.adjust(unlist(pval), method = "BH")<=0.1)
DFDR.p.adjust(pval = pval,t=0.1)
DFDR2.p.adjust(pval = pval,t=0.1)
sum(unlist(DFDR.p.adjust(pval = pval,t=0.1))<=0.1)
sum(unlist(DFDR2.p.adjust(pval = pval,t=0.1))<=0.1)

GBH.p.adjust(pval = pval,t=0.1)
sum(unlist(GBH.p.adjust(pval = pval,t=0.1))<=0.1)

t=select.thres(pval,select.method = "BH", comb.method = "minP", alpha = 0.1)
cFDR.cp.adjust(pval, t=t, comb.method="minP")

t1=select.thres(pval, select.method = "bonferroni", comb.method = "minP", alpha = 0.1, k=3)
cFDR.cp.adjust(pval, t=t1, comb.method="minP")

t2=select.thres(pval, select.method = "sidak", comb.method = "minP", alpha = 0.1, k=3)
cFDR.cp.adjust(pval, t=t2, comb.method="minP")
```

---

# gbonf.cv — *Critical Value for the generalized Bonferroni Procedure Controlling k-FWER*

---

## Description

The function for computing the critical value based on number of hypotheses $m$, fold $k$ and significant level $\alpha$.

## Usage

```
gbonf.cv(m, k, alpha)
```

### Arguments

| | |
|---|---|
| `m` | number of hypotheses to be tested. |
| `k` | number of allowed type 1 errors in k-FWER controls. |
| `alpha` | significant level used to compare with adjusted p-values to make decisions, the default value is 0.05. |

### Value

A numeric vector of the adjusted p-values (of the same length as `p`) if `make.decision = FALSE`, or a list including original p-values, adjusted p-values and decision rules if `make.decision = TRUE`.

### Author(s)

Yalin Zhu

### See Also

`gbonf.p.adjust`, `p.adjust`, `Sidak.p.adjust`.

### Examples

```
p <- c(0.031,0.023,0.029,0.005,0.031,0.000,0.874,0.399,0.293,0.077)
gbonf.cv(m=length(p), k=2)
```

---

## `gbonf.p.adjust` *Adjusted P-Values for the Generalized Bonferroni Procedure Controlling k-FWER*

---

### Description

The function for computing the adjusted p-values based on original p-values and fold $k$.

### Usage

```
gbonf.p.adjust(p, k, alpha, make.decision)
```

### Arguments

| | |
|---|---|
| `p` | numeric vector of p-values (possibly with `NA`s). Any other R is coerced by `as.numeric`. Same as in `p.adjust`. |
| `k` | number of allowed type 1 errors in k-FWER controls. |
| `alpha` | significant level used to compare with adjusted p-values to make decisions, the default value is 0.05. |
| `make.decision` | logical; if `TRUE`, then the output include the decision rules compared adjusted p-values with significant level $\alpha$ |

## Value

A numeric vector of the adjusted p-values (of the same length as `p`) if `make.decision = FALSE`, or a list including original p-values, adjusted p-values and decision rules if `make.decision = TRUE`.

## Author(s)

Yalin Zhu

## References

Lehmann, E. L., & Romano, J. P. (2005). Generalizations of the familywise error rate. *The Annals of Statistics*, **33**: 1138-1154.

## See Also

`gsidak.p.adjust`, `p.adjust`, `Sidak.p.adjust`.

## Examples

```
p <- c(0.031,0.023,0.029,0.005,0.031,0.000,0.874,0.399,0.293,0.077)
gbonf.p.adjust(p, k=2)
```

---

# gsidak.cv — *Critical Value for the generalized Sidak Procedure Controlling k-FWER*

---

## Description

The function for computing the critical value based on number of hypotheses $m$, fold $k$ and significant level $\alpha$.

## Usage

```
gsidak.cv(m, k, alpha)
```

## Arguments

| | |
|---|---|
| `m` | number of hypotheses to be tested. |
| `k` | number of allowed type 1 errors in k-FWER controls. |
| `alpha` | significant level used to compare with adjusted p-values to make decisions, the default value is 0.05. |

## Value

A numeric vector of the adjusted p-values (of the same length as `p`) if `make.decision = FALSE`, or a list including original p-values, adjusted p-values and decision rules if `make.decision = TRUE`.

### Author(s)

Yalin Zhu

### See Also

`gsidak.p.adjust`, `p.adjust`, `Sidak.p.adjust`.

### Examples

```
p <- c(0.031,0.023,0.029,0.005,0.031,0.000,0.874,0.399,0.293,0.077)
gsidak.cv(m=length(p), k=2)
```

---

## `gsidak.p.adjust` *Adjusted P-Values for the Generalized Sidak Procedure Controlling k-FWER*

---

### Description

The function for computing the adjusted p-values based on original p-values and fold $k$.

### Usage

```
gsidak.p.adjust(p, k, alpha, make.decision)
```

### Arguments

| | |
|---|---|
| `p` | numeric vector of p-values (possibly with `NA`s). Any other R is coerced by `as.numeric`. Same as in `p.adjust`. |
| `k` | number of allowed type 1 errors in k-FWER controls. |
| `alpha` | significant level used to compare with adjusted p-values to make decisions, the default value is 0.05. |
| `make.decision` | logical; if `TRUE`, then the output include the decision rules compared adjusted p-values with significant level $\alpha$ |

### Value

A numeric vector of the adjusted p-values (of the same length as `p`) if `make.decision = FALSE`, or a list including original p-values, adjusted p-values and decision rules if `make.decision = TRUE`.

### Author(s)

Yalin Zhu

### References

Guo, W., & Romano, J. (2007). A generalized Sidak-Holm procedure and control of generalized error rates under independence. *Statistical Applications in Genetics and Molecular Biology*, **6**(1).

## See Also

gbonf.p.adjust, p.adjust, Sidak.p.adjust.

## Examples

```
p <- c(0.031,0.023,0.029,0.005,0.031,0.000,0.874,0.399,0.293,0.077)
gsidak.p.adjust(p, k=2)
```

---

select.thres *Selecting Threshold for cFDR Controlling Procedures*

---

## Description

Given the structural p-values, choose a selecting method for controlling generalized familywise error rate or false discovery rate across families, and a combining mehtod, returns a vector of thresholds for the first stage of cFDR controlling procedures.

## Usage

```
select.thres(pval, select.method, comb.method, alpha, k)
```

## Arguments

| | |
|---|---|
| pval | the structural p-values, the type should be "list". |
| select.method | global p-value selecting methods. For generalized FWER controlling, k-Bonferroni or k-Sidak procedures can be used; for FDR controlling, BH procedure can be used. |
| comb.method | p-value combining methods including "Fisher", "Stouffer", and "minP" combining methods. |
| alpha | significant level for selecting significant families in the first stage. The default value is 0.05. |
| k | number of allowed type 1 errors in k-FWER controls. |

## Value

A list of the adjusted conditional p-values, a list of NULL means the family is not selected to do the test in the second stage.

## Author(s)

Yalin Zhu

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