Package 'FixSeqMTP'

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Type Package

Title Fixed Sequence Multiple Testing Procedures

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Author Yalin Zhu, Wenge Guo

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

BugReports https://github.com/allenzhuaz/FixSeqMTP/issues

Description Several generalized / directional Fixed Sequence Multiple Testing Procedures (FSMTPs) are developed for testing a sequence of pre-ordered hypotheses while controlling the FWER, FDR and Directional Error (mdFWER). All three FWER controlling generalized FSMTPs are designed under arbitrary dependence, which allow any number of acceptances. Two FDR controlling generalized FSMTPs are respectively designed under arbitrary dependence and independence, which allow more but a given number of acceptances. Two mdFWER controlling directional FSMTPs are respectively designed under arbitrary dependence and independence, which can also make directional decisions based on the signs of the test statistics. The main functions for each proposed generalized / directional FSMTPs are designed to calculate adjusted p-values and critical values, respectively. For users' convenience, the functions also provide the output option for printing decision rules.

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Encoding UTF-8

LazyData TRUE

R topics documented:

`bisection.FDR` *Bisection algorithm (FDR)*

Description

Bisection algorithm to find the solution for the adjusted p-value for FDR controlling g-FSMTPs.

Usage

```
bisection.FDR(f, a=0, b=1, p, k, j, n = 1000, tol)
```

Arguments

`f`	the objective function to be optimized for the solution.
`a`	mininum of the interval which contains the solution from bisection algorithm.
`b`	maxinum of the interval which contains the solution from bisection algorithm.
`p`	numeric vector of p-values (possibly with `NA`s). Any other R is coerced by `as.numeric`. Same as in `p.adjust`.
`k`	pre-specified number of acceptances allowed in the testing procedure (cannot exceed the length of `p`)
`j`	the index of the hypothesis.
`n`	the number of sections that the interval which from bisection algorithm.
`tol`	the desired accuracy.

Value

a solution of the objective function which is between the interval from `a` to `b`.

Author(s)

Yalin Zhu

See Also

`bisection.FWER`

bisection.FWER *Bisection algorithm (FWER)*

Description

Bisection algorithm to find the solution for the adjusted p-value for FWER controlling g-FSMTPs.

Usage

```
bisection.FWER(f, a=0, b=1, p, beta, j, n = 1000, tol)
```

Arguments

f	the objective function to be optimized for the solution.
a	mininum of the interval which contains the solution from bisection algorithm.
b	maxinum of the interval which contains the solution from bisection algorithm.
p	numeric vector of p-values (possibly with NAs). Any other R is coerced by as.numeric. Same as in p.adjust.
beta	pre-specified constant satisfying $0 \leq \beta < 1$, only for method="accept".
j	index of the hypothesis.
n	number of sections that the interval which from bisection algorithm.
tol	desired accuracy.

Value

a solution of the objective function which is between the interval from a to b.

Author(s)

Yalin Zhu

See Also

bisection.FDR

FixSeqMTP *FixSeqMTP : Tools for Fixed Sequence Multiple Testing Procedures*

Description

The FixSeqMTP package provides three categories of functions for generalized/directional fixed sequence mutliple testing procedures:

FWER controlling procedures

FSFWER.arbidept.p.adjust and FSFWER.arbidept.cv

FDR controlling procedures

FSFDR.arbidept.p.adjust and FSFDR.arbidept.cv

FSFDR.indept.p.adjust and FSFDR.indept.cv

mdFWER controlling procedures

FSmdFWER.arbidept.p.adjust and FSmdFWER.arbidept.cv

FSmdFWER.indept.p.adjust and FSmdFWER.indept.cv

Author(s)

Yalin Zhu, Wenge Guo

References

Qiu, Z., Guo, W., & Lynch, G. (2015). On generalized fixed sequence procedures for controlling the FWER. *Statistics in medicine*, 34(30), 3968-3983.

