Package ‘FixSeqMTP’

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Type Package

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

Description The FixSeqMTP package is designed to test a sequence of pre-ordered hypotheses using several generalized Fixed Sequence Multiple Testing Procedures (g-FSMTPs). The proposed three FWER controlling g-FSMTPs utilize numbers of rejections and acceptances, all of the procedures are designed under arbitrary dependence. The proposed two FDR controlling g-FSMTPs allows more but a given number of acceptances (>=1), the procedures are designed for arbitrary dependence and independence. The main functions for each proposed g-FSMTPs are designed to calculate adjusted p-values and critical values, respectively. For users' convenience, the output results also include the option of decision rules for convenience.

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Encoding UTF-8

LazyData true

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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 which to be optimized for the solution.

`a` mininum of the interval which cantains the solution from bisection algorithm.

`b` maxinum of the interval which cantains 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 between the interwal 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 which to be optimized for the solution.
`a`	mininum of the interval which cantains the solution from bisection algorithm.
`b`	maxinum of the interval which cantains 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`.
`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 between the interwal 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 two categories of functions for generalized fixed sequence multiple hypothese testing:

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`

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.

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.

`FSFDR.arbidept.cv` *Critical Values for Fixed Sequence FDR Controlling Procedures*

Description

Given a set of pre-ordered p-values and accuracy for the result, returns critical values using one of several generalized fixed sequence multiple testing procedures. 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 `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`)
`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 100 hypotheses, where 60% are true nulls
set.seed(1234); n <- 50; pi0 <- 0.6
mu <- sample(c(0,3), n, replace = TRUE, prob = c(pi0,1-pi0))
Zstat <- rnorm(n = n, 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 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 several generalized fixed sequence multiple testing procedures. 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 `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 procedures designed to control FDR should be stop on the k-th acceptances and automatically accept 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 control 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 100 hypotheses, where 60% are true nulls
set.seed(1234); n <- 50; pi0 <- 0.6
mu <- sample(c(0,3), n, replace = TRUE, prob = c(pi0,1-pi0))
Zstat <- rnorm(n = n, 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 Procedures*

Description

Given a set of pre-ordered p-values and accuracy for the result, returns critical values using one of several generalized fixed sequence multiple testing procedures. 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 `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`)

`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 100 hypotheses, where 60% are true nulls
set.seed(1234); n <- 50; pi0 <- 0.6
mu <- sample(c(0,3), n, replace = TRUE, prob = c(pi0,1-pi0))
Zstat <- rnorm(n = n, 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 Procedures under Independence*

Description

Given a set of pre-ordered p-values and accuracy for the result, returns adjusted p-values using one of several generalized fixed sequence multiple testing procedures. 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 procedures designed to control FDR should be stop on the k-th acceptances and automatically accept 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 control FDR if the true null p-valuesare 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 thetrue 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 100 hypotheses, where 60% are true nulls
set.seed(1234); n <- 50; pi0 <- 0.6
mu <- sample(c(0,3), n, replace = TRUE, prob = c(pi0,1-pi0))
Zstat <- rnorm(n = n, 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*

Description

Given a set of pre-ordered p-values and accuracy for the result, returns critical values using one of several generalized fixed sequence multiple testing 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 NAs). 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 the 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 need to be specified only for the Procedure A2 ("accept"), 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

Description

Given a set of pre-ordered p-values and accuracy for the result, returns adjusted p-values using one of several generalized fixed sequence multiple testing 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 the 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 need to be specified only for the Procedure A2 ("accept"), 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")
```

`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 `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.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 `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.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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