Package ‘MHTdiscrete’

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Description A comprehensive tool for almost all existing multiple testing methods for discrete data. The package also provides some novel multiple testing procedures controlling FWER/FDR for discrete data. Given discrete p-values and their domains, the [method].p.adjust function returns adjusted p-values, which can be used to compare with the nominal significant level alpha and make decisions. For users' convenience, the functions also provide the output option for printing decision rules.
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getPval

Calculating p-values for discrete data

Description

The function for calculating the original available p-values and all attainable p-values for the corresponding hypothesis.

Usage

getPval(raw.data, test.type, alternative)

Arguments

raw.data original data set with count number for treatment group and study group. The data set type could be matrix or data.frame.
test.type there are two discrete test available now, must be one of "FET" for Fisher's Exact Test and "BET" for Binomial Exact Test.alternative indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less".

Value

A numeric vector of the adjusted p-values (of the same length as p).

Author(s)

Yalin Zhu

References


Examples

```r
## Using Fisher's Exact Test to get the available and attainable p-values
# import raw data set as data.frame type
df <- data.frame(X1=c(4, 2, 2, 13, 6, 8, 4, 0, 1), N1 = rep(148, 9),
                 X2 = c(0, 0, 1, 3, 2, 1, 2, 2, 2), N2 = rep(132, 9))
# obtain the available p-values and attainable p-values using two-sided Fisher's Exact Test
getPval(raw.data=df, test.type = "FET", alternative = "two.sided")
# store the available p-values
p <- getPval(raw.data=df, test.type = "FET", alternative = "two.sided")[[1]]; p
# store the attainable p-values
p.set <- getPval(raw.data=df, test.type = "FET", alternative = "two.sided")[[2]]; p.set
```

**GTBH.p.adjust**

The adjusted p-values for Gilbert-Tarone-BH step-up FDR controlling procedure.

Description

The function for calculating the adjusted p-values based on original available p-values and all attainable p-values.

Usage

`GTBH.p.adjust(p, p.set, 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`.
- `p.set`: a list of numeric vectors, where each vector is the vector of all attainable p-values containing the available p-value for the corresponding hypothesis.
- `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).

Author(s)

Yalin Zhu
References


See Also

`GTBY.p.adjust`, `MBH.p.adjust`, `MBY.p.adjust`

Examples

```r
p <- c(pbinom(1,8,0.5),pbinom(1,5,0.75),pbinom(1,6,0.6))
p.set <- list(pbinom(0:8,8,0.5),pbinom(0:5,5,0.75),pbinom(0:6,6,0.6))
GTBH.p.adjust(p,p.set)
```

**GTBY.p.adjust**

The adjusted p-values for Gilbert-Tarone-BY step-up FDR controlling procedure.

Description

The function for calculating the adjusted p-values based on original available p-values and all attainable p-values.

Usage

`GTBY.p.adjust(p, p.set, alpha, make.decision)`

Arguments

- `p` numeric vector of p-values (possibly with NAs). Any other R is coerced by `as.numeric`. Same as in `p.adjust`.
- `p.set` a list of numeric vectors, where each vector is the vector of all attainable p-values containing the available p-value for the corresponding hypothesis.
- `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`).
**MBH.p.adjust**

Author(s)
Yalin Zhu

References


See Also
`GTBH.p.adjust`, `MBH.p.adjust`, `MBY.p.adjust`

Examples
```r
p <- c(pbinom(1:8,0.5),pbinom(1:5,0.75),pbinom(1:6,0.6))
p.set <- list(pbinom(0:8,0.5),pbinom(0:5,0.75),pbinom(0:6,0.6))
GTBY.p.adjust(p,p.set)
```

---

**MBH.p.adjust**

*The adjusted p-values for Modified Benjamini-Hochberg (BH) step-up FDR controlling procedure.*

Description
The function for calculating the adjusted p-values based on original available p-values and all attainable p-values.

Usage
`MBH.p.adjust(p, p.set, 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`.
- **p.set**: a list of numeric vectors, where each vector is the vector of all attainable p-values containing the available p-value for the corresponding hypothesis.
- **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).