Lynch, G., Guo, W., Sarkar, S. K., & Finner, H. (2016). The Control of the False Discovery Rate in Fixed Sequence Multiple Testing. *arXiv preprint* arXiv:1611.03146.

Grandhi, A., Guo, W., & Romano, J. P. (2016). Control of Directional Errors in Fixed Sequence Multiple Testing. *arXiv preprint* arXiv:1602.02345.

FSFDR.arbidept.cv *Critical Values for Fixed Sequence FDR Controlling Procedure under Arbitrary Dependence*

Description

Given a set of pre-ordered p-values and accuracy for the result, return the corresponding critical values using the generalized fixed sequence FDR controlling procedure under arbitrary dependence (See Theorem 3.1 and 4.1 in Lynch et al. (2016)). The function also provides an option to make decisions given a pre-specified significant level α.

Usage

```
FSFDR.arbidept.cv(p, k=1, alpha = 0.05, make.decision = TRUE)
```

Arguments

p	numeric vector of p-values (possibly with NAs). Any other R is coerced by as.numeric. Same as in p.adjust.
k	pre-specified number of acceptances allowed in the testing procedure (cannot exceed the length of p)
alpha	significant level used to calculate the critical values to make decisions, the default value is 0.05.
make.decision	logical; if TRUE (default), then the output include the decision rules compared adjusted p-values with significant level $alpha$

Value

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

Author(s)

Yalin Zhu

References

Lynch, G., Guo, W., Sarkar, S. K., & Finner, H. (2016). The Control of the False Discovery Rate in Fixed Sequence Multiple Testing. *arXiv preprint* arXiv:1611.03146.

See Also

`FSFWER.arbidept.cv` for fixed sequence FWER controlling procedures.

Examples

```
## generate a pre-ordered pvalue vector for 50 hypotheses, where 80% are true nulls
set.seed(1234); m <- 50; pi0 <- 0.8; m0 <- m*pi0; m1 <- m-m0
mu <- c(4*0.9^(1:m1), rep(0,m0))
Zstat <- rnorm(n = m, mean = mu)
Pval <- 1-pnorm(Zstat)
## conventional fixed sequence procedure
FSFDR.arbidept.cv(p = Pval, alpha = 0.05)
## generalized fixed sequence procedure allowing stop at 5th acceptance
FSFDR.arbidept.cv(p = Pval, alpha = 0.05, k=5)
```

`FSFDR.arbidept.p.adjust`

Adjusted P-values for Fixed Sequence FDR Controlling Procedure under Arbitrary Dependence

---

Description

Given a set of pre-ordered p-values and accuracy for the result, returns adjusted p-values using the generalized fixed sequence multiple testing procedures under arbitrary dependence (See Theorem 3.1 and 4.1 in Lynch et al. (2016)). The function also provides an option to make decisions given a pre-specified significant level α.

Usage

```
FSFDR.arbidept.p.adjust(p, alpha=0.05, k=1, tol = 1e-6, make.decision = TRUE)
```

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.

k	pre-specified number of acceptances allowed in the testing procedure (cannot exceed the length of p)
tol	desired accuracy. The default value is 1e-6 .
make.decision	logical; if TRUE (default), then the output include the decision rules compared adjusted p-values with significant level $alpha$

Details

The generalized fixed sequence FDR controlling procedure stops on the k-th acceptances and automatically accepts the rest of hypotheses, where k is a pre-specified positive integer. When $k = 1$, the generalized procedure becomes conventional one (Theorem 3.1 in Lynch et al. (2016)), which stops testing once one acceptance appears. This method strongly controls FDR under arbitrary dependence.

Value

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

Author(s)

Yalin Zhu

References

Lynch, G., Guo, W., Sarkar, S. K., & Finner, H. (2016). The Control of the False Discovery Rate in Fixed Sequence Multiple Testing. *arXiv preprint* arXiv:1611.03146.

