

# Package ‘FixSeqMTP’

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**Type** Package

**Title** Fixed Sequence Multiple Testing Procedures

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**BugReports** <https://github.com/allenzhuaz/FixSeqMTP/issues>

**Description** Several generalized Fixed Sequence Multiple Testing Procedures (g-FSMTPs) are developed for testing a sequence of pre-ordered hypotheses while controlling the FWER and FDR. All three FWER controlling g-FSMTPs are designed under arbitrary dependence, which allow any number of acceptances, and two FDR controlling g-FSMTPs are respectively designed under arbitrary dependence and independence, which allow more but a given number of acceptances. 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.

**License** GPL (>= 2)

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bisection.FDR	<i>Bisection algorithm (FDR)</i>
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### 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	minimum of the interval which contains the solution from bisection algorithm.
b	maximum 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 <a href="#">as.numeric</a> . Same as in <a href="#">p.adjust</a> .
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](#)

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bisection.FWER	<i>Bisection algorithm (FWER)</i>
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**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	minimum of the interval which contains the solution from bisection algorithm.
b	maximum of the interval which contains the solution from bisection algorithm.
p	numeric vector of p-values (possibly with <i>NA</i> s). Any other R is coerced by <a href="#">as.numeric</a> . Same as in <a href="#">p.adjust</a> .
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](#)

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FixSeqMTP

*FixSeqMTP : Tools for Fixed Sequence Multiple Testing Procedures*

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### Description

The FixSeqMTP package provides two categories of functions for generalized fixed sequence multiple 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](#)

### 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*.

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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  $\alpha$ .

### 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 <code>as.numeric</code> . Same as in <code>p.adjust</code> .
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 <i>alpha</i>

**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  $\alpha$ .

### 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 <a href="#">as.numeric</a> . Same as in <a href="#">p.adjust</a> .
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 <i>alpha</i>

### 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  $\alpha$ .

## 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 <a href="#">as.numeric</a> . Same as in <a href="#">p.adjust</a> .
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 <i>alpha</i>

**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**

[FSFDR.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  $\alpha$ .

**Usage**

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



**Arguments**

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

**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  $\alpha$ .

### 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 <a href="#">as.numeric</a> . Same as in <a href="#">p.adjust</a> .
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 <i>alpha</i>

### 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  $\alpha$ .

## 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 <a href="#">as.numeric</a> . Same as in <a href="#">p.adjust</a> .
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 <i>alpha</i>

**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")
```

---

optim.accept.adj

*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.adj(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 <a href="#">as.numeric</a> . Same as in <a href="#">p.adjust</a> .
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.adj    *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.adj(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 <a href="#">as.numeric</a> . Same as in <a href="#">p.adjust</a> .
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.

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optim.both.adj	<i>Objective function to be optimized (3)</i>
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---

**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.adj(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 <a href="#">as.numeric</a> . Same as in <a href="#">p.adjust</a> .
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.adj      *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.adj(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 <a href="#">as.numeric</a> . Same as in <a href="#">p.adjust</a> .
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.adj      *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.adj(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 <a href="#">as.numeric</a> . Same as in <a href="#">p.adjust</a> .
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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