Author(s)

Yalin Zhu

References


See Also

MBY.p.adjust, MBL.p.adjust

Examples

```r
p <- c(pbinom(1,8,0.5),pbinom(1,5,0.75),pbinom(1,6,0.6))
p.set <-list(pbinom(0:8,8,0.5),pbinom(0:5,5,0.75),pbinom(0:6,6,0.6))
MBL.p.adjust(p,p.set)
```

---

**MBL.p.adjust**

The adjusted p-values for Modified Benjamini-Liu (BL) step-down FDR controlling procedure.

Description

The function for calculating the adjusted p-values based on original available p-values and all attainable p-values.

Usage

```r
MBL.p.adjust(p, p.set, alpha, make.decision)
```

Arguments

- `p` numeric vector of p-values (possibly with NAs). Any other R is coerced by `as.numeric`. Same as in `p.adjust`.
- `p.set` a list of numeric vectors, where each vector is the vector of all attainable p-values containing the available p-value for the corresponding hypothesis.
- `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 α.
Value

A numeric vector of the adjusted p-values (of the same length as `p`).

Note

The MBL procedure for discrete data controls FDR under the specific dependence assumption where the joint distribution of statistics from true nulls are independent of the joint distribution of statistics from false nulls.

Author(s)

Yalin Zhu

References


See Also

`MBH.p.adjust`, `MBY.p.adjust`

Examples

```r
p <- c(pbinom(1,8,0.5),pbinom(1,5,0.75),pbinom(1,6,0.6))
p.set <- list(pbinom(0:8,0.5),pbinom(0:5,5,0.75),pbinom(0:6,6,0.6))
MBL.p.adjust(p,p.set)
```

---

The adjusted p-values for Modified Bonferroni single-step FWER controlling procedure.

Description

The function for calculating the adjusted p-values based on original available p-values and all attainable p-values.

Usage

```r
MBonf.p.adjust(p, p.set, alpha, make.decision)
```
Arguments

- **p**: numeric vector of p-values (possibly with NAs). Any other R is coerced by `as.numeric`. Same as in `p.adjust`.
- **p.set**: a list of numeric vectors, where each vector is the vector of all attainable p-values containing the available p-value for the corresponding hypothesis.
- **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`.

Note

The attainable p-value refers to the element of domain set of p-value for the corresponding hypothesis. For continuous test statistics, the p-value under true null are uniform distributed in (0,1), thus the p-values are attainable everywhere between 0 and 1. But for discrete test statistics, the p-value can only take finite values between 0 and 1, that is the attainable p-values for discrete case are finite and countable, so we can assign them in a finite list `p.set`.

Author(s)

Yalin Zhu

References


See Also


Examples

```r
p <- c(pbinom(1,8,0.5),pbinom(1,5,0.75),pbinom(1,6,0.6))
p.set <- list(pbinom(0:8,8,0.5),pbinom(0:5,5,0.75),pbinom(0:6,6,0.6))
MBonf.p.adjust(p,p.set)
## Compare with the traditional Bonferroni adjustment
p.adjust(p,method = "bonferroni")
## Compare with the Tarone adjustment
Tarone.p.adjust(p,p.set)
```
The adjusted p-values for Modified Benjamini-Yekutieli (BY) step-up FDR controlling procedure.

Description

The function for calculating the adjusted p-values based on original available p-values and all attainable p-values.

Usage

MBY.p.adjust(p, p.set, alpha, make.decision)

Arguments

p numeric vector of p-values (possibly with NAs). Any other R is coerced by as.numeric. Same as in p.adjust.

p.set a list of numeric vectors, where each vector is the vector of all attainable p-values containing the available p-value for the corresponding hypothesis.

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).

Author(s)

Yalin Zhu

References


See Also

MBH.p.adjust, MBL.p.adjust

Examples

p <- c(pbinom(1,8,0.5),pbinom(1,5,0.75),pbinom(1,6,0.6))
p.set <- list(pbinom(0:8,8,0.5),pbinom(0:5,5,0.75),pbinom(0:6,6,0.6))
MBY.p.adjust(p,p.set)
The adjusted p-values for Modified Hochberg step-up FWER controlling procedure.

Description

The function for calculating the adjusted p-values based on original available p-values and all attainable p-values.

Usage

MHoch.p.adjust(p, p.set, alpha, make.decision)

Arguments

- `p` numeric vector of p-values (possibly with NAs). Any other R is coerced by `as.numeric`. Same as in `p.adjust`.
- `p.set` a list of numeric vectors, where each vector is the vector of all attainable p-values containing the available p-value for the corresponding hypothesis.
- `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`).