See Also

FSFWER.arbidept.p.adjust for fixed sequence FWER controlling procedures.

Examples

```
## generate a pre-ordered pvalue vector for 50 hypotheses, where 80% are true nulls
set.seed(1234); m <- 50; pi0 <- 0.8; m0 <- m*pi0; m1 <- m-m0
mu <- c(4*0.9^(1:m1), rep(0,m0))
Zstat <- rnorm(n = m, mean = mu)
Pval <- 1-pnorm(Zstat)
## conventional fixed sequence procedure
FSFDR.arbidept.p.adjust(p = Pval, alpha = 0.05)
## generalized fixed sequence procedure allowing stop at 5th acceptance
FSFDR.arbidept.p.adjust(p = Pval, alpha = 0.05, k=5)
```

FSFDR.indept.cv *Critical Values for Fixed Sequence FDR Controlling Procedure under Independence*

Description

Given a set of pre-ordered p-values and accuracy for the result, return the corresponding critical values using the generalized fixed sequence FDR controlling procedure under independence for true nulls (See Theorem 3.2 and 4.2 in Lynch et al. (2016)). The function also provides an option to make decisions given a pre-specified significant level α.

Usage

```
FSFDR.indept.cv(p, k=1, alpha = 0.05, tol = 1e-6, make.decision = TRUE)
```

Arguments

p	numeric vector of p-values (possibly with NAs). Any other R is coerced by as.numeric. Same as in p.adjust.
k	pre-specified number of acceptances allowed in the testing procedure (cannot exceed the length of p)
alpha	significant level used to calculate the critical values to make decisions, the default value is 0.05.
tol	desired accuracy. The default value is 1e-6 .
make.decision	logical; if TRUE (default), then the output include the decision rules compared adjusted p-values with significant level $alpha$

Value

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

Author(s)

Yalin Zhu

References

Lynch, G., Guo, W., Sarkar, S. K., & Finner, H. (2016). The Control of the False Discovery Rate in Fixed Sequence Multiple Testing. *arXiv preprint* arXiv:1611.03146.

See Also

FSFWER.arbidept.cv for fixed sequence FWER controlling procedures.

Examples

```
## generate a pre-ordered pvalue vector for 50 hypotheses, where 80% are true nulls
set.seed(1234); m <- 50; pi0 <- 0.8; m0 <- m*pi0; m1 <- m-m0
mu <- c(4*0.9^(1:m1), rep(0,m0))
Zstat <- rnorm(n = m, mean = mu)
Pval <- 1-pnorm(Zstat)
## conventional fixed sequence procedure
FSFDR.indept.cv(p = Pval, alpha = 0.05)
## generalized fixed sequence procedure allowing stop at 5th acceptance
FSFDR.indept.cv(p = Pval, alpha = 0.05, k=5)
```

`FSFDR.indept.p.adjust` *Adjusted P-values for Fixed Sequence FDR Controlling Procedure under Independence*

Description

Given a set of pre-ordered p-values and accuracy for the result, returns adjusted p-values using the generalized fixed sequence multiple testing procedures under independence for true nulls (See Theorem 3.2 and 4.2 in Lynch et al. (2016)). The function also provides an option to make decisions given a pre-specified significant level α.

Usage

```
FSFDR.indept.p.adjust(p, alpha=0.05, k=1, tol = 1e-6, make.decision = TRUE)
```

Arguments

`p`	numeric vector of p-values (possibly with `NA`s). 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.
`k`	pre-specified number of acceptances allowed in the testing procedure (cannot exceed the length of `p`)
`tol`	desired accuracy. The default value is `1e-6` .
`make.decision`	logical; if `TRUE` (default), then the output include the decision rules compared adjusted p-values with significant level $alpha$

Details

The generalized fixed sequence FDR controlling procedure stops on the k-th acceptances and automatically accepts the rest of hypotheses, where k is a pre-specified positive integer. When $k = 1$, the generalized procedure becomes conventional one (Theorem 3.2 in Lynch et al. (2016)), which stops testing once one acceptance appears. This method strongly controls FDR if the true null p-values are mutually independent and are independent of the false null p-values. When k=1, the conventional procedure strongly controls FDR if the p-values are negatively associated on the true null p-values.