Author(s)

Yalin Zhu

References


See Also

Roth.p.adjust, p.adjust.
Examples

```r
p <- c(pbinom(1,8,0.5),pbinom(1,5,0.75),pbinom(1,6,0.6))
p.set <- list(pbinom(0:8,8,0.5),pbinom(0:5,5,0.75),pbinom(0:6,6,0.6))
Mholm.p.adjust(p,p.set)
## Compare with the traditional Hochberg adjustment
p.adjust(p,method = "hochberg")
## Compare with the Roth adjustment
Roth.p.adjust(p,p.set)
```

**Description**

The function for calculating the adjusted p-values based on original available p-values and all attainable p-values.

**Usage**

```r
Mholm.p.adjust(p, p.set, alpha, make.decision)
```

**Arguments**

- `p` numeric vector of p-values (possibly with NAs). Any other R is coerced by `as.numeric`. Same as in `p.adjust`.
- `p.set` a list of numeric vectors, where each vector is the vector of all attainable p-values containing the available p-value for the corresponding hypothesis.
- `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).

**Author(s)**

Yalin Zhu

**References**


See Also

`TH.p.adjust`, `p.adjust`.

Examples

```r
p <- c(pbinom(1,8,0.5), pbinom(1,5,0.75), pbinom(1,6,0.6))
p.set <- list(pbinom(0:8,8,0.5), pbinom(0:5,5,0.75), pbinom(0:6,6,0.6))
MHolm.p.adjust(p, p.set)
## Compare with the traditional Holm adjustment
p.adjust(p, method = "holm")
## Compare with the Tarone-Holm adjustment
TH.p.adjust(p, p.set)
```

Description

The MHTdiscrete package provides two categories of important functions for discrete data multiple hypothesis testing:

FWER controlling procedures


FDR controlling procedures

Step-down: `MBL.p.adjust`.

Author(s)

Yalin Zhu

References


MixBonf.p.adjust

The adjusted p-values for Mixed Bonferroni single-step FWER controlling procedure.

**Description**

The function for calculating the adjusted p-values based on original available p-values and the attainable p-values for the discrete test statistics.

**Usage**

MixBonf.p.adjust(pc, pd, pd.set, alpha, make.decision)

**Arguments**

- `pc`: numeric vector of the available p-values (possibly with NAs) for the continuous test statistics. Any other R is coerced by as.numeric. Same as in p.adjust.
- `pd`: numeric vector of the available p-values (possibly with NAs) for the discrete test statistics. Any other R is coerced by as.numeric. Same as in p.adjust.
- `pd.set`: a list of numeric vectors, where each vector is the vector of all attainable p-values containing the available p-value for the corresponding hypothesis for discrete data.
- `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.
Note

The arguments include three parts, the available p-values need to be reorganized in advance. Gather all available p-values for continuous data as \( pc \), and all available p-values for discrete data as \( pd \). The attainable p-value refers to the element of domain set of p-value for the corresponding hypothesis for discrete test statistics, the p-value can only take finite values between 0 and 1, that is, the attainable p-values for discrete case are finite and countable, so we can assign them in a finite list \( pd.set \). The function returns the adjusted p-values with the first part for continuous data of the same length as \( pc \), and second part for discrete data of the same length as \( pd \).

Author(s)

Yalin Zhu

References


See Also


Examples

```r
pd <- c(pbinom(1,8,0.5),pbinom(1,5,0.75)); pc <- c(0.04, 0.1)
pd.set <- list(pbinom(0:8,8,0.5),pbinom(0:5,5,0.75))
MixBonf.p.adjust(pc,pd,pd.set)
## Compare with the traditional Bonferroni adjustment
p.adjust(c(pc,pd),method = "bonferroni")
```

Roth.p.adjust

*The adjusted p-values for Roth’s step-up FWER controlling procedure.*

Description

The function for calculating the adjusted p-values based on original available p-values and all attainable p-values.

Usage

```
Roth.p.adjust(p, p.set, digits, alpha, make.decision)
```
Roth.rej

Arguments

p numeric vector of p-values (possibly with NAs). Any other R is coerced by \texttt{as.numeric}. Same as in \texttt{p.adjust}.

p.set a list of numeric vectors, where each vector is the vector of all attainable p-values containing the available p-value for the corresponding hypothesis.

digits minimal number of significant digits for the adjusted p-values, the default value is 4, see \texttt{print.default}.