Value

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

Author(s)

Yalin Zhu

References

Lynch, G., Guo, W., Sarkar, S. K., & Finner, H. (2016). The Control of the False Discovery Rate in Fixed Sequence Multiple Testing. *arXiv preprint* arXiv:1611.03146.

See Also

`FSFWER.arbidept.p.adjust` for fixed sequence FWER controlling procedures.

Examples

```
## generate a pre-ordered pvalue vector for 50 hypotheses, where 80% are true nulls
set.seed(1234); m <- 50; pi0 <- 0.8; m0 <- m*pi0; m1 <- m-m0
mu <- c(4*0.9^(1:m1), rep(0,m0))
Zstat <- rnorm(n = m, mean = mu)
Pval <- 1-pnorm(Zstat)
## conventional fixed sequence procedure
FSFDR.indept.p.adjust(p = Pval, alpha = 0.05)
## generalized fixed sequence procedure allowing stop at 5th acceptance
FSFDR.indept.p.adjust(p = Pval, alpha = 0.05, k=5)
```

`FSFWER.arbidept.cv` *Critical Values for Fixed Sequence FWER Controlling Procedures under Arbitrary Dependence*

Description

Given a set of pre-ordered p-values and accuracy for the result, return the corresponding critical values using one of three generalized fixed sequence FWER controlling procedures. The function also provides an option to make decisions given a pre-specified significant level α.

Usage

```
FSFWER.arbidept.cv(p, alpha=0.05, beta=0.5, tol = 1e-6,
  method = c("reject","accept","both"), make.decision = TRUE)
```

Arguments

`p`	numeric vector of p-values (possibly with `NA`s). Any other R is coerced by `as.numeric`. Same as in `p.adjust`.
`alpha`	significant level used to calculate the critical values to make decisions, the default value is 0.05.
`beta`	pre-specified constant satisfying $0 \leq \beta < 1$, only for `method="accept"`. The default value is `0.5`.
`tol`	desired accuracy. The default value is `1e-6` .
`method`	critical value calculation method. See details.
`make.decision`	logical; if `TRUE` (default), then the output include the decision rules compared adjusted p-values with significant level $alpha$

Details

The critical value calculation methods for Fixed Sequence multiple testing include Procedure A1 only using numbers of rejections ("reject"), Procedure A2 only using numbers of acceptances ("accept") and Procedure A3 using both numbers of rejections and numbers of acceptances ("both"). The three methods strongly control FWER under arbitrary dependence. The constant `beta` needs to be specified for the Procedure A2 (`"accept"`), while one can ignore this argument when using other methods.

Value

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

Author(s)

Yalin Zhu

References

Qiu, Z., Guo, W., & Lynch, G. (2015). On generalized fixed sequence procedures for controlling the FWER. *Statistics in medicine*, 34(30), 3968-3983.

See Also

`FSFDR.arbidept.cv` and `FSFDR.indept.cv` for fixed sequence FDR controlling procedures.

Examples

```
  ## Clinical trial example in Qiu et al. (2015)
Pval <- c(0.0008, 0.0135, 0.0197, 0.7237, 0.0003, 0.2779, 0.0054, 0.8473)
FSFWER.arbidept.cv(p=Pval, alpha=0.05, method = "reject")
FSFWER.arbidept.cv(p=Pval, alpha=0.05, beta=0.1, method = "accept")
FSFWER.arbidept.cv(p=Pval, alpha=0.05, beta=0.5, method = "accept")
FSFWER.arbidept.cv(p=Pval, alpha=0.05, beta=0.9, method = "accept")
FSFWER.arbidept.cv(p=Pval, alpha=0.05, method = "both")
```

FSFWER.arbidept.p.adjust

Adjusted P-values for Fixed Sequence FWER Controlling Procedures under Arbitrary Dependence

---

Description

Given a set of pre-ordered p-values and accuracy for the result, returns adjusted p-values using one of three generalized fixed sequence FWER controlling procedures. The function also provides an option to make decisions given a pre-specified significant level α.

Usage

```
FSFWER.arbidept.p.adjust(p, alpha=0.05, beta=0.5, tol = 1e-6,
  method = c("reject","accept","both"), make.decision = TRUE)
```

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.
beta	pre-specified constant satisfying $0 \leq \beta < 1$, only for method="accept". The default value is 0.5.
tol	desired accuracy. The default value is 1e-6 .
method	adjustment method. See details.
make.decision	logical; if TRUE (default), then the output include the decision rules compared adjusted p-values with significant level $alpha$

Details

The adjustment methods for Fixed Sequence multiple testing include Procedure A1 only using numbers of rejections ("reject"), Procedure A2 only using numbers of acceptances ("accept") and Procedure A3 using both numbers of rejections and numbers of acceptances ("both"). The three methods strongly control FWER under arbitrary dependence. The constant beta needs to be specified for the Procedure A2 ("accept"), while one can ignore this argument when using other methods.

Value

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

Author(s)

Yalin Zhu

References

Qiu, Z., Guo, W., & Lynch, G. (2015). On generalized fixed sequence procedures for controlling the FWER. *Statistics in medicine*, 34(30), 3968-3983.

See Also

FSFDR.arbidept.p.adjust and FSFDR.arbidept.p.adjust for fixed sequence FDR controlling procedures.

Examples

```
  ## Clinical trial example in Qiu et al. (2015)
Pval <- c(0.0008, 0.0135, 0.0197, 0.7237, 0.0003, 0.2779, 0.0054, 0.8473)
FSFWER.arbidept.p.adjust(p=Pval, alpha=0.05, method = "reject")
FSFWER.arbidept.p.adjust(p=Pval, alpha=0.05, beta=0.1, method = "accept")
FSFWER.arbidept.p.adjust(p=Pval, alpha=0.05, beta=0.5, method = "accept")
FSFWER.arbidept.p.adjust(p=Pval, alpha=0.05, beta=0.9, method = "accept")
FSFWER.arbidept.p.adjust(p=Pval, alpha=0.05, method = "both")
```

FSmdFWER.arbidept.cv *Critical values for Fixed Sequence mdFWER Controlling Procedure under Arbitrary Dependence Along with Directional Decisions Regarding Parameters of Interest*

Description

Given a set of pre-ordered test statistics and the corresponding p-values, returns critical values using the directional fixed sequence multiple testing procedures under arbitrary dependence (See Procedure 1 and Theorem 1 in Grandhi et al. (2016)). The function also provides an option to make decisions and determine the sign given a pre-specified significant level α and the test statistics.

Usage

```
FSmdFWER.arbidept.cv(p, test.stat, alpha=0.05, make.decision = TRUE)
```

Arguments

p	numeric vector of p-values (possibly with NAs). Any other R is coerced by as.numeric. Same as in p.adjust.
test.stat	numeric vector of test statistics, which are used to determine the direction of decisions, with the same length of p.
alpha	significant level used to compare with Critical values to make decisions, the default value is 0.05.
make.decision	logical; if TRUE (default), then the output include the decision rules compared original p-values with the critical values, and directions of the decision based on the sign of test statistics.

Value

A numeric vector of the critical values (of the same length as p) if make.decision = FALSEALSE, or a data frame including original p-values, critical values, test statistics and directional decision rules if make.decision = TRUE.