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 \texttt{p}).

Author(s)

Yalin Zhu

References


See Also

\texttt{M Hoch.p.adjust,p.adjust}.

Examples

\begin{verbatim}
 p <- c(pbinom(1,8,0.5),pbinom(1,5,0.75),pbinom(1,6,0.6))
 p.set <-list(pbinom(0:8,8,0.5),pbinom(0:5,5,0.75),pbinom(0:6,6,0.6))
 Roth.p.adjust(p,p.set,digits=5)
\end{verbatim}

\begin{verbatim}
 Roth.rej The number of rejected hypotheses for Roth’s step-up FWER controlling procedure.
\end{verbatim}

Description

The function for calculating the number of rejected hypotheses (rejection region) based on original available p-values, all attainable p-values and the given significant level.

Usage

\begin{verbatim}
 Roth.rej(p,p.set,alpha)
\end{verbatim}
Arguments

- **p**: numeric vector of p-values (possibly with NAs). Any other R is coerced by `as.numeric`. Same as in `p.adjust`.
- **p.set**: a list of numeric vectors, where each vector is the vector of all attainable p-values containing the available p-value for the corresponding hypothesis.
- **alpha**: the given significant level for Roth’s procedure, the default value is 0.05.

Value

An integer value of the number of rejected hypotheses.

Author(s)

Yalin Zhu

References


Examples

```r
p <- c(pbinom(1,8,0.5),pbinom(1,5,0.75),pbinom(1,6,0.6))
p.set <-list(pbinom(0:8,8,0.5),pbinom(0:5,5,0.75),pbinom(0:6,6,0.6))
Roth.rej(p,p.set,0.05)
```

**Sidak.p.adjust**

The adjusted p-values for Sidak single-step FWER controlling procedure.

Description

The function for calculating the adjusted p-values based on original available p-values.

Usage

`Sidak.p.adjust(p, alpha, make.decision)`

Arguments

- **p**: numeric vector of p-values (possibly with NAs). Any other R is coerced by `as.numeric`. Same as in `p.adjust`.
- **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 α.
**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**

`p.adjust`.

**Examples**

```r
p <- c(pbinom(1,8,0.5),pbinom(1,5,0.75),pbinom(1,6,0.6))
Sidak.p.adjust(p)
```

---

**Description**

The function for calculating the adjusted p-values based on original available p-values and all attainable p-values.

**Usage**

`Tarone.p.adjust(p, p.set, alpha, make.decision)`

**Arguments**

- `p` numeric vector of p-values (possibly with NAs). Any other R is coerced by `as.numeric`. Same as in `p.adjust`.
- `p.set` a list of numeric vectors, where each vector is the vector of all attainable p-values containing the available p-value for the corresponding hypothesis.
- `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

See Also
*MBonf.p.adjust, MixBonf.p.adjust, p.adjust*.

Examples
```r
p <- c(pbinom(1,8,0.5),pbinom(1,5,0.75),pbinom(1,6,0.6))
p.set <-list(pbinom(0:8,8,0.5),pbinom(0:5,5,0.75),pbinom(0:6,6,0.6))
Tarone.p.adjust(p,p.set)
```

---

**TH.p.adjust**

*The adjusted p-values for Tarone-Holm step-down FWER controlling procedure.*

Description
The function for calculating the adjusted p-values based on original available p-values and all attainable p-values.

Usage
```
TH.p.adjust(p, p.set, alpha, make.decision)
```

Arguments
- **p**: numeric vector of p-values (possibly with NAs). Any other R is coerced by `as.numeric`. Same as in `p.adjust`.
- **p.set**: a list of numeric vectors, where each vector is the vector of all attainable p-values containing the available p-value for the corresponding hypothesis.
- **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).

Author(s)
Yalin Zhu
References


See Also

*MHoml.p.adjust, p.adjust.*

Examples

```r
p <- c(pbinom(1,8,0.5),pbinom(1,5,0.75),pbinom(1,6,0.6))
p.set <-list(pbinom(0:8,8,0.5),pbinom(0:5,5,0.75),pbinom(0:6,6,0.6))
TH.p.adjust(p,p.set)
```
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