Author(s)

Yalin Zhu

References

Grandhi, A., Guo, W., & Romano, J. P. (2016). Control of Directional Errors in Fixed Sequence Multiple Testing. *arXiv preprint* arXiv:1602.02345.

See Also

FSmdFWER.indept.cv for fixed sequence mdFWER controlling procedures under independence.

Examples

```
## Clinical trial example in Grandhi et al. (2016)
Pval <- c(0.0008, 0.0135, 0.0197, 0.7237, 0.0003, 0.2779, 0.0054, 0.8473)
Zstat <- c(3.4434, 2.5085, 2.3642, -0.3543, 3.7651, 1.0900, 2.8340, 0.1930)
FSmdFWER.arbidept.cv(p = Pval, test.stat = Zstat, make.decision = TRUE)
```

`FSmdFWER.arbidept.p.adjust`

Adjusted P-values for Fixed Sequence mdFWER Controlling Procedure under Arbitrary Dependence Along with Directional Decisions Regarding Parameters of Interest

---

Description

Given a set of pre-ordered test statistics and the corresponding p-values, returns adjusted p-values using the directional fixed sequence multiple testing procedures under arbitrary dependence (See Procedure 1 and Theorem 1 in Grandhi et al. (2016)). The function also provides an option to make decisions and determine the sign given a pre-specified significant level α and the test statistics.

Usage

```
FSmdFWER.arbidept.p.adjust(p, test.stat, alpha=0.05, make.decision = TRUE)
```

Arguments

`p`	numeric vector of p-values (possibly with `NA`s). Any other R is coerced by `as.numeric`. Same as in `p.adjust`.
`test.stat`	numeric vector of test statistics, which are used to determine the direction of decisions, with the same length of `p`.
`alpha`	significant level used to compare with adjusted p-values to make decisions, the default value is 0.05.
`make.decision`	logical; if `TRUE` (default), then the output include the decision rules compared adjusted p-values with significant level $alpha$, and directions of the decision based on the sign of test statistics.

Value

A numeric vector of the adjusted p-values (of the same length as `p`) if `make.decision = FALSEALSE`, or a data frame including original p-values, adjusted p-values, test statistics and directional decision rules if `make.decision = TRUE`.

Author(s)

Yalin Zhu

References

Grandhi, A., Guo, W., & Romano, J. P. (2016). Control of Directional Errors in Fixed Sequence Multiple Testing. *arXiv preprint* arXiv:1602.02345.

See Also

FSmdFWER.indept.p.adjust for fixed sequence mdFWER controlling procedures under independence.

Examples

```
## Clinical trial example in Grandhi et al. (2016)
Pval <- c(0.0008, 0.0135, 0.0197, 0.7237, 0.0003, 0.2779, 0.0054, 0.8473)
Zstat <- c(3.4434, 2.5085, 2.3642, -0.3543, 3.7651, 1.0900, 2.8340, 0.1930)
FSmdFWER.arbidept.p.adjust(p = Pval, test.stat = Zstat, make.decision = TRUE)
```

FSmdFWER.indept.cv *Critical values for Fixed Sequence mdFWER Controlling Procedure under Independence Along with Directional Decisions Regarding Parameters of Interest*

Description

Given a set of pre-ordered test statistics and the corresponding p-values, returns critical values using the directional fixed sequence multiple testing procedures under independence (See Procedure 2 and Theorem 2 in Grandhi et al. (2016)). The function also provides an option to make decisions and determine the sign given a pre-specified significant level α and the test statistics.

Usage

```
FSmdFWER.indept.cv(p, test.stat, alpha=0.05, make.decision = TRUE)
```

Arguments

p	numeric vector of p-values (possibly with NAs). Any other R is coerced by as.numeric. Same as in p.adjust.
test.stat	numeric vector of test statistics, which are used to determine the direction of decisions, with the same length of p.
alpha	significant level used to compare with Critical values to make decisions, the default value is 0.05.
make.decision	logical; if TRUE (default), then the output include the decision rules compared original p-values with the critical values, and directions of the decision based on the sign of test statistics.

Value

A numeric vector of the critical values (of the same length as p) if make.decision = FALSEALSE, or a data frame including original p-values, critical values, test statistics and directional decision rules if make.decision = TRUE.

Author(s)

Yalin Zhu

References

Grandhi, A., Guo, W., & Romano, J. P. (2016). Control of Directional Errors in Fixed Sequence Multiple Testing. *arXiv preprint* arXiv:1602.02345.

See Also

FSmdFWER.arbidept.cv for fixed sequence mdFWER controlling procedures under arbitrary dependence.

Examples

```
## Clinical trial example in Grandhi et al. (2016)
Pval <- c(0.0008, 0.0135, 0.0197, 0.7237, 0.0003, 0.2779, 0.0054, 0.8473)
Zstat <- c(3.4434, 2.5085, 2.3642, -0.3543, 3.7651, 1.0900, 2.8340, 0.1930)
FSmdFWER.indept.cv(p = Pval, test.stat = Zstat, make.decision = TRUE)
```

FSmdFWER.indept.p.adjust

Adjusted P-values for Fixed Sequence mdFWER Controlling Procedure under Independence Along with Directional Decisions Regarding Parameters of Interest

---

Description

Given a set of pre-ordered test statistics and the corresponding p-values, returns adjusted p-values using the directional fixed sequence multiple testing procedures under independence (See Procedure 2 and Theorem 2 in Grandhi et al. (2016)). The function also provides an option to make decisions and determine the sign given a pre-specified significant level α and the test statistics.

Usage

```
FSmdFWER.indept.p.adjust(p, test.stat, alpha=0.05, make.decision = TRUE)
```

Arguments

p	numeric vector of p-values (possibly with NAs). Any other R is coerced by as.numeric. Same as in p.adjust.
test.stat	numeric vector of test statistics, which are used to determine the direction of decisions, with the same length of p.
alpha	significant level used to compare with adjusted p-values to make decisions, the default value is 0.05.
make.decision	logical; if TRUE (default), then the output include the decision rules compared adjusted p-values with significant level $alpha$, and directions of the decision based on the sign of test statistics.

Value

A numeric vector of the adjusted p-values (of the same length as p) if make.decision = FALSEALSE, or a data frame including original p-values, adjusted p-values, test statistics and directional decision rules if make.decision = TRUE.

Author(s)

Yalin Zhu

References

Grandhi, A., Guo, W., & Romano, J. P. (2016). Control of Directional Errors in Fixed Sequence Multiple Testing. *arXiv preprint* arXiv:1602.02345.

See Also

`FSmdFWER.indept.p.adjust` for fixed sequence mdFWER controlling procedures under independence.

Examples

```
## Clinical trial example in Grandhi et al. (2015)
Pval <- c(0.0008, 0.0135, 0.0197, 0.7237, 0.0003, 0.2779, 0.0054, 0.8473)
Zstat <- c(3.4434, 2.5085, 2.3642, -0.3543, 3.7651, 1.0900, 2.8340, 0.1930)
FSmdFWER.indept.p.adjust(p = Pval, test.stat = Zstat, make.decision = TRUE)
```

---

optim.accept.adjp *Objective function to be optimized (2)*

Description

Objective function to be optimized for the adjusted p-values for FWER controlling g-FSMTP based on the numbers of acceptances only. (See Procedure A2 in Qiu et al. (2015))

Usage

```
optim.accept.adjp(alpha, p, beta)
```

Arguments

`alpha`	the parameter we need to solve for the adjusted p-values.
`p`	numeric vector of p-values (possibly with `NA`s). Any other R is coerced by `as.numeric`. Same as in `p.adjust`.
`beta`	pre-specified constant satisfying $0 \leq \beta < 1$, only for `method="accept"`.

Value

difference between adjusted p-value and significant level alpha.

Author(s)

Yalin Zhu

References

Qiu, Z., Guo, W., & Lynch, G. (2015). On generalized fixed sequence procedures for controlling the FWER. *Statistics in medicine*, 34(30), 3968-3983.

optim.arbidept.adjp *Objective function to be optimized (4)*

Description

Objective function to be optimized for the adjusted p-values for FDR controlling g-FSMTP under arbitrary dependence. (See Theorem 3.1 and Theorem 4.1 in Lynch et al. (2016))

Usage

```
optim.arbidept.adjp(alpha, p, k)
```

Arguments

alpha	the parameter we need to solve for the adjusted p-values.
p	numeric vector of p-values (possibly with NAs). Any other R is coerced by as.numeric. Same as in p.adjust.
k	pre-specified number of acceptances allowed in the testing procedure (cannot exceed the length of p)

Value

difference between adjusted p-value and significant level alpha.

Author(s)

Yalin Zhu

References

Lynch, G., Guo, W., Sarkar, S. K., & Finner, H. (2016). The Control of the False Discovery Rate in Fixed Sequence Multiple Testing. *arXiv preprint* arXiv:1611.03146.

optim.both.adjp *Objective function to be optimized (3)*

Description

Objective function to be optimized for the adjusted p-values for FWER controlling g-FSMTP based on the numbers of both rejections and acceptances. (See Procedure A3 in Qiu et al. (2015))

Usage

```
optim.both.adjp(alpha, p, beta)
```

Arguments

alpha	the parameter we need to solve for the adjusted p-values.
p	numeric vector of p-values (possibly with NAs). Any other R is coerced by as.numeric. Same as in p.adjust.
beta	pre-specified constant satisfying $0 \leq \beta < 1$, only for method="accept".

Value

difference between adjusted p-value and significant level alpha.

Author(s)

Yalin Zhu

References

Qiu, Z., Guo, W., & Lynch, G. (2015). On generalized fixed sequence procedures for controlling the FWER. *Statistics in medicine*, 34(30), 3968-3983.

`optim.indept.adjp` *Objective function to be optimized (5)*

Description

Objective function to be optimized for the adjusted p-values for FDR controlling g-FSMTP under independence. (See Theorem 3.2 and Theorem 4.2 in Lynch et al. (2016))

Usage

```
optim.indept.adjp(alpha, p, k)
```

Arguments

`alpha`	the parameter we need to solve for the adjusted p-values.
`p`	numeric vector of p-values (possibly with `NA`s). Any other R is coerced by `as.numeric`. Same as in `p.adjust`.
`k`	pre-specified number of acceptances allowed in the testing procedure (cannot exceed the length of `p`)

Value

difference between adjusted p-value and significant level alpha.

Author(s)

Yalin Zhu

References

Lynch, G., Guo, W., Sarkar, S. K., & Finner, H. (2016). The Control of the False Discovery Rate in Fixed Sequence Multiple Testing. *arXiv preprint* arXiv:1611.03146.

`optim.reject.adjp` *Objective function to be optimized (1)*

Description

Objective function to be optimized for the adjusted p-values for FWER controlling g-FSMTP based on the numbers of rejections only. (See Procedure A1 in Qiu et al. (2015))

Usage

```
optim.reject.adjp(alpha, p, beta)
```

Arguments

`alpha`	the parameter we need to solve for the adjusted p-values.
`p`	numeric vector of p-values (possibly with `NA`s). Any other R is coerced by `as.numeric`. Same as in `p.adjust`.
`beta`	pre-specified constant satisfying $0 \leq \beta < 1$, only for `method="accept"`.

Value

difference between adjusted p-value and significant level alpha.

Author(s)

Yalin Zhu

References

Qiu, Z., Guo, W., & Lynch, G. (2015). On generalized fixed sequence procedures for controlling the FWER. *Statistics in medicine*, 34(30), 3968-3983.